

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:34:54 ; Search time 75 Seconds
(without alignments)
920.318 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 518
Sequence: 1 MGALARALLPLLAQWLLRA.....RRRDPEVNVDESSLVRHRWK 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 segs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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 - 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
 - 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	100.0	518	19 AAW61362	Aspartic proteinas
2	518	100.0	518	20 AAY41714	Human PRO852 prote
3	518	100.0	518	20 AAY22239	Human CSP56, aspar
4	518	100.0	518	20 AAY13799	Human aspartyl pro
5	518	100.0	518	21 AAB44270	Human PRO852 (UNQ4
6	518	100.0	518	21 AAY88424	Human aspartyl pro
7	518	100.0	518	22 AAE10628	Human aspartyl pro
8	518	100.0	518	22 AAE10656	Human Asp 1 protei
9	518	100.0	518	22 AAU29059	Human PRO polypept
10	518	100.0	518	22 AAE06858	Human aspartyl pro

11	518	100.0	518	22 AAU06602	Human Aspartyl pro
12	518	100.0	518	22 AAU07201	Human aspartyl pro
13	518	100.0	518	22 AAE02580	Human aspartyl pro
14	518	100.0	518	22 AAE02608	Human Aspartyl pro
15	518	100.0	518	23 ABB78589	Human Asp-1 protei
16	518	100.0	518	23 ABB78617	Human Asp-1delatM
17	518	100.0	518	23 ABB06531	Human aspartyl pro
18	518	100.0	518	23 ABB07453	Human BACE2 amino
19	481	92.9	481	22 AAG75592	Human colon cancer
20	469	90.5	475	22 AAE10657	Secreted recombina
21	469	90.5	475	22 AAE02609	Human secreted asp
22	469	90.5	475	23 ABB78618	Human polypeptide
23	439	84.7	439	23 ABB90365	Human aspartyl pro
24	423	81.7	423	22 AAE04796	Human aspartyl pro
25	407	78.6	413	22 AAE10658	Acid-processed hu-
26	407	78.6	413	22 AAE02610	Human acid-process
27	407	78.6	413	23 ABB78619	Asp-1delatM(his)6
28	344	66.4	355	22 AAB93925	Human protein sequ
29	285	55.0	423	22 AAB88479	Human membrane or
30	59	11.4	514	22 AAB84204	Amino acid sequenc
31	50	9.7	50	22 AAM18665	Peptide #5099 enco
32	44	8.5	44	22 ABB32242	Peptide #4893 enco
33	44	8.5	44	22 ABB37490	Peptide #4996 enco
34	44	8.5	44	22 ABB22791	Protein #4790 enco
35	44	8.5	44	22 AAM70610	Human bone marrow
36	44	8.5	44	22 AAM18450	Peptide #4884 enco
37	44	8.5	44	22 AAM30925	Peptide #4962 enco
38	44	8.5	44	22 AAM06046	Peptide #4728 enco
39	44	8.5	44	23 ABB40288	Human peptide enco
40	23	4.4	67	23 ABP11020	Human ORFX protein
41	22	4.2	22	22 AAE10665	Human aspartyl pro
42	22	4.2	22	22 AAU06618	Human Aspartyl pro
43	22	4.2	25	21 AAY88440	Amino acid sequenc
44	22	4.2	25	22 AAE10644	Human aspartyl pro
45	22	4.2	25	22 AAE06874	Human aspartyl pro
46	22	4.2	25	22 AAU07217	Human C-terminal A
47	22	4.2	25	22 AAE02596	Human Asp1 peptide
48	22	4.2	25	23 ABB78605	Human BACE2 C-term
49	16	3.1	16	23 ABB07455	Human protein sequ
50	15	2.9	89	22 AAM25497	Novel human enzyme
51	12	2.3	62	22 AAU23633	Novel human enzyme
52	12	2.3	387	22 AAU23068	Novel human enzyme
53	12	2.3	390	22 AAU23069	Novel human enzyme
54	12	2.3	415	21 AAB07889	Amino acid sequenc
55	12	2.3	425	21 AAY88437	Human Asp2 amino a
56	12	2.3	425	22 AAE10641	T7-Caspase-Caspase
57	12	2.3	425	22 AAE06871	T7-Caspase-Caspase
58	12	2.3	425	22 AAU06615	T7-Caspase-caspase
59	12	2.3	425	22 AAU07214	T7-Caspase-Caspase
60	12	2.3	425	22 AAE02593	T7-Caspase-caspase
61	12	2.3	425	23 ABB78602	T7-caspase-caspase
62	12	2.3	427	22 AAM93866	Human polypeptide,
63	12	2.3	428	22 AAE10646	Human-Asp 2(b) pro
64	12	2.3	428	22 AAE06891	Human-Asp2(b) del
65	12	2.3	428	22 AAU06620	Human-pro-Asp 2(b)
66	12	2.3	428	22 AAU07219	Human aspartyl pro
67	12	2.3	428	22 AAE02598	Human aspartyl pro
68	12	2.3	428	23 ABB78607	Human Asp-2(b)del
69	12	2.3	433	21 AAY88433	Human-pro-Asp-2(a)
70	12	2.3	433	22 AAE10640	Human-pro-Asp 2(a)
71	12	2.3	433	22 AAE06870	Human-pro-Asp2(a)
72	12	2.3	433	22 AAU06614	Human-pro-Asp 2(a)
73	12	2.3	433	22 AAU07213	T7-human aspartyl
74	12	2.3	433	22 AAE02592	Human-pro-Asp-2(a)
75	12	2.3	433	23 ABB78601	Human-pro-Asp-2(a)
76	12	2.3	434	22 AAE10647	Human-Asp 2(b) pro
77	12	2.3	434	22 AAE06892	Human-Asp2(b) del
78	12	2.3	434	22 AAU06621	Human-Asp-2(b)
79	12	2.3	434	22 AAU07220	Human aspartyl pro
80	12	2.3	434	22 AAE02599	Human aspartyl pro
81	12	2.3	434	23 ABB78608	Human Asp-2(b)del
82	12	2.3	446	21 AAY88431	T7-caspase-human-p
83	12	2.3	446	22 AAE10638	T7-Human-pro-Asp 2

84	12	2.3	446	22	AAE06868	T7-Human-pro-Asp2 (157	8	1.5	8	22	AAE10659	Human Aspartyl pro
85	12	2.3	446	22	AAU06612	Human T7-Human-pro	158	8	1.5	8	22	AAE02611	Human Aspartyl pro
86	12	2.3	446	22	AAU07211	T7-human aspartyl	159	8	1.5	8	23	ABB78620	Human Asp-1 substr
87	12	2.3	446	22	AAE02590	T7-Human-pro-Asp-2	160	8	1.5	105	21	AAAG45058	Arabidopsis thalia
88	12	2.3	446	23	ABB78599	Modified human asp	161	8	1.5	131	22	AAU23632	Novel human enzyme
89	12	2.3	453	21	AAV88438	Human-Asp 2(a) pro	162	8	1.5	197	16	AAAR80012	Human LBP (1-197)
90	12	2.3	453	22	AAE10642	Human-Asp2(a) delc	163	8	1.5	205	19	AAV98673	H. pylori GHPO 530
91	12	2.3	453	22	AAE06872	Human-pro-Asp 2(a)	164	8	1.5	224	17	AAW16833	Recombinant endoto
92	12	2.3	453	22	AAU06616	Human aspartyl pro	165	8	1.5	239	22	ABG09608	Novel human diagno
93	12	2.3	453	22	AAU07215	Human-Asp-2(a) del	166	8	1.5	262	22	AAW41741	Human polypeptide
94	12	2.3	453	22	AAE02594	Human Asp-2(a)delc	167	8	1.5	285	21	AAAG12862	Arabidopsis thalia
95	12	2.3	456	21	AAE07897	Active enzyme port	168	8	1.5	287	23	ABB91441	Herbically activ
96	12	2.3	459	21	AAV88432	T7-caspase-human-p	169	8	1.5	297	22	AAV78949	C. glutamicum SRT
97	12	2.3	459	21	AAV88439	Modified human asp	170	8	1.5	307	21	AAAG12861	Arabidopsis thalia
98	12	2.3	459	21	AAV88439	T7-Caspase-human-p	171	8	1.5	313	22	ABG09606	Novel human diagno
99	12	2.3	459	22	AAE10639	Human-Asp 2(a) pro	172	8	1.5	335	22	ABG18051	Novel human diagno
100	12	2.3	459	22	AAE10643	Human-Asp 2(a) delc	173	8	1.5	341	20	AAV32039	Bovine pregnancy a
101	12	2.3	459	22	AAE06873	Human-Asp2(a) delc	174	8	1.5	356	22	AAV79898	Human protein SEQ
102	12	2.3	459	22	AAU06613	Human T7-Caspase-H	175	8	1.5	358	22	AAU41391	Propionibacterium
103	12	2.3	459	22	AAU06617	Human-pro-Asp 2(a)	176	8	1.5	380	20	AAV32041	Bovine pregnancy a
104	12	2.3	459	22	AAU07212	T7-caspase-human a	177	8	1.5	446	17	AAW16810	Recombinant endoto
105	12	2.3	459	22	AAU07216	Human aspartyl pro	178	8	1.5	457	17	AAW16811	Recombinant endoto
106	12	2.3	459	22	AAE02591	T7-Caspase-human-p	179	8	1.5	458	22	AAAG89932	Recombinant endoto
107	12	2.3	459	22	AAE02595	Human-Asp-2(a) del	180	8	1.5	465	16	AAAR76242	C glutamicum prote
108	12	2.3	459	22	AAE02595	T7-caspase-human-p	181	8	1.5	472	22	AAV39955	Recombinant LBP.
109	12	2.3	459	23	ABB78600	Human Asp-2(a)delc	182	8	1.5	473	22	ABB71149	Recombinant LBP.
110	12	2.3	459	23	ABB78604	Human Asp-2(a)delc	183	8	1.5	475	23	ABB91454	Human polypeptide
111	12	2.3	460	21	AAE07898	Amino acid sequenc	184	8	1.5	477	14	AAAR41660	Drosophila melanog
112	12	2.3	476	21	AAV88426	Human aspartyl pro	185	8	1.5	477	15	AAAR53459	Herbically activ
113	12	2.3	476	22	AAE10630	Human aspartyl pro	186	8	1.5	479	17	AAW16795	Human gram-negativ
114	12	2.3	476	22	AAE06860	Human aspartyl pr	187	8	1.5	479	17	AAW16799	Human lipopolysacc
115	12	2.3	476	22	AAE06909	Murine aspartyl pr	188	8	1.5	479	17	AAW16808	Recombinant endoto
116	12	2.3	476	22	AAU06604	Human Aspartyl pro	189	8	1.5	479	17	AAW16795	Recombinant endoto
117	12	2.3	476	22	AAU07203	Human aspartyl pro	190	8	1.5	480	17	AAW16821	Recombinant endoto
118	12	2.3	476	22	AAE02582	Murine aspartyl pr	191	8	1.5	480	17	AAW16822	Recombinant endoto
119	12	2.3	476	22	AAE02619	Human Asp-2(b) pro	192	8	1.5	481	14	AAAR34140	LBP-beta. Synthet
120	12	2.3	476	23	ABB78591	Human aspartyl pr	193	8	1.5	481	15	AAAR62501	LBP amino terminal
121	12	2.3	476	23	ABB06410	Human aspartyl pro	194	8	1.5	481	16	AAAR80994	Recombinant lipopo
122	12	2.3	476	23	ABB06120	Human NS protein s	195	8	1.5	481	16	AAAR81246	Human LBP. Homo s
123	12	2.3	488	22	AAE06572	Human memapsin 2.	196	8	1.5	481	16	AAAR80014	Lipopolysaccharide
124	12	2.3	488	22	AAE06572	Memapsin 2 protein	197	8	1.5	481	16	AAAR68922	rlBP. Homo sapien
125	12	2.3	488	23	AAU99488	Human memapsin 2.	198	8	1.5	481	16	AAAR68000	Recombinant human
126	12	2.3	501	19	AAW59807	Amino acid sequenc	199	8	1.5	481	16	AAAR76601	Recombinant endoto
127	12	2.3	501	21	AAV94767	Murine beta-secret	200	8	1.5	481	17	AAW16829	Recombinant endoto
128	12	2.3	501	21	AAV94768	Human beta-secret	201	8	1.5	481	17	AAW16830	Recombinant endoto
129	12	2.3	501	21	AAV94769	Rat beta-secretase	202	8	1.5	481	17	AAW16831	Recombinant endoto
130	12	2.3	501	21	AAE07896	Amino acid sequenc	203	8	1.5	481	17	AAW16836	Recombinant endoto
131	12	2.3	501	21	AAV88425	Human aspartyl pr	204	8	1.5	481	17	AAW16837	Recombinant endoto
132	12	2.3	501	21	AAE10631	Murine aspartyl pr	205	8	1.5	481	17	AAW16838	Recombinant endoto
133	12	2.3	501	22	AAE10629	Human aspartyl pr	206	8	1.5	481	17	AAW16839	Recombinant endoto
134	12	2.3	501	22	AAE10631	Murine aspartyl pr	207	8	1.5	481	17	AAW16840	Recombinant endoto
135	12	2.3	501	22	AAE06859	Human aspartyl pro	208	8	1.5	481	17	AAW19010	Recombinant endoto
136	12	2.3	501	22	AAE06861	Murine aspartyl pr	209	8	1.5	481	17	AAW19011	Recombinant endoto
137	12	2.3	501	22	AAU06603	Human Aspartyl pro	210	8	1.5	481	17	AAW16809	Recombinant endoto
138	12	2.3	501	22	AAU06605	Mouse Aspartyl pro	211	8	1.5	481	17	AAW16807	Recombinant endoto
139	12	2.3	501	22	AAU07202	Human aspartyl pro	212	8	1.5	481	17	AAW16806	Recombinant endoto
140	12	2.3	501	22	AAU07204	Mouse aspartyl pro	213	8	1.5	481	17	AAW05851	Recombinant endoto
141	12	2.3	501	22	AAE04948	Mouse aspartic sec	214	8	1.5	481	19	AAW77093	Recombinant lipopo
142	12	2.3	501	22	AAE02581	Human aspartyl pro	215	8	1.5	481	19	AAW63305	Lipopolysaccharide
143	12	2.3	501	22	AAE02583	Murine aspartyl pr	216	8	1.5	481	19	AAW40139	Lipopolysaccharide
144	12	2.3	501	23	ABB78590	Human Asp-2(a) pro	217	8	1.5	481	19	AAW40812	Human recombinant
145	12	2.3	501	23	ABB78592	Human Asp-2(a) pro	218	8	1.5	481	19	AAW78356	Human lipopolysacc
146	12	2.3	501	23	ABB06409	Human aspartyl pr	219	8	1.5	481	20	AAW78356	Human lipopolysacc
147	12	2.3	503	22	AAE06573	Human Asp-2(a) pro	220	8	1.5	481	21	AAV57150	Lipopolysaccharide
148	12	2.3	503	22	AAE06573	Human pro-memapsin	221	8	1.5	481	21	AAV57150	Human lipopolysacc
149	12	2.3	503	23	AAU99489	T7 promoter and ve	222	8	1.5	481	22	AAAG7902	Human lipopolysacc
150	12	2.3	509	23	AAU99489	Pro-memapsin 2 enc	223	8	1.5	481	22	AAU09006	Human lipopolysacc
151	12	2.3	790	19	AAW59808	FLAG-tagged human	224	8	1.5	481	22	AAAG89151	Human secreted pro
152	12	2.3	969	22	ABG09611	Partial amino acid	225	8	1.5	481	22	AAAB66059	Human Recombinant
153	12	2.3	969	22	ABG09611	Novel human diagno	226	8	1.5	481	22	AAAB66059	rlBP protein. Uni
154	9	1.7	45	23	AAU78524	N terminus of 15kD	227	8	1.5	482	17	AAW16819	Recombinant endoto
155	9	1.7	269	22	ABG18048	Novel human diagno	228	8	1.5	482	17	AAW16820	Recombinant endoto
156	9	1.7	322	22	AAE04797	Human aspartyl pro	229	8	1.5	504	23	AAU84277	Human endometrial
	9	1.7	351	20	AAV35918	Extended human sec		8	1.5	548	22	AAAG98365	Escherichia coli p

230	8	1.5	592	22	ABB62801	Drosophila melanog	303	7	1.4	145	22	ABB50641	Human secreted pro
231	8	1.5	592	22	ABB67339	Drosophila melanog	304	7	1.4	145	23	ABP34658	Human ORF3631 prot
232	8	1.5	692	22	AA93225	C glutamicum prote	305	7	1.4	146	22	ABG24335	Novel human diago
233	8	1.5	1246	23	AAU84295	Human endometrial	306	7	1.4	149	22	ABB59178	Drosophila melanog
234	8	1.5	1247	23	AAO17366	Human nidogen. Ho	307	7	1.4	156	22	AAU23445	Novel human enzyme
235	8	1.5	1247	23	ABB90742	Human Tumour Endot	308	7	1.4	157	22	ABG22859	Novel human diago
236	7	1.4	9	21	ABBI9593	Human CASB616 epit	309	7	1.4	160	17	AAW01000	Apoptosis-regulati
237	7	1.4	10	21	ABBI9598	Human CASB616 epit	310	7	1.4	160	20	AAW05436	Human BIK protein
238	7	1.4	14	14	AAK32965	Mastoparan analogu	311	7	1.4	160	20	AAW94326	Human BiP1a protei
239	7	1.4	14	14	AAK32978	Mastoparan analogu	312	7	1.4	161	20	AAV38638	Neisseria meningit
240	7	1.4	14	14	AAK32960	Mastoparan analogu	313	7	1.4	161	20	AAV38640	Human gonorrhoe
241	7	1.4	23	22	ABB35198	Human transmembran	314	7	1.4	166	23	ABP01194	Human ORFX protein
242	7	1.4	25	22	ABB42277	Peptide #9783 enco	315	7	1.4	168	18	AAW55521	H. pylori ORF 12ge
243	7	1.4	25	22	AA663163	Human brain expres	316	7	1.4	168	18	AAW20521	Helicobacter pylor
244	7	1.4	25	22	AAW75977	Human bone marrow	317	7	1.4	168	18	AAW24680	H. pylori cell env
245	7	1.4	25	22	AAK36085	Peptide #10122 enc	318	7	1.4	168	22	ABB52931	Escherichia coli p
246	7	1.4	28	22	AAE02657	Human gene 2 enco	319	7	1.4	168	22	ABB52965	Escherichia coli p
247	7	1.4	30	22	AAE85337	Human oaf protein	320	7	1.4	170	23	AAO22050	Hepatitis C virus
248	7	1.4	34	21	ABBI2350	Fragment of human	321	7	1.4	170	23	ABB47867	listeria monocytog
249	7	1.4	34	21	AA656900	Arabidopsis thalia	322	7	1.4	171	22	AAU51854	Propionibacterium
250	7	1.4	41	22	ABB51187	Human secreted pro	323	7	1.4	174	22	AA689195	Human secreted pro
251	7	1.4	43	19	AAV21020	Human glial fibril	324	7	1.4	175	22	AAI17175	Peptide #3609 enco
252	7	1.4	47	22	AAU31051	Novel human secret	325	7	1.4	175	22	AAI29668	Peptide #3705 enco
253	7	1.4	61	19	AAW75196	Human secreted pro	326	7	1.4	175	22	AAW40930	Human polypeptide
254	7	1.4	61	22	AAU42241	Propionibacterium	327	7	1.4	175	22	AAW04870	Peptide #3552 enco
255	7	1.4	68	22	AAU20237	Human novel endocr	328	7	1.4	175	22	AA674083	Human colon cancer
256	7	1.4	69	23	ABP03389	Human ORFX protein	329	7	1.4	175	23	ABP41517	Human ovarian anti
257	7	1.4	71	21	AA600466	Human secreted pro	330	7	1.4	180	22	AAO09655	Human polypeptide
258	7	1.4	72	22	AA683313	Human immune/haema	331	7	1.4	185	19	AAW988220	H. pylori GHPO 234
259	7	1.4	76	22	AAU48836	Propionibacterium	332	7	1.4	187	22	AAI23494	Human EST encoded
260	7	1.4	79	21	AA656899	Arabidopsis thalia	333	7	1.4	192	22	AAI6973	Hepatitis C virus
261	7	1.4	86	22	ABB51186	Human secreted pro	334	7	1.4	192	16	AAK69640	Hepatitis C virus
262	7	1.4	88	22	AAO13578	Human polypeptide	335	7	1.4	192	16	AAK69656	Hepatitis C virus
263	7	1.4	90	22	AAU47158	Propionibacterium	336	7	1.4	192	16	AAK69644	Hepatitis C virus
264	7	1.4	91	22	ABB44259	Peptide #11765 enc	337	7	1.4	192	17	AAK89527	Hepatitis C virus
265	7	1.4	91	22	ABB27130	Protein #9129 enco	338	7	1.4	192	17	AAK89529	Hepatitis C virus
266	7	1.4	91	22	AA65297	Human brain expres	339	7	1.4	192	17	AAK89511	Hepatitis C virus
267	7	1.4	91	22	AAI21888	Peptide #8322 enco	340	7	1.4	192	17	AAK89515	Hepatitis C virus
268	7	1.4	91	22	AAI38214	Peptide #12251 enc	341	7	1.4	193	22	AAU16973	Human novel secret
269	7	1.4	94	23	ABB78860	Tumour necrosis fa	342	7	1.4	194	22	AAI53465	Human colon cancer
270	7	1.4	95	22	AAI00047	Plastidic trioseph	343	7	1.4	206	21	AAV91339	Group B Streptococ
271	7	1.4	105	23	ABP02682	Human ORFX protein	344	7	1.4	208	16	AAK77167	Arabidopsis thalia
272	7	1.4	106	22	AAE02654	Human gene 2 enco	345	7	1.4	209	21	AAI04117	Arabidopsis thalia
273	7	1.4	109	22	ABG11071	Novel human diago	346	7	1.4	209	21	AAI11858	Arabidopsis thalia
274	7	1.4	109	22	ABG23787	Novel human diago	347	7	1.4	209	21	AAI11858	Arabidopsis thalia
275	7	1.4	112	22	ABB67791	Drosophila melanog	348	7	1.4	210	18	AAI11261	Streptococcus pneu
276	7	1.4	115	18	AAW55383	H. pylori ORF hp4p	349	7	1.4	217	22	AAW40476	Human polypeptide
277	7	1.4	115	18	AAW21006	H. pylori cell env	350	7	1.4	219	21	AAW58938	Arabidopsis thalia
278	7	1.4	115	21	AA658939	Arabidopsis thalia	351	7	1.4	222	19	AAW72187	Arabidopsis thalia
279	7	1.4	115	22	AAK88647	Human immune/haema	352	7	1.4	222	19	AAW72118	HSV-2 strain SBS C
280	7	1.4	117	23	ABP33337	Human ORF2310 prot	353	7	1.4	222	19	AAW72040	HSV-2 strain SBS C
281	7	1.4	119	23	ABB54744	Lactococcus lactis	354	7	1.4	231	22	AAI75438	Human colon cancer
282	7	1.4	120	21	AA603247	Human secreted pro	355	7	1.4	231	22	AAI750087	Human secreted pro
283	7	1.4	121	20	AAV12208	Human 5' EST secre	356	7	1.4	232	23	ABB90294	Human polypeptide
284	7	1.4	123	22	AAO13332	Human polypeptide	357	7	1.4	233	22	AAI61608	Human protein HP03
285	7	1.4	126	19	AAW77364	Human Tumour Suppr	358	7	1.4	234	16	AAK82605	Eph transmembrane
286	7	1.4	126	22	AAI39144	Human polypeptide	359	7	1.4	235	20	AAI35512	Chlamydia pneumoni
287	7	1.4	126	22	AAI39144	Human protein sequ	360	7	1.4	238	16	AAI71481	Human hek-l protei
288	7	1.4	130	22	AAO01648	Human polypeptide	361	7	1.4	241	20	AAI37435	Human acid sequenc
289	7	1.4	139	22	AAI99857	Human excretory re	362	7	1.4	245	22	AAI38690	Human polypeptide
290	7	1.4	139	22	AAI42672	Human kidney relat	363	7	1.4	253	22	AAI0135	Streptomyces nous
291	7	1.4	140	20	AAI06823	P. methanolica pro	364	7	1.4	255	22	AAI63235	Human breast cance
292	7	1.4	140	20	AAI93839	P. methanolica PEP	365	7	1.4	262	21	AAI58184	Propionibacterium
293	7	1.4	140	20	AAI93840	S. cerevisiae prot	366	7	1.4	262	21	AAI58184	lung cancer associ
294	7	1.4	140	21	AAI19018	Amino acid sequenc	367	7	1.4	265	23	ABBI72311	Rat protein isolat
295	7	1.4	140	21	AAI51057	P. methanolica PEP	368	7	1.4	267	22	ABBI72311	Escherichia coli e
296	7	1.4	140	22	AAE05416	P. methanolica PEP	369	7	1.4	268	22	AAI69751	Novel human diago
297	7	1.4	140	22	AAI67567	Amino acid sequenc	370	7	1.4	269	22	ABG07213	Propionibacterium
298	7	1.4	140	22	AAI61993	P. methanolica PEP	371	7	1.4	272	22	AAI49513	Novel human diago
299	7	1.4	140	22	AAI72372	P. methanolica PEP	372	7	1.4	273	22	AAI85336	Human oaf protein
300	7	1.4	140	22	AAI49227	P. methanolica prot	373	7	1.4	273	22	AAI03825	Human gene 8 enco
301	7	1.4	140	23	AAI19974	Protein derived fr	374	7	1.4	273	22	AAI03851	Human gene 8 enco
302	7	1.4	145	22	ABG08183	Novel human diago	375	7	1.4	273	23	ABG64540	Human albumin fusi

376	7	1.4	273	23	ABG64541	Human albumin fusi
377	7	1.4	273	23	AAU83188	Novel secreted pro
378	7	1.4	276	23	AAE14745	Human triacylglyce
379	7	1.4	279	21	AAB08981	Human secreted pro
380	7	1.4	280	22	AAG89194	Human secreted pro
381	7	1.4	280	23	AAE14743	Human triacylglyce
382	7	1.4	289	21	AAG04116	Arabidopsis thalia
383	7	1.4	289	21	AAG11857	Arabidopsis thalia
384	7	1.4	289	21	AAG54003	Arabidopsis thalia
385	7	1.4	289	23	AAU77494	Human lipid metabo
386	7	1.4	290	21	AAV74500	Neisseria gonorrhe
387	7	1.4	290	21	AAV74501	Neisseria meningit
388	7	1.4	290	21	AAV74502	Neisseria meningit
389	7	1.4	290	22	AAU63105	Propionibacterium
390	7	1.4	294	22	ABE66598	Drosophila melanog
391	7	1.4	295	22	AAG72119	Human olfactory re
392	7	1.4	298	14	AAR36678	Ethylene-induced a
393	7	1.4	298	14	ABE64796	Drosophila melanog
394	7	1.4	306	22	AAG98408	Escherichia coli p
395	7	1.4	313	22	ABE64037	Drosophila melanog
396	7	1.4	320	15	AAE62044	Leptospiira Omp1.
397	7	1.4	320	18	AAW14278	Leptospiira alstoni
398	7	1.4	323	21	AAE12341	Fragment of human
399	7	1.4	326	22	ABE66589	Human pepsin. Hom
400	7	1.4	326	22	AAE61351	Pepsin proteain. H
401	7	1.4	327	22	AAW00099	Plastidic trioseph
402	7	1.4	330	20	AAV05383	Mouse GCR9 protein
403	7	1.4	330	21	AAV94269	Mouse 7-transmembr
404	7	1.4	330	23	ABP28764	Streptococcus poly
405	7	1.4	339	22	ABG15392	Novel human diagno
406	7	1.4	346	23	ABE54038	Lactococcus lactis
407	7	1.4	354	17	AAW14463	Yeast glycoprotein
408	7	1.4	359	22	ABG24341	Novel human diagno
409	7	1.4	359	23	ABE90878	Herbicidally activ
410	7	1.4	363	18	AAW24256	Ammonifex histidin
411	7	1.4	366	23	AAV91299	Human protein NOV6
412	7	1.4	368	22	ABG29719	Novel human diagno
413	7	1.4	369	22	ABG01477	Novel human diagno
414	7	1.4	373	21	AAAG04115	Arabidopsis thalia
415	7	1.4	373	21	AAG11856	Arabidopsis thalia
416	7	1.4	373	21	AAAG54002	Arabidopsis thalia
417	7	1.4	379	23	AAU72876	Human aspartyl pro
418	7	1.4	380	20	AAV32036	Bovine pregnancy a
419	7	1.4	387	20	AAV32052	Bovine pregnancy a
420	7	1.4	388	20	AAV32058	Cat pregnancy asso
421	7	1.4	388	20	AAV32058	Human full-length
422	7	1.4	388	22	AAU27708	Bovine pregnancy a
423	7	1.4	392	20	AAV32057	Putative P. abyssi
424	7	1.4	392	22	AAE96350	Human triacylglyce
425	7	1.4	395	23	AAE14744	Aspergillus oryzae
426	7	1.4	397	18	AAW31628	Human lysosomal ac
427	7	1.4	397	23	AAE17308	Amino acid sequenc
428	7	1.4	399	22	AAE67513	Human lipid metabo
429	7	1.4	399	23	AAU77496	Canine cholecystok
430	7	1.4	407	16	AAR80749	Canine cholecystok
431	7	1.4	407	17	AAE92291	Canine cholecystok
432	7	1.4	407	17	AAR88460	Canine cholecystok
433	7	1.4	409	15	AAR48060	Sequence of protea
434	7	1.4	410	13	AAR28030	Pichia pastoris pr
435	7	1.4	417	23	AAW49396	Human zinc finger
436	7	1.4	420	21	ABE80665	Candida boidinii p
437	7	1.4	428	20	AAV09000	E. coli sura prote
438	7	1.4	433	21	AAG30824	Arabidopsis thalia
439	7	1.4	433	21	AAE31636	Arabidopsis thalia
440	7	1.4	436	23	ABP29086	Streptococcus poly
441	7	1.4	445	16	AAR80750	Canine cholecystok
442	7	1.4	445	17	AAR92292	Canine cholecystok
443	7	1.4	445	17	AAR88461	Canine cholecystok
444	7	1.4	449	19	AAW57043	Human aspartic pro
445	7	1.4	450	21	AAV57041	Plasmodium vivax p
446	7	1.4	451	22	ABE6063	Murine protein: SE
447	7	1.4	453	14	AAR41675	Canine gastrin rec
448	7	1.4	453	22	ABE66628	Canine gastrin rec

449	7	1.4	456	21	AAV71062	Human membrane tra
450	7	1.4	456	22	AAW78336	Human protein sequ
451	7	1.4	460	22	AAE94655	Human protein sequ
452	7	1.4	465	22	ABE66239	Drosophila melanog
453	7	1.4	470	22	ABE66083	Murine TANGO 202.
454	7	1.4	477	22	ABE61772	Drosophila melanog
455	7	1.4	477	22	ABE67670	Amino acid sequenc
456	7	1.4	486	23	ABE91908	Herbicidally activ
457	7	1.4	489	22	ABE11767	Human membrane tra
458	7	1.4	489	22	AAW79320	Human protein SEQ
459	7	1.4	490	21	AAV75584	Neisseria meningit
460	7	1.4	490	21	AAV75585	Neisseria meningit
461	7	1.4	491	22	AAE81101	Mycobacterium tube
462	7	1.4	494	15	AAR62825	Human steroid-21-h
463	7	1.4	506	21	AAE17818	Arabidopsis thalia
464	7	1.4	508	21	AAE31635	Arabidopsis thalia
465	7	1.4	513	21	AAE45529	Arabidopsis thalia
466	7	1.4	517	21	AAV32390	Herpesvirus entry
467	7	1.4	517	23	AAE23294	Human nectin-lalph
468	7	1.4	522	21	AAE17817	Arabidopsis thalia
469	7	1.4	525	23	ABP28514	Streptococcus poly
470	7	1.4	529	21	AAE51569	Arabidopsis thalia
471	7	1.4	529	23	ABE93699	Herbicidally activ
472	7	1.4	537	22	ABE61550	Drosophila melanog
473	7	1.4	537	22	ABE67157	Drosophila melanog
474	7	1.4	550	18	AAW23282	Brevibacterium lac
475	7	1.4	550	18	AAW06584	B. lactofermentum
476	7	1.4	550	19	AAE68149	Brevibacterium lac
477	7	1.4	550	19	AAW69551	B. lactofermentum
478	7	1.4	550	19	AAW47398	C glutamicum prote
479	7	1.4	550	22	AAE93196	Enterococcus faeca
480	7	1.4	569	22	AAU34910	Polyhydroxybutyrat
481	7	1.4	589	12	AAE10681	Sequence encoded b
482	7	1.4	589	14	AAE32190	Alcaligenes eutrop
483	7	1.4	589	22	AAE10892	S. pneumoniae deri
484	7	1.4	590	19	AAE85912	Propionibacterium
485	7	1.4	590	22	AAU42564	Rhodobacter spaero
486	7	1.4	601	22	AAE10894	Sequence of human
487	7	1.4	604	15	AAE51267	Cyclooxygenase-2.
488	7	1.4	604	15	AAE56660	Human cyclooxygena
489	7	1.4	604	16	AAR72228	Human cyclooxygena
490	7	1.4	604	18	AAW12698	Human prostaglandi
491	7	1.4	604	22	AAE72199	Human cyclooxygena
492	7	1.4	604	23	ABE07244	Human cyclooxygena
493	7	1.4	604	23	ABE07247	Guinea pig cycloo
494	7	1.4	604	23	ABE07248	Rabbit cyclooxygen
495	7	1.4	604	23	ABE07249	Horse cyclooxygena
496	7	1.4	604	23	ABE07250	Sheep cyclooxygena
497	7	1.4	613	22	AAU04887	Micromonospora eve
498	7	1.4	621	20	AAV21549	Porcine heparin-bi
499	7	1.4	622	22	ABE58015	Drosophila melanog
500	7	1.4	622	22	ABE67236	Drosophila melanog
501	7	1.4	634	20	AAV21548	Human heparin-bind
502	7	1.4	638	18	AAW32098	Miniature swine re
503	7	1.4	638	22	AAE70633	Porcine endogenous
504	7	1.4	638	22	AAE70634	Porcine endogenous
505	7	1.4	638	22	AAE73287	Retoviral protein
506	7	1.4	638	22	AAE35114	PERV-C env protein
507	7	1.4	652	22	AAU42709	Proplionibacterium
508	7	1.4	656	22	ABE26839	Novel human diagno
509	7	1.4	659	23	AAU11356	Human DNAX cytokin
510	7	1.4	659	22	AAU35112	PERV-1-15 env prot
511	7	1.4	667	22	AAU04957	Human Interleukin
512	7	1.4	667	23	AAU83601	Human PRO protein,
513	7	1.4	668	22	AAE36888	Portuguese Water d
514	7	1.4	672	16	AAR71325	Poly-beta-hydroxya
515	7	1.4	674	22	AAE94461	Human protein sequ
516	7	1.4	674	22	AAE95164	Human protein sequ
517	7	1.4	674	23	ABE66691	Human novel polype
518	7	1.4	677	22	ABE61957	Drosophila melanog
519	7	1.4	690	5	AAE40306	Sequence encoded b
520	7	1.4	692	22	ABE22381	Novel human diagno
521	7	1.4	702	23	ABP28373	Streptococcus poly

522	7	1.4	702	23	AAM47575	Drosophila cell cy	595	6	1.2	12	22	AAB50475	Bacterial AiaA pep
523	7	1.4	704	21	AAB15891	E. coli proliferat	596	6	1.2	12	23	AAM52423	Putative protease
524	7	1.4	704	22	AAU34770	B. coli cellular p	597	6	1.2	14	22	ABB55906	Vascular dementia-
525	7	1.4	704	22	AAU38372	Salmonella typhi c	598	6	1.2	14	22	AAB72296	ADAMTS-R1 immunoge
526	7	1.4	715	23	ABB53379	Lactococcus lactis	599	6	1.2	14	23	ABJ00604	B lymphocyte stimu
527	7	1.4	723	22	AAM39467	Human polypeptide	600	6	1.2	14	23	ABG33465	B lymphocyte stimu
528	7	1.4	726	22	AA667116	Human transcriptio	601	6	1.2	15	22	AA678131	Human actin 49 pep
529	7	1.4	730	22	AAM41253	Human polypeptide	602	6	1.2	15	22	AA699299	Human ribosomal ph
530	7	1.4	731	23	AAE14746	Human triacylglyce	603	6	1.2	15	22	AA667721	Cytochrome b559 10
531	7	1.4	760	23	AAE20507	Streptococcus muta	604	6	1.2	15	23	ABB81892	Transcriptional el
532	7	1.4	760	23	AAE20592	Streptococcus muta	605	6	1.2	16	22	AAM99379	Vaccine related MH
533	7	1.4	773	23	ABB57374	Mouse ischaemic co	606	6	1.2	18	23	AAU78513	Human and mouse BA
534	7	1.4	775	21	AA67250	Mouse protein tyro	607	6	1.2	19	18	AAU72374	S. pneumoniae HSP7
535	7	1.4	775	21	AA67251	Mutant mouse PTP-P	608	6	1.2	19	22	AAB72292	ADAMTS-7 immunogen
536	7	1.4	784	23	ABB47322	Listeria monocytog	609	6	1.2	19	23	AAE23897	PIR-A1 receptor pe
537	7	1.4	802	17	AA690848	Gibberellin (GA1),	610	6	1.2	20	9	AA682056	Pep-13 comprising \
538	7	1.4	802	23	ABB92819	Herbicideally activ	611	6	1.2	20	12	AA610788	S-antigen polypept
539	7	1.4	862	22	AA690202	C glutamicum prote	612	6	1.2	21	18	AA610215	Endoglycoceramidas
540	7	1.4	863	22	ABB63583	Drosophila melanog	613	6	1.2	21	19	AA648387	Synthetic don-1 po
541	7	1.4	863	22	ABB63583	Novel human diagno	614	6	1.2	22	19	AA659850	Amino acid sequenc
542	7	1.4	880	22	ABG24427	Streptococcus poly	615	6	1.2	22	22	AA672346	Membrane attachmen
543	7	1.4	896	22	ABG28532	Novel human diagno	616	6	1.2	22	23	AAU10579	Mammalian T8 signa
544	7	1.4	902	22	ABB60606	Drosophila melanog	617	6	1.2	23	22	AAB60685	PTT01A 103L-encode
545	7	1.4	925	22	ABG15391	Novel human diagno	618	6	1.2	23	23	AA649118	Cationic amphipath
546	7	1.4	933	23	ABP28348	Streptococcus poly	619	6	1.2	24	15	AA647014	Cathepsin E positi
547	7	1.4	942	21	AAB25536	Eucalyptus grandis	620	6	1.2	24	22	AA699380	Vaccine related MH
548	7	1.4	981	23	ABB78727	Human calsynntenin-	621	6	1.2	25	18	AA635870	Leader sequence fo
549	7	1.4	987	21	AAB19590	Human CASB616. Ho	622	6	1.2	25	19	AA659838	RAMyIA signal pept
550	7	1.4	993	20	AA649897	Rat TAO2 kinase.	623	6	1.2	25	23	ABB77596	Human cancer assoc
551	7	1.4	993	22	ABB66086	Drosophila melanog	624	6	1.2	26	21	AA6784367	Amino acid sequenc
552	7	1.4	994	16	AA687018	Receptor tyrosine	625	6	1.2	26	21	AA676928	Human colon cancer
553	7	1.4	994	18	AA626366	Mouse Nuk tyrosine	626	6	1.2	26	22	AA624389	Human prokineticin
554	7	1.4	994	22	AAU01907	Murine neural kina	627	6	1.2	27	21	AA688094	Preproinsulin secr
555	7	1.4	1055	21	AAB19591	Human CASB616. Ho	628	6	1.2	27	21	AA643836	Secretory signal s
556	7	1.4	1062	21	AAB40294	Human ORFX ORF58 p	629	6	1.2	27	22	AA694075	Human reproductive
557	7	1.4	1127	22	AAB95541	Human protein sequ	630	6	1.2	27	22	AA645954	Transdominant effe
558	7	1.4	1133	22	ABG28516	Novel human diagno	631	6	1.2	27	22	AAB35084	Preproinsulin secr
559	7	1.4	1191	22	AAM80219	Human protein SEQ	632	6	1.2	27	23	AA649941	Human D40 associat
560	7	1.4	1193	22	ABG18089	Novel human diagno	633	6	1.2	27	23	AA649962	Human D40 associat
561	7	1.4	1235	21	AAB41663	Human ORFX ORF1427	634	6	1.2	27	23	AAU76403	Preproinsulin secr
562	7	1.4	1379	22	ABB57823	Drosophila melanog	635	6	1.2	30	23	AA649997	Human D40 associat
563	7	1.4	1429	20	AA693941	Human brx protein.	636	6	1.2	31	21	AAB15670	Alpha v beta 3 rec
564	7	1.4	1429	22	ABG05537	Novel human diagno	637	6	1.2	31	21	AA646497	Human 5' EST relat
565	7	1.4	1520	22	AA690690	C glutamicum prote	638	6	1.2	31	22	AA677180	Human colon cancer
566	7	1.4	1822	15	AA655273	Beta subunit of in	639	6	1.2	31	23	AAE18959	Rice alpha-amylase
567	7	1.4	1873	23	AAE14708	Human beta4 integr	640	6	1.2	32	18	AA620205	H. pylori secreted
568	7	1.4	1873	23	AAE14714	Human beta4 integr	641	6	1.2	32	20	AA611389	Human 5' EST secre
569	7	1.4	1875	22	AAB68089	Amino acid sequenc	642	6	1.2	32	21	AA686536	Human gene 77-enco
570	7	1.4	2042	22	ABB59689	Drosophila melanog	643	6	1.2	32	22	AA642768	Peptide #10274 enco
571	7	1.4	2047	22	AAB99541	Human CLASP-7 prot	644	6	1.2	32	22	ABB26061	Protein #8060 enco
572	7	1.4	2047	23	ABG61707	Human cadherin-lik	645	6	1.2	32	22	AA663659	Human brain expres
573	7	1.4	2404	20	AA630640	HIV-1-NC7 envelope	646	6	1.2	32	22	AA676473	Human bone marrow
574	6	1.2	8	22	ABP14602	HIV A03 super moti	647	6	1.2	32	22	AA620905	Peptide #7339 enco
575	6	1.2	8	22	ABP16775	HIV B07 super moti	648	6	1.2	32	22	AAM36581	Peptide #10618 enco
576	6	1.2	8	22	ABP18951	HIV B62 super moti	649	6	1.2	32	22	ABG45734	Human peptide enco
577	6	1.2	8	22	ABP20976	HIV A03 motif nef	650	6	1.2	33	22	AA007615	Human polypeptide
578	6	1.2	8	22	ABP23037	HIV A11 motif nef	651	6	1.2	33	22	AAB60686	Human polypeptide
579	6	1.2	8	23	ABB06440	Beta-secretase rel	652	6	1.2	33	22	AA660688	Plasmid TTO1A 103L
580	6	1.2	8	23	ABB07485	Theobroma cacao as	653	6	1.2	34	20	AA692216	PTTUDABP-encoded r
581	6	1.2	9	22	ABP11718	HIV A01 super moti	654	6	1.2	34	20	AA603951	Analogue of parath
582	6	1.2	9	22	ABP15783	HIV A24 super moti	655	6	1.2	34	21	AA637357	Human secreted pep
583	6	1.2	9	22	ABP17991	HIV B58 super moti	656	6	1.2	34	21	AAU20673	Human novel foetal
584	6	1.2	9	22	ABP20919	HIV A03 motif nef	657	6	1.2	35	22	AA656638	Arabidopsis thalia
585	6	1.2	10	22	ABP13056	HIV A02 super moti	658	6	1.2	35	22	AA630124	Peptide #2775 enco
586	6	1.2	10	22	ABP15796	HIV A24 super moti	659	6	1.2	35	22	ABB35296	Peptide #2802 enco
587	6	1.2	10	22	ABP16792	HIV B07 super moti	660	6	1.2	35	22	ABB39561	Peptide #7067 enco
588	6	1.2	10	22	ABP23034	HIV A11 motif nef	661	6	1.2	35	22	ABB20738	Protein #2737 enco
589	6	1.2	10	22	ABP24173	HIV A24 motif nef	662	6	1.2	35	22	AA624282	Human brain expres
590	6	1.2	11	21	AA676394	Fragment of human	663	6	1.2	35	22	AA656125	Human brain expres
591	6	1.2	11	22	ABP13083	HIV A02 super moti	664	6	1.2	35	22	AA660260	Human bone marrow
592	6	1.2	11	22	ABP15818	HIV A24 super moti	665	6	1.2	35	22	AA668497	Human bone marrow
593	6	1.2	11	22	ABP17992	HIV B58 super moti	666	6	1.2	35	22	AA672887	Human bone marrow
594	6	1.2	12	21	AAB09319	Hepatitis GB virus	667	6	1.2	35	22	AA616303	Peptide #2737 enco

668	6	1.2	35	22	AAW19767	Peptide #6201 enco	741	6	1.2	48	22	AAO07651	Human polypeptide
669	6	1.2	35	22	AAW28796	Peptide #2833 enco	742	6	1.2	48	23	ABG44108	Human peptide enco
670	6	1.2	35	22	AAW33118	Peptide #7155 enco	743	6	1.2	49	21	AAG56387	Arabidopsis thalia
671	6	1.2	35	22	AAW04039	Peptide #2721 enco	744	6	1.2	49	22	ABB29630	Peptide #2281 enco
672	6	1.2	35	23	ABB80917	Human sprouty-4 or	745	6	1.2	49	22	ABB34808	Peptide #2314 enco
673	6	1.2	35	23	ABG38078	Human peptide enco	746	6	1.2	49	22	ABB50577	Human secreted pro
674	6	1.2	35	23	ABG42721	Human peptide enco	747	6	1.2	49	22	ABB20224	Protein #2223 enco
675	6	1.2	36	16	AAW75130	PLAP glycosyl-phos	748	6	1.2	49	22	AAM55610	Human brain expres
676	6	1.2	36	20	AAW49764	Compact structure	749	6	1.2	49	22	AAM67995	Human bone marrow
677	6	1.2	36	20	AAW11642	Human 5' EST secre	750	6	1.2	49	22	AAO11940	Human polypeptide
678	6	1.2	36	21	AAW88082	Lamp-1 lysosomal t	751	6	1.2	49	22	AAO13242	Human polypeptide
679	6	1.2	36	21	AAW43825	Lysosomal membrane	752	6	1.2	49	22	AAM15811	Peptide #2245 enco
680	6	1.2	36	21	AAW56348	Streptococcus pyog	753	6	1.2	49	22	AAM28321	Peptide #2358 enco
681	6	1.2	36	22	ABW03311	Human musculoskele	754	6	1.2	49	22	AAM03549	Peptide #2231 enco
682	6	1.2	36	22	AAW5941	Transdominant effe	755	6	1.2	49	23	ABG37527	Human peptide enco
683	6	1.2	36	22	AAW35073	Lamp-1 lysosomal m	756	6	1.2	50	19	AAW35017	Human peptide used in po
684	6	1.2	36	23	AAW76179	Lysosome associate	757	6	1.2	50	20	AAW29804	Human GABA B recep
685	6	1.2	37	21	AAW56637	Arabidopsis thalia	758	6	1.2	50	22	AAW40556	Propionibacterium
686	6	1.2	38	13	AAW20962	Sequence of human	759	6	1.2	50	22	AAW43237	Propionibacterium
687	6	1.2	38	18	AAW27479	Preproinsulin lead	760	6	1.2	51	19	AAW57744	Propionibacterium
688	6	1.2	38	18	AAW27480	Preproinsulin lead	761	6	1.2	51	22	AAW71570	Hepatocyte nuclear
689	6	1.2	38	18	AAW27481	Preproinsulin lead	762	6	1.2	51	21	AAW64665	Human 5' EST relat
690	6	1.2	38	18	AAW27482	Preproinsulin lead	763	6	1.2	51	22	AAU41435	Propionibacterium
691	6	1.2	38	20	AAW48503	Human breast tumou	764	6	1.2	51	22	AAW86756	Human immune/haema
692	6	1.2	38	22	ABW41697	Peptide #9203 enco	765	6	1.2	51	22	AAO07411	Human polypeptide
693	6	1.2	38	22	ABW25470	Protein #7469 enco	766	6	1.2	51	22	AAW37342	Chaperone cpn60 pr
694	6	1.2	38	22	AAW62570	Human brain expres	767	6	1.2	51	22	AAG77229	Human colon cancer
695	6	1.2	38	22	AAW75381	Human bone marrow	768	6	1.2	52	20	AAW11651	Human 5' EST secre
696	6	1.2	38	22	AAW20580	Peptide #7014 enco	769	6	1.2	52	22	AAU48976	Propionibacterium
697	6	1.2	38	22	AAW35493	Peptide #9530 enco	770	6	1.2	52	22	AAM86713	Human colon cancer
698	6	1.2	38	22	AAW60745	Human secreted pro	771	6	1.2	52	22	AAO03436	Human polypeptide
699	6	1.2	38	23	ABG44975	Human peptide enco	772	6	1.2	52	23	ABP26180	Streptococcus poly
700	6	1.2	38	23	AAW47896	Zinc finger protei	773	6	1.2	52	23	ABP26181	Streptococcus poly
701	6	1.2	40	10	AAW90808	N-terminal sequenc	774	6	1.2	53	21	AAB53997	Human colon cancer
702	6	1.2	41	22	AAW68296	Plasmid RED1-encod	775	6	1.2	53	21	AAB53998	Human colon cancer
703	6	1.2	41	22	AAW68296	Human bone marrow	776	6	1.2	53	21	AAB53999	Human colon cancer
704	6	1.2	41	23	ABG37843	Human peptide enco	777	6	1.2	53	21	AAB58425	Human ovarian anti
705	6	1.2	42	18	AAW34597	C-terminal "signal	778	6	1.2	53	22	AAU41231	Human ORFX protein
706	6	1.2	42	20	AAW02721	Human secreted pro	779	6	1.2	53	22	AAM84849	Human secreted pro
707	6	1.2	42	23	AAW50531	Anchor peptide seq	780	6	1.2	53	22	AAG76074	Propionibacterium
708	6	1.2	43	19	AAW74930	Human secreted pro	781	6	1.2	53	22	AAG77781	Human colon cancer
709	6	1.2	43	22	AAW71247	Human gene 5-encod	782	6	1.2	53	23	ABP42223	Human ovarian anti
710	6	1.2	43	22	AAW71277	Human gene 5-encod	783	6	1.2	53	23	ABP42819	Human colon cancer
711	6	1.2	43	22	AAW01241	Human gene 10 enco	784	6	1.2	53	23	ABP02592	Human ORFX protein
712	6	1.2	43	22	AAW01278	Human gene 10 enco	785	6	1.2	54	20	AAW78192	Human secreted pro
713	6	1.2	43	23	ABG63470	Human albumin fusi	786	6	1.2	54	21	AAB51724	Human secreted pro
714	6	1.2	43	23	ABG63471	Human albumin fusi	787	6	1.2	54	22	AAU50698	Propionibacterium
715	6	1.2	43	23	ABG63702	Human albumin fusi	788	6	1.2	54	22	AAU65073	Propionibacterium
716	6	1.2	43	23	ABG63703	Human albumin fusi	789	6	1.2	54	22	ABB03379	Human musculoskele
717	6	1.2	44	21	AAW64715	Human 5' EST relat	790	6	1.2	55	16	AAW80193	Internal portion o
718	6	1.2	44	22	ABG16321	Novel human diagn	791	6	1.2	55	19	AAW79444	Staphylococcus aur
719	6	1.2	44	23	AAW78527	N terminus of 11kD	792	6	1.2	55	21	AAB35778	Rat CART peptide f
720	6	1.2	45	19	AAW79315	Staphylococcus aur	793	6	1.2	55	21	AAB35782	Murine CART peptid
721	6	1.2	45	20	AAW41440	Fragment of human	794	6	1.2	55	21	AAG02879	Human secreted pro
722	6	1.2	45	22	AAW87000	Human immune/haema	795	6	1.2	55	22	ABG60250	Human ovarian anti
723	6	1.2	45	22	AAO13181	Human polypeptide	796	6	1.2	55	22	AAU63757	Propionibacterium
724	6	1.2	46	21	AAB38062	Fragment of human	797	6	1.2	55	22	AAU64206	Propionibacterium
725	6	1.2	46	21	AAW48490	Arabidopsis thalia	798	6	1.2	55	22	ABB39033	Peptide #6539 enco
726	6	1.2	46	22	ABB41398	Peptide #8904 enco	799	6	1.2	55	22	ABB40396	Peptide #7902 enco
727	6	1.2	46	22	AAW62268	Human brain expres	800	6	1.2	55	22	ABB23977	Protein #5976 enco
728	6	1.2	46	22	AAW75072	Human bone marrow	801	6	1.2	55	22	ABB24768	Human reproductive
729	6	1.2	46	22	AAW86213	Human immune/haema	802	6	1.2	55	22	AAW94384	Human brain expres
730	6	1.2	46	22	AAW35190	Peptide #9227 enco	803	6	1.2	55	22	AAW59687	Human brain expres
731	6	1.2	47	13	AAW20963	Sequence of human	804	6	1.2	55	22	AAW61204	Human bone marrow
732	6	1.2	47	19	AAW59847	Anchoring sequence	805	6	1.2	55	22	AAW72263	Peptide #5956 enco
733	6	1.2	47	22	ABB31222	Peptide #3873 enco	806	6	1.2	55	22	AAW73923	Peptide #6593 enco
734	6	1.2	47	22	ABB36429	Peptide #3935 enco	807	6	1.2	55	22	AAW19522	Peptide #6559 enco
735	6	1.2	47	22	AAW57187	Human brain expres	808	6	1.2	55	22	AAW20159	Peptide #8139 enco
736	6	1.2	47	22	AAW69592	Human bone marrow	809	6	1.2	55	22	AAW32522	Peptide #8139 enco
737	6	1.2	47	22	AAW29928	Peptide #3965 enco	810	6	1.2	55	22	AAW34102	Human secreted pro
738	6	1.2	47	22	AAW05091	Peptide #3773 enco	811	6	1.2	55	23	AAB90584	Novel ovarian rela
739	6	1.2	47	23	ABG39213	Human peptide enco	812	6	1.2	55	23	ABG61721	Human albumin fusi
740	6	1.2	47	23	AAU10577	Human placental al	813	6	1.2	55	23	ABG65465	

814	6	1.2	55	23	ABG42078	Human peptide enco	887	6	1.2	66	22	AAM03819	Peptide #2501 enco
815	6	1.2	55	23	ABG43811	Human peptide enco	888	6	1.2	66	23	ABG37807	Human peptide enco
816	6	1.2	56	21	AAG01468	Human secreted pro	889	6	1.2	67	22	ABB67943	Drosophila melanog
817	6	1.2	56	22	AAU47306	Propionibacterium	890	6	1.2	67	22	ABG27225	Novel human diagno
818	6	1.2	56	22	AAU20338	Human novel endocr	891	6	1.2	67	22	ABB30615	Peptide #3266 enco
819	6	1.2	56	22	AAM85195	Human immune/haema	892	6	1.2	67	22	ABB35779	Peptide #3285 enco
820	6	1.2	56	22	ABP60781	Scorpion leiuropep	893	6	1.2	67	22	ABB17373	Human nervous syst
821	6	1.2	56	23	ABP34242	Human ORF3215 prot	894	6	1.2	67	22	ABB21202	Human brain expres
822	6	1.2	57	21	ABAB32846	Eucalyptus grandis	895	6	1.2	67	22	AAM56587	Human bone marrow
823	6	1.2	57	22	ABB42299	Peptide #9805 enco	896	6	1.2	67	22	AAM68968	Peptide #3314 enco
824	6	1.2	57	22	ABAB25802	Protein #7801 enco	897	6	1.2	67	22	AAM16795	Peptide #3229 enco
825	6	1.2	57	22	AAM63185	Human brain expres	898	6	1.2	67	22	AAM29277	Peptide #3195 enco
826	6	1.2	57	22	AAM75999	Human bone marrow	899	6	1.2	67	22	AAM04513	Peptide #4636 enco
827	6	1.2	57	22	AAM23573	Human EST encoded	900	6	1.2	67	23	ABG38553	Human peptide enco
828	6	1.2	57	22	AAM36107	Peptide #10144 enc	901	6	1.2	67	23	ABP03159	Human ORFX protein
829	6	1.2	57	23	ABG45406	Human peptide enco	902	6	1.2	67	23	ABB49594	Listeria monocytog
830	6	1.2	57	23	ABP02519	Human ORFX protein	903	6	1.2	68	21	AAV84596	Fragment of human
831	6	1.2	58	20	AAV59754	Human normal ovari	904	6	1.2	68	22	ABB31892	Peptide #4543 enco
832	6	1.2	58	22	AAU47118	Propionibacterium	905	6	1.2	68	22	ABB37130	Peptide #4636 enco
833	6	1.2	58	22	AAU18640	Human lung antigen	906	6	1.2	68	22	ABB22441	Protein #4440 enco
834	6	1.2	58	23	ABP31864	Human glycoprotein	907	6	1.2	68	22	AAM80954	Human haematologic
835	6	1.2	59	13	AAAR27732	SalF20.5R. Vaccin	908	6	1.2	68	22	AAM57849	Human brain expres
836	6	1.2	59	14	AAAR43264	RGAI N-terminal.	909	6	1.2	68	22	AAM70267	Human bone marrow
837	6	1.2	59	22	AAU20680	Human novel foetal	910	6	1.2	68	22	AAM18095	Peptide #4529 enco
838	6	1.2	59	22	AAU94522	Human reproductive	911	6	1.2	68	22	AAM32699	Human EST encoded
839	6	1.2	59	22	AAAM87918	Human immune/haema	912	6	1.2	68	22	AAM30604	Peptide #4641 enco
840	6	1.2	59	23	ABP42252	Human ovarian anti	913	6	1.2	68	22	AAAM05730	Peptide #4412 enco
841	6	1.2	59	23	ABP02996	Human ORFX protein	914	6	1.2	68	23	ABG39911	Human peptide enco
842	6	1.2	59	23	AAU80947	Caulobacter cresce	915	6	1.2	68	23	ABP03696	Human ORFX protein
843	6	1.2	60	19	AAU98556	H. pylori GHPO 167	916	6	1.2	68	23	ABP07588	Human ORFX protein
844	6	1.2	60	22	AAU54616	Propionibacterium	917	6	1.2	68	23	ABP09809	Human ORFX protein
845	6	1.2	60	22	AAU62553	Propionibacterium	918	6	1.2	68	23	ABB54500	Lactococcus lactis
846	6	1.2	60	22	AAAM87965	Human immune/haema	919	6	1.2	69	21	AAAG17411	Arabidopsis thalia
847	6	1.2	60	22	AAAO07148	Human polypeptide	920	6	1.2	69	22	AAAM99898	Human excretory re
848	6	1.2	60	22	AAAB69147	M. catarrhalis str	921	6	1.2	69	22	AAAM43697	Human bladder anti
849	6	1.2	61	21	AAAG20221	Arabidopsis thalia	922	6	1.2	69	23	ABP00667	Human ORFX protein
850	6	1.2	61	21	AAAG00525	Human secreted pro	923	6	1.2	70	21	AAAB53996	Human colon cancer
851	6	1.2	61	21	AAAG03465	Human secreted pro	924	6	1.2	70	21	AAAG18531	Zea mays protein f
852	6	1.2	61	22	AAU56087	Propionibacterium	925	6	1.2	70	22	ABG18828	Novel human diagno
853	6	1.2	61	22	AAAO10476	Human polypeptide	926	6	1.2	70	22	AAAM24095	Human EST encoded
854	6	1.2	61	23	ABBP33124	Human ORF2097 prot	927	6	1.2	70	23	ABP42243	Human ovarian anti
855	6	1.2	62	21	AAAG37069	Arabidopsis thalia	928	6	1.2	71	19	AAAM60973	Streptococcus pneu
856	6	1.2	62	21	AAAY86274	Human secreted pro	929	6	1.2	71	21	AAAG25363	Arabidopsis thalia
857	6	1.2	62	22	ABG01887	Novel human diagno	930	6	1.2	71	22	AAU45743	Propionibacterium
858	6	1.2	62	22	AAAB63837	Human prostate can	931	6	1.2	71	22	AAU64516	Propionibacterium
859	6	1.2	62	23	ABP09488	Human ORFX protein	932	6	1.2	71	22	AAAM91322	Human immune/haema
860	6	1.2	63	20	AAAY29800	Human GABA B recep	933	6	1.2	72	13	AAAR25119	Non-A, Non-B Hepat
861	6	1.2	63	20	AAAY29801	Human GABA B recep	934	6	1.2	72	21	AAAG20172	Arabidopsis thalia
862	6	1.2	63	20	AAAY29802	Human GABA B recep	935	6	1.2	72	22	AAU62168	Propionibacterium
863	6	1.2	63	20	AAAY29803	Human GABA B recep	936	6	1.2	72	22	AAU02065	Synthetic human ta
864	6	1.2	63	22	AAU42008	Propionibacterium	937	6	1.2	72	23	ABP05481	Human ORFX protein
865	6	1.2	63	22	AAU50416	Propionibacterium	938	6	1.2	73	17	AAAM04202	Peptide encoded by
866	6	1.2	63	22	AAU57838	Propionibacterium	939	6	1.2	73	17	AAAM04190	Peptide encoded by
867	6	1.2	63	22	AAU59994	Propionibacterium	940	6	1.2	73	17	AAAM04199	Peptide encoded by
868	6	1.2	63	22	AAOI2008	Human polypeptide	941	6	1.2	73	21	AAAB34462	Human secreted pro
869	6	1.2	64	21	AAAB39473	Human secreted pro	942	6	1.2	73	21	AAAG43580	Arabidopsis thalia
870	6	1.2	64	21	AAAB38199	Human secreted pro	943	6	1.2	73	22	AAU45304	Propionibacterium
871	6	1.2	64	22	AAU47819	Propionibacterium	944	6	1.2	73	22	ABG03752	Novel human diagno
872	6	1.2	64	22	AAO07361	Human polypeptide	945	6	1.2	73	23	ABP33587	Human protease-1lk
873	6	1.2	64	22	AAAB60687	Human polypeptide	946	6	1.2	73	23	ABP05087	Human ORFX protein
874	6	1.2	65	21	AAAB45293	PTTOSAI APE-encode	947	6	1.2	73	23	ABP10788	Human ORFX protein
875	6	1.2	65	21	AAAB45294	Sequence #7 homolo	948	6	1.2	74	22	AAU53361	Propionibacterium
876	6	1.2	65	21	AAAG00484	Human secreted pro	949	6	1.2	74	22	AAAM83188	Human immune/haema
877	6	1.2	65	23	ABP04162	Human ORFX protein	950	6	1.2	74	22	AAO07082	Human polypeptide
878	6	1.2	66	20	AAAY74034	Human prostate tum	951	6	1.2	75	21	AAAB35777	Rat CART peptide f
879	6	1.2	66	21	AAAB42112	Human ORFX ORF1876	952	6	1.2	75	21	AAAB35781	Murine CART peptid
880	6	1.2	66	21	AAAG32863	Zea mays protein f	953	6	1.2	75	21	AAAB08492	Amino acid sequenc
881	6	1.2	66	22	ABBB29901	Peptide #2552 enco	954	6	1.2	75	22	AAAM99788	Human excretory re
882	6	1.2	66	22	ABBB20496	Protein #2495 enco	955	6	1.2	75	22	AAAG67855	Human leukemia vi
883	6	1.2	66	22	AAAM55895	Human brain expres	956	6	1.2	75	22	AAO08074	Human polypeptide
884	6	1.2	66	22	AAAM68269	Human bone marrow	957	6	1.2	75	22	AAAM42603	Human kidney relat
885	6	1.2	66	22	AAAM16091	Peptide #2525 enco	958	6	1.2	76	21	AAAG12275	Zea mays protein f
886	6	1.2	66	22	AAAM28582	Peptide #2619 enco	959	6	1.2	76	22	AAU67129	Propionibacterium

960	6	1.2	76	22	ABG05836	Novel human diagno
961	6	1.2	76	23	ABP03498	Human ORFX protein
962	6	1.2	77	19	AAW44726	Amino acid sequenc
963	6	1.2	77	22	AAW90374	Human immune/haema
964	6	1.2	77	22	AAO10251	Human polypeptide
965	6	1.2	77	23	ABP02872	Human ORFX protein
966	6	1.2	78	19	AAW98260	H. pylori GHPO 144
967	6	1.2	78	21	AAW33208	Pinus radiata tran
968	6	1.2	79	22	AAW04846	Human SGP003 parti
969	6	1.2	79	23	ABP00842	Human ORFX protein
970	6	1.2	79	23	ABP05175	Human ORFX protein
971	6	1.2	80	21	AAW42338	Human ORFX ORF2102
972	6	1.2	80	22	ABG00065	Novel human diagno
973	6	1.2	80	22	ABG11887	Novel human diagno
974	6	1.2	80	22	ABG17171	Novel human diagno
975	6	1.2	80	22	AAW20323	Human novel endocr
976	6	1.2	80	22	AAW85491	Human immune/haema
977	6	1.2	80	23	ABP43203	Human ovartian anti
978	6	1.2	80	23	ABP08150	Human ORFX protein
979	6	1.2	81	22	AAO03474	Human polypeptide
980	6	1.2	81	22	AAO06868	Human polypeptide
981	6	1.2	82	18	AAW28194	Amino acid sequenc
982	6	1.2	82	19	AAW21011	Human glial fibril
983	6	1.2	82	20	AAW35995	Extended human sec
984	6	1.2	82	20	AAW88606	Secreted protein e
985	6	1.2	82	21	AAW12159	Hydrophobic domain
986	6	1.2	82	21	AAW28196	Human artemin neur
987	6	1.2	82	22	ABW31944	Peptide #4595 enco
988	6	1.2	82	22	ABW37183	Peptide #4689 enco
989	6	1.2	82	22	ABW50373	Human secreted pro
990	6	1.2	82	22	ABW22487	Protein #4486 enco
991	6	1.2	82	22	AAW57895	Human brain expres
992	6	1.2	82	22	AAW70313	Peptide #4585 enco
993	6	1.2	82	22	AAW18151	Human bone marrow
994	6	1.2	82	22	AAW30654	Human protein sequ
995	6	1.2	82	22	AAW55544	Peptide #4691 enco
996	6	1.2	82	22	AAW05777	Peptide #4459 enco
997	6	1.2	82	23	ABG39957	Human peptide enco
998	6	1.2	83	20	AAW78170	Human secreted pro
999	6	1.2	83	22	AAW44883	Propionibacterium
1000	6	1.2	83	22	ABG28088	Novel human diagno

ALIGNMENTS

RESULT 1
AAW61362
ID AAW61362 standard; Protein; 518 AA.
XX AC AAW61362;
XX DT 25-SEP-1998 (first entry)
XX DE Aspartic proteinase ASP1.
XX KW ASP1; Aspartic proteinase; Alzheimer's disease; cancer; melanoma.
XX OS Homo sapiens.
XX PN EP848062-A2.
XX PD 17-JUN-1998.
XX PF 01-DEC-1997; 97EP-0309648.
XX PR 14-DEC-1996; 96GB-0026022.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PA (SMIK) SMITHKLINE BEECHAM PLC.
XX PI Chapman CG, Evans JR, Powell DJ, Southan C;
XX

DR WPI; 1998-314477/28.
DR N-PSDB; AAV27962.
XX
PT New isolated polynucleotide encodes Aspartic protease polypeptide -
PT used to diagnosis, treat and vaccinate against Alzheimer's disease,
PT cancer and melanoma
XX
PS Claim 11; Page 7; 19pp; English.
XX
CC The human ASP1 protein is structurally related to other proteins of the
CC Aspartic proteinase family. ASP 1 polypeptides and polynucleotides can
CC be used to diagnosis, treat and vaccinate against Alzheimer's disease,
CC cancer and melanoma.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 19; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGALRALLLPLLAQWLRAPELAPAPFTLPLRVAAATNRVAPTPGPGTAEHRHADGL	60
DB	1	MGALARALLPLLAQWLRAPELAPAPFTLPLRVAAATNRVAPTPGPGTAEHRHADGL	60
QY	61	ALALEPALASPAGAAFLAWDNLQDSDGRGYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
DB	61	ALALEPALASPAGAAFLAWDNLQDSDGRGYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
QY	121	TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTFVGEDLVTI PKGFNTSFLVNIATI	180
DB	121	TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTFVGEDLVTI PKGFNTSFLVNIATI	180
QY	181	FESSENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA	240
DB	181	FESSENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA	240
QY	241	GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCEYNADKA	300
DB	241	GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCEYNADKA	300
QY	301	IYDSGTTLLRLPQKVFDAVEAVARASLIPFSDGFWTGSQACWTNSETPWSYFPKISI	360
DB	301	IYDSGTTLLRLPQKVFDAVEAVARASLIPFSDGFWTGSQACWTNSETPWSYFPKISI	360
QY	361	YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYIFD	420
DB	361	YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYIFD	420
QY	421	RAQKRVGAASPCAIEIAGAASEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG	480
DB	421	RAQKRVGAASPCAIEIAGAASEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG	480
QY	481	AILLVILVLLLPFRCCQRRPRDPEVVNDESSLVRHRWK	518
DB	481	AILLVILVLLLPFRCCQRRPRDPEVVNDESSLVRHRWK	518

RESULT 2
AAW41714
ID AAY41714 standard; Protein; 518 AA.
XX AC AAY41714;
XX DT 07-DEC-1999 (first entry)
XX DE Human PRO852 protein sequence.
XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX OS Homo sapiens.
XX

348

PN WO9946281-A2.
XX 16-SEP-1999.
PD 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.

PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34056.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX
PS Claim 12; Fig 73; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPTPAERHADGL 60

QY 61 ALALEPALASPAGANFLAMVDNLQGDGGRGYILEMLICTPPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQGDGGRGYILEMLICTPPQKLQILVDTGSSNFAVAG 120

QY 121 TPHSYIDTYFDTERSSITYRSKGFVDVTWKYTOGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSITYRSKGFVDVTWKYTOGSWTGFVGEDLVITPKGFNTSFLVNIATI 180

QY 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFEDSLVTOANIPNVFSMCGAGLPVA 240
Db 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFEDSLVTOANIPNVFSMCGAGLPVA 240

QY 241 GSGTNGGSLVLTGIEPISLYKGDIMWYTPIKEENWYQIEILKLEIGGQSLNDCREYNADKA 300
Db 241 GSGTNGGSLVLTGIEPISLYKGDIMWYTPIKEENWYQIEILKLEIGGQSLNDCREYNADKA 300

QY 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATWMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATWMEGFYVIFD 420
QY 421 RAQKRVGAASPCAETIAGAAVSEISGFSTEDVASNVCVPAQSLSEPIILMIVSYALMSVCG 480
Db 421 RAQKRVGAASPCAETIAGAAVSEISGFSTEDVASNVCVPAQSLSEPIILMIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518
Db 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518

RESULT 3

AYY22239
ID AAY22239 standard; Protein; 518 AA.
XX
AC AAY22239;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human CSP56, aspartyl-typse protease, protein sequence.
XX
KW Metastatic marker protein; human; cancer metastasis; breast cancer;
KW colon cancer; diagnosis; therapy; tumour; metastatic potential;
KW CSP56; aspartyl-typse protease.
XX
OS Homo sapiens.
XX
PN WO9934004-A2.
XX
PD 08-JUL-1999.

XX
PF 24-DEC-1998; 98WO-US27608.
XX
PR 31-DEC-1997; 97US-0070112.
XX
PA (CHIR) CHIRON CORP.
XX
PI Giese K, Xin H;
XX
DR WPI; 1999-430248/36.
DR N-PSDB; AAX84708.

XX
PT New polynucleotides associated with cancer metastasis
XX
PS Claim 4; Page 78-80; 80pp; English.
XX
CC This sequence represents a polypeptide of the invention, and is
CC an aspartyl-typse protease, designated CSP56. The polynucleotides (PNS) of
CC the invention encode metastatic marker protein variants. The PNS and
CC polypeptides can be used as markers for cancer metastasis. The products
CC can be used for identifying metastatic tissue or metastatic potential of
CC a tissue, e.g. breast or colon tissue. They can also be used for
CC screening test compounds for the ability to suppress the metastatic
CC potential of a tumour. The products can be used for developing products
CC for the therapy of cancers, particularly breast or colon cancer.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLAOWLLRAAPBLAPFTLPRVAATAATNRVVAFTPGPGTPAERHADGL 60
Db 1 MGALARALLPLAOWLLRAAPBLAPFTLPRVAATAATNRVVAFTPGPGTPAERHADGL 60

QY 61 ALALEPALASPAAGANFLAMVDNLQDSDGGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120

Db 61 ALALEPALASPAAGANFLAMVDNLQDSDGGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERRSSTYRSKGFVDVTVKYTGSGWTFVGEDLVTIIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERRSSTYRSKGFVDVTVKYTGSGWTFVGEDLVTIIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGIIGLAYATLAKPSSSLETFEDSLVTOANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGIIGLAYATLAKPSSSLETFEDSLVTOANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDGREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDGREYNADKA 300
QY 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATWMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATWMEGFYVIFD 420
QY 421 RAQKRVGAASPCAETIAGAAVSEISGFSTEDVASNVCVPAQSLSEPIILMIVSYALMSVCG 480
Db 421 RAQKRVGAASPCAETIAGAAVSEISGFSTEDVASNVCVPAQSLSEPIILMIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518
Db 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518

RESULT 4

AYY13799
ID AAY13799 standard; Protein; 518 AA.
XX
AC AAY13799;
XX
DT 21-SEP-1999 (first entry)
XX
DE Human aspartyl protease, CSP56.
XX
KW CSP56; human; aspartyl protease; diagnosis; neoplasia; tumour;
KW breast tumour; colon tumour.
XX
OS Homo sapiens.
XX
PN WO9933963-A1.
XX
PD 08-JUL-1999.

XX
PF 14-DEC-1998; 98WO-US26547.
XX
PR 31-DEC-1997; 97US-0070112.
XX
PA (CHIR) CHIRON CORP.

XX
PI Giese KW, Xin H;
XX
DR WPI; 1999-430240/36.
DR N-PSDB; AAX89297.

XX
PT Human CSP56 protein for diagnosis of neoplasia
XX
PS Claim 2; Fig 2A; 51pp; English.
XX
CC This represents a human Csp56 protein, a novel aspartyl protease. The
CC CSP56 protein can be used in methods for diagnosing neoplasia, for
CC determining the metastatic potential of a tumour, and for screening test
CC compounds for the ability to suppress the metastatic potential of a
CC tumour. The tumours are preferably from breast or colon.

QY Sequence 518 AA;

Query Match 100.0%; Score 518; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPFTLLPLRVAATNRVVAFTPGPTPAERHADGL 60
1 MGALARALLPLLAQWLLRAAPELAPFTLLPLRVAATNRVVAFTPGPTPAERHADGL 60
Db 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKLIIVDTGSSNFAVAG 120
61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKLIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDIMWTPIKEEWYQIEILKLEIGQSINLDCREYNADKA 300
241 GSGTNGSLVLGGIEPSLYKGDIMWTPIKEEWYQIEILKLEIGQSINLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDIMWTPIKEEWYQIEILKLEIGQSINLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
361 YLRDENSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAPASPCAEIAGAASEISGPFSTEDVASNCVPAQSLSEPIIIVSYALMSVCG 480
421 RAQKRVGFAPASPCAEIAGAASEISGPFSTEDVASNCVPAQSLSEPIIIVSYALMSVCG 480
Db 421 RAQKRVGFAPASPCAEIAGAASEISGPFSTEDVASNCVPAQSLSEPIIIVSYALMSVCG 480
QY 481 AILLVILVLLLPFCQRRPRDPEVNDDESSLVRHRWK 518
481 AILLVILVLLLPFCQRRPRDPEVNDDESSLVRHRWK 518
Db 481 AILLVILVLLLPFCQRRPRDPEVNDDESSLVRHRWK 518

RESULT 5
AAB44270
ID AAB44270 standard; Protein; 518 AA.
XX
AC AAB44270;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
XX expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Gertsen ME; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Hillan KJ; Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78500.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
PT
XX
PS Claim 12; Fig 73; 636bp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytosstatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting CC can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
CC
XX
SQ Sequence 518 AA;
QY
Query Match 100.0%; Score 518; DB 21; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLLAQWLLRAAPELAPFTLLPLRVAATNRVVAFTPGPTPAERHADGL 60
1 MGALARALLPLLAQWLLRAAPELAPFTLLPLRVAATNRVVAFTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPFTLLPLRVAATNRVVAFTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKLIIVDTGSSNFAVAG 120
61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKLIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDIMWTPIKEEWYQIEILKLEIGQSINLDCREYNADKA 300
241 GSGTNGSLVLGGIEPSLYKGDIMWTPIKEEWYQIEILKLEIGQSINLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDIMWTPIKEEWYQIEILKLEIGQSINLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
361 YLRDENSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAPASPCAEIAGAASEISGPFSTEDVASNCVPAQSLSEPIIIVSYALMSVCG 480
421 RAQKRVGFAPASPCAEIAGAASEISGPFSTEDVASNCVPAQSLSEPIIIVSYALMSVCG 480

Db 421 RAQKRVGFASPCAEIAGAAVSEISGFSTEDVASNVCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518
Db 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518

RESULT 6
AAE10628
ID AAY88424 standard; Protein; 518 AA.
XX
AC AAY88424;
XX
DT 03-AUG-2000 (first entry)
XX

DE Human aspartyl protease 1 (Asp1) amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;
KW Alzheimer's disease; beta secretase site.
XX

OS Homo sapiens.
XX
PN WO200017369-A2.
XX

PD 30-MAR-2000.
XX

PF 23-SEP-1999; 99WO-US20881.
XX

PR 24-SEP-1998; 98US-0101594.
XX

PA (PHAA) PHARMACIA & UPJOHN CO.
XX

PI Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;
XX

DR WPI; 2000-303209/26.
XX

DR N-PSDB; AAA15661.
XX

PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at
PT the beta secretase site to produce amyloid beta peptide -
XX
PS Claim 54; Fig 1; 183pp; English.

XX
CC This sequence represents the human aspartyl protease amino acid sequence.
CC The invention relates to a protease capable of cleaving the beta
CC secretase site of amyloid precursor protein (APP). The protease contains
CC a sequence encoding the amino acid sequence DTG and a sequence encoding
CC DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
CC causes an autosomal dominant form of Alzheimer's disease. APP localises
CC to the cell surface membrane and have a single C-terminal transmembrane
CC domain. Proteolytic processing of APP produces the amyloid beta protein,
CC which is possibly very important in Alzheimer's disease. The invention
CC includes a nucleotide sequence encoding the protease, a vector containing
CC the nucleotide sequence, and a cell line comprising the vector. Methods
CC for screening for inhibitors of beta secretase activity are also given in
CC the invention. The human aspartase protein and nucleotide sequences and
CC the methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease.
XX

SO Sequence 518 AA;

Query Match 100.0%; Score 518; DB 21; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLLPILAQWLLRAAPELAPAPFTPLLRVAAATNRVAVPTPGGTPAERHADGL 60
Db 1 MGALARALLLPILAQWLLRAAPELAPAPFTPLLRVAAATNRVAVPTPGGTPAERHADGL 60

QY 61 ALALEPALASPAGANFLAMVDNLQDGSGRGYLLEMLIGTPPOKQLIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDGSGRGYLLEMLIGTPPOKQLIVDTGSSNFAVAG 120

QY 121 TPHSYIDTYFDTERSSYYRSKGFDTVTKYQTQGSWTGVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSYYRSKGFDTVTKYQTQGSWTGVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVEDAVEAVARASLIPEFSDGFWTGSQACWTSNSETPWSYFPKISI 360
Db 301 IVDSGTTLLRLPQKVEDAVEAVARASLIPEFSDGFWTGSQACWTSNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFASPCAEIAGAAVSEISGFSTEDVASNVCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPCAEIAGAAVSEISGFSTEDVASNVCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518
Db 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518

RESULT 7
AAE10628
ID AAE10628 standard; Protein; 518 AA.
XX
AC AAE10628;
XX

DT 10-DEC-2001 (first entry)
XX

DE Human aspartyl protease 1 (hu-Asp1) protein.
XX

XX
KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW chromosome 21.
XX

OS Homo sapiens.
XX

XX
FH Key Location/Qualifiers
FH Peptide 1..20
FT /label= signal_peptide
FT Protein 21..518
FT /note= "Mature human aspartyl protease 1"
FT Domain 469..492
FT /label= Transmembrane_domain

GB2357767-A.
XX

04-JUL-2001.
XX

22-SEP-2000; 2000GB-0023315.
XX

23-SEP-1999; 99US-0155493.
XX

23-SEP-1999; 99US-0404133.
XX

23-SEP-1999; 99WO-US20881.
XX

13-OCT-1999; 99US-0416901.
XX

06-DEC-1999; 99US-0169232.
XX

(PHAA) PHARMACIA & UPJOHN CO.
XX

Bienkowski MJ, Gurney M;
XX

WPI; 2001-444208/48.
XX

N-PSDB; AAD17864.
XX

Polypeptide comprising fragments of human aspartyl protease with amyloid precursor protein processing activity and alpha-secretase activity, for identifying modulators useful in treating Alzheimer's disease -

Claim 36, Fig 1; 187bp; English.

The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1 proteins which lack transmembrane domain or amino terminal domain or cytoplasmic domain and retains alpha-secretase activity and amyloid protein precursor (APP) processing activity. The proteins of the invention are useful for assaying hu-Asp1 alpha-secretase activity, which in turn is useful for identifying modulators of hu-Asp1 alpha-secretase activity, where modulators that increase hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's disease (AD) which causes progressive dementia with consequent formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with the substrate under acidic conditions and determining the level of hu-Asp1 proteolytic activity. The present sequence is Asp1 protein from human. Asp1 gene is localised on chromosome 21.

Query Match	100.0%;	Score 518;	DB 22;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 518; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MGALARALLPLLAQWLLRAAPELAPFTLLPLRVAATNRVAPTPGPTPAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAAPELAPFTLLPLRVAATNRVAPTPGPTPAERHADGL	60
QY	61	ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPQKLQILVTGSSNFAVAG	120
Db	61	ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPQKLQILVTGSSNFAVAG	120
QY	121	TPHSYIDTYFDTERSSTYRSKGFVTVYKYTQGSWTGFVGEDLVITPKGNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFVTVYKYTQGSWTGFVGEDLVITPKGNTSFLVNIATI	180
QY	181	FESENFPLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANI PNVSQMCGAGLPVA	240
Db	181	FESENFPLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANI PNVSQMCGAGLPVA	240
QY	241	GSGTNGGSLVLGGIEPSLYKGDIMWTPIKEEMWYQI EILKLEIGGQSLNDCREYNADKA	300
Db	241	GSGTNGGSLVLGGIEPSLYKGDIMWTPIKEEMWYQI EILKLEIGGQSLNDCREYNADKA	300
QY	301	IYDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDFWGTGSQLA CWTNSETPWSYFPKISI	360
Db	301	IYDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDFWGTGSQLA CWTNSETPWSYFPKISI	360
QY	361	YLRDENSSRSFRITILPOLYIQPMNGAGLNYECYRFGISPTNALVIGATWMEGFYVIFD	420
Db	361	YLRDENSSRSFRITILPOLYIQPMNGAGLNYECYRFGISPTNALVIGATWMEGFYVIFD	420
QY	421	RAQKRVGFAASPCAETAGAAVSEISGPFSTEDVASNCVPAQSLSEPIMLWTSYALMSVCG	480
Db	421	RAQKRVGFAASPCAETAGAAVSEISGPFSTEDVASNCVPAQSLSEPIMLWTSYALMSVCG	480
QY	481	AILLVLIVLLLLPFRCCQRRPRDPEVYNDESSLVRHRWK	518
Db	481	AILLVLIVLLLLPFRCCQRRPRDPEVYNDESSLVRHRWK	518

RESULT 8
AAE10656
ID AAE10656 standard; Protein; 518 AA.
XX
AC AAE10656;
XX

DT	10-DEC-2001	(first entry)
XX		
DE	Human-Asp 1 protein lacking TM domain and containing (His)6 tag.	
XX		
KW	Human; aspartyl protease 1; Aspi; amyloid precursor protein; APP;	
KW	Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;	
KW	amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	GB2357767-A.	
XX		
PD	04-JUL-2001.	
XX		
PF	22-SEP-2000; 2000GB-0023315.	
XX		
PR	23-SEP-1999; 99US-0155493.	
PR	23-SEP-1999; 99US-0404133.	
PR	23-SEP-1999; 99WO-US20881.	
PR	13-OCT-1999; 99US-0416901.	
PR	06-DEC-1999; 99US-0169232.	
XX		
PA	(PHAA) PHARMACIA & UPJOHN CO.	
XX		
PI	Bienkowski MJ, Gurney M;	
XX		
DR	DPI; 2001-444208/48.	

PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
PS Example 14; Page 155-156; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human Asp 1
CC protein lacking a transmembrane (TM) domain and containing (His) 6
CC tag. This sequence is generated from human Asp 1 protein by the
CC deletion of its C-terminal TM domain and addition of hexa-histidine
CC tag at its C-terminus.

Query Match	100.0%;	Score 518;	DB 22;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 518; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	MGALARALLLPILAQWLLRAAPELAPFTLLPLRVAATNRVVAPTPPGPGTPAERHADGL	60
Dd	1	MGALARALLLPILAQWLLRAAPELAPFTLLPLRVAATNRVVAPTPPGPGTPAERHADGL	60
OY	61	ALALEPALASPAGANFLAMVDNIQGDSGRGYLLEMLIGTEPQKLQILVDTGSSNFAVAG	120
Dd	61	ALALEPALASPAGANFLAMVDNIQGDSGRGYLLEMLIGTEPQKLQILVDTGSSNFAVAG	120
OY	121	TPHSYIDTYEDTERSSSTYSKGFDTVTKYTQGSWTGVGEDLVTIIPKGNTSFLVNIAATI	180
Dd	121	TPHSYIDTYEDTERSSSTYSKGFDTVTKYTQGSWTGVGEDLVTIIPKGNTSFLVNIAATI	180

QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTOANIPNVFSMOMCGAGLPVA 240
|||
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTOANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPRIKEEMWYQIIEILKLEIGQSINLDCREYNADKA 300
|||
Db 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPRIKEEMWYQIIEILKLEIGQSINLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
|||
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMWAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
|||
Db 361 YLRDENSSRSFRITILPOLYIQPMWAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAIEIAGA VSEISGPFSTEDVASNCVPAQSLSEPIIMIVSYALMSVCG 480
|||
Db 421 RAQKRVGFPAASPCAIEIAGA VSEISGPFSTEDVASNCVPAQSLSEPIIMIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518
|||
Db 481 AILLVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518

RESULT 9
AAU29059
ID AAU29059 standard; Protein; 518 AA.
XX
AC AAU29059;
XX

DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #36.

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX Homo sapiens.

XX WO200168848-A2.

XX PD 20-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.

PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

XX (GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-602746/68.
DR N-PSDB; AAS45960.

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -

PS Claim 11; Fig 72; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

XX SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAAPELAPAPFTLPLRVAATNRVAVPTPGPTPAERHADGL 60
|||
Db 1 MGALARALLPLLAQWLRAAPELAPAPFTLPLRVAATNRVAVPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYYLEMLICTPPQKLQILVDTGSSNFAVAG 120
|||
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYYLEMLICTPPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSITYRSKGFDTVTKYTQGSWTFVGEDLVITPKGFNTSFLVNIATI 180
|||
Db 121 TPHSYIDTYFDTERSSITYRSKGFDTVTKYTQGSWTFVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTOANIPNVFSMOMCGAGLPVA 240
|||
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTOANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPRIKEEMWYQIIEILKLEIGQSINLDCREYNADKA 300
|||
Db 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPRIKEEMWYQIIEILKLEIGQSINLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360

Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFASPACAEIAGAAVSEISGFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPACAEIAGAAVSEISGFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFRCCRRPRDPEVNVNDESSLVHRWK 518
Db 481 AILLVLIVLLLLPFRCCRRPRDPEVNVNDESSLVHRWK 518
RESULT 10
AAE06858
ID AAE06858 standard; Protein; 518 AA.
XX
AC AAE06858;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human aspartyl protease 1 (Hu-Asp1) protein.
XX
KW Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy; chromosome 21.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= signal_peptide
FT 21..518
FT /note= "Mature human aspartyl protease 1 (Hu-Asp1)"
FT Domain 469..492
FT /label= Transmembrane_domain
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00799.
XX
PR 09-MAY-2001; 2001WO-IB00799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX
DR WPI: 2001-483072/52.
DR N-PSDB; AAD13020.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity
XX
PS Example 2; Fig 1; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,

CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is human aspartyl protease 1 (Hu-Asp1).
CC Hu-Asp 1 gene is localised on chromosome 21.
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 518; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLLAQWLIRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLIRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFVDVTVKYTGSGTWGVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFVDVTVKYTGSGTWGVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEYQIEILKLEIGGOSLNDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEYQIEILKLEIGGOSLNDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFASPACAEIAGAAVSEISGFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPACAEIAGAAVSEISGFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFRCCRRPRDPEVNVNDESSLVHRWK 518
Db 481 AILLVLIVLLLLPFRCCRRPRDPEVNVNDESSLVHRWK 518
RESULT 11
AAU06602
ID AAU06602 standard; Protein; 518 AA.
XX
AC AAU06602;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human Aspartyl protease 1 (Asp1).
XX
KW Human; Aspartyl protease; Asp1; Asp2; beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta.
XX
OS Homo sapiens.
XX
PN WO200149098-A2.
XX

PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00798.
XX
PR 09-MAY-2001; 2001WO-IB00798.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502549/55.
DR N-PSDB; AAS11516.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -

Example 2; Fig 1; 185bp; English.

XX
PS The invention relates to a purified polypeptide comprising a fragment of
XX mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridise to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is human Asp1.

XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVAVPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVAVPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDGGRGYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDGGRGYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTFYFDTERSTYRSKGFDTVKYQGSWTGFVEDLVTIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTFYFDTERSTYRSKGFDTVKYQGSWTGFVEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQCGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQCGAGLPVA 240
QY 241 GSGTNGGSLVVGIEPSLYKGDWYTPIKEMYQIILKLEIGGQSLNDCREYNADKA 300
Db 241 GSGTNGGSLVVGIEPSLYKGDWYTPIKEMYQIILKLEIGGQSLNDCREYNADKA 300

QY 301 IVDSGTLLRLPQKVEDAVEAVARASLIPEFSDGFWTGSQACWTNSETPMSYFPKISI 360
Db 301 IVDSGTLLRLPQKVEDAVEAVARASLIPEFSDGFWTGSQACWTNSETPMSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATWEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATWEGFYVIFD 420
QY 421 RAQKRVGFAASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFAASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 ALLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518
Db 481 ALLVLIVLLLLPFCQRRPRDPEVNVDESSLVHRWK 518

RESULT 12

AU07201
AAU07201 standard; Protein; 518 AA.

AC AAU07201;

DT 24-OCT-2001 (first entry)

XX Human aspartyl protease 1 (Asp-1).

XX Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease.

XX Homo sapiens.

XX WO200149097-A2.

PN 12-JUL-2001.

PD 09-MAY-2001; 2001WO-IB00797.

XX 09-MAY-2001; 2001WO-IB00797.

PR 09-MAY-2001; 2001WO-IB00797.

XX (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

XX WPI; 2001-502548/55.

DR N-PSDB; AAS11701.

XX Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

PT activity -

XX Example 2; Fig 1; 185bp; English.

PS The invention relates to a novel purified polypeptide comprising a
XX fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing
CC an APP cleavage site recognisable by a mammalian beta-secretase, and
CC further comprising two lysine residues at the carboxyl terminus of the
CC amino acid sequence of the mammalian APP or APP fragment. The
CC polypeptides are used for assaying for modulators of beta-secretase
CC activity; identifying agents that inhibit the APP processing activity
CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of

CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence represents the
CC amino acid sequence of human Asp-1.

XX Sequence 518 AA;

Query Match 100.0%; Score 518; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPRIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPRIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQLAQWTNSETPMSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQLAQWTNSETPMSYFPKISI 360
QY 361 YLRDENSRSRFRITILPOLYIOPMMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSRSRFRITILPOLYIOPMMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFASPACAIAGAASEISGPFSTEDVASNCVPAQSISEPIIMIVSYALMSVCG 480
Db 421 RAQKRVGFASPACAIAGAASEISGPFSTEDVASNCVPAQSISEPIIMIVSYALMSVCG 480
QY 481 AILLVLIVLILLPFCQRRPRDEEVNDESSLVRHRWK 518
Db 481 AILLVLIVLILLPFCQRRPRDEEVNDESSLVRHRWK 518

RESULT 13
AAE02580
ID AAE02580 standard; Protein; 518 AA.
XX

AC AAE02580;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human aspartyl protease 1 (Asp 1).
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;
KW beta-secretase; chromosome 21.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Signal_peptide
FT Peptide 22..62
FT /label= Asp_1_prepropeptide

FT Peptide 23..62
FT /label= Asp_1_propeptide
FT Protein 63..518
FT /label= Mature human_Asp_1_protein
FT /note= "Specifically claimed"
FT Active-site 87..89
FT /label= Active_site_1
FT Active-site 110..113
FT /label= Active_site_2
FT Active-site 303..305
FT /label= Active_site_3
FT Domain 469..492
FT Domain /label= Transmembrane_domain.
FT Domain 493..518
FT Region /label= Cytoplasmic_domain
FT /note= "Peptide #1"

PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US26080.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX

PI Gurney M, Bienkowski MJ;
XX
XX WPI; 2001-290516/30.
DR N-PSDB; AAD06738.
XX

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
protein, useful for the treatment of Alzheimer's disease -
XX
PS Claim 29; Fig 1; 189pp; English.

XX The present invention relates to enzymes for cleaving the alpha-
secretase site of the amyloid precursor protein (APP) and methods of
identifying those enzymes. The methods may be used to identify enzymes
that may be used to cleave the alpha-secretase cleavage site of the APP
protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human aspartyl protease 1
CC (Asp 1). Asp 1 has alpha-secretase protease and beta-secretase
CC protease activities. Asp 1 gene is located on chromosome 21.
XX

SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPRIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300

Db 241 GSGTNGSLVLGGIEPSLYKGDWYTPRIKEEMWYQIILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNDSSLVRHRWK 518
Db 481 AILLVLIVLLLLPFCQRRPRDPEVNDSSLVRHRWK 518

RESULT 14

AAE02608 standard; Protein; 518 AA.

AAE02608;

10-AUG-2001 (first entry)

Human Aspartyl protease-1 (Asp-1) deltatM (His)6 protein.

Human; alpha-secretase; amyloid precursor protein; APP; therapy; Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1; beta-secretase; Asp-1 deltatM (His)6 protein.

Homo sapiens.
OS Synthetic.

WO200123533-A2.

05-APR-2001.

22-SEP-2000; 2000WO-US26080.

23-SEP-1999; 99US-0155493.

23-SEP-1999; 99WO-US20881.

13-OCT-1999; 99US-0416901.

06-DEC-1999; 99US-0169232.

(PHAA) PHARMACIA & UPJOHN CO.

Gurney M, Bienkowski MJ;

WPI; 2001-290516/30.

Example 14; Page 183-184; 189pp; English.

The present invention relates to enzymes for cleaving the alpha-secretase site of the amyloid precursor protein (APP) and methods of identifying those enzymes. The methods may be used to identify enzymes that may be used to cleave the alpha-secretase cleavage site of the APP protein. The enzymes may be used to treat or modulate the progress of Alzheimer's disease. The present sequence is human Aspartyl protease-1 (Asp-1) deltatM (His)6 protein which is used for the expression of pre-pro-human-Aspartyl protease 1 (Asp1). This protein is obtained by replacing C-terminal transmembrane and cytoplasmic domains with a hexahistidine purification tag in the human Aspartyl protease 1.

Sequence 518 AA;

Query Match 100.0%; Score 518; DB 22; Length 518;

Best Local Similarity 100.0%; Pred. No. 0; Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAABELAPAFTLPLRVAATNRVVAFTPGPGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAABELAPAFTLPLRVAATNRVVAFTPGPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGSGRYILEMLIGTPPKQLIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGSGRYILEMLIGTPPKQLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSITYRSKGFDTVTKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSITYRSKGFDTVTKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFEDSLVTOANIPNVFSMQCGAGLPVA 240
Db 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFEDSLVTOANIPNVFSMQCGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDWYTPRIKEEMWYQIILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDWYTPRIKEEMWYQIILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNDSSLVRHRWK 518
Db 481 AILLVLIVLLLLPFCQRRPRDPEVNDSSLVRHRWK 518

RESULT 15

ABB78589 standard; Protein; 518 AA.

ABB78589;

16-JUL-2002 (first entry)

Human Asp-1 protein sequence SEQ ID NO:2.

Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease; proteolytic; chromosome 21.

Homo sapiens.

GB2367060-A.

27-MAR-2002.

29-OCT-2001; 2001GB-0025934.

23-SEP-1999; 99US-155493P.

23-SEP-1999; 99US-0404133.

23-SEP-1999; 99WO-US20881.

13-OCT-1999; 99US-0416901.

06-DEC-1999; 99US-169232P.

22-SEP-2000; 2000GB-0023315.

(PHAA) PHARMACIA & UPJOHN CO.

Bienkowski MJ, Gurney M;

WPI; 2002-396337/43.

DR N-PSDB; ABL52456.

XX Human aspartyl protease 1 substrates useful in assays to detect
PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT disease -
XX
XX
PS Claim 7; Fig 1; 182pp; English.

CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the
CC non-coding strand complementary to a defined 1804 nucleotide sequence
CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain; (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents hu-Asp1 from the present invention.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 23; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVAPTPPGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVAPTPPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNIQDSGRGYLLEMLIGTPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNIQDSGRGYLLEMLIGTPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSTYRSKGFDTVKYTOGSGMTGFGVEDLVTIPKGFNTSFLVNIAIT 180
Db 121 TPHSYIDTYFDTERSTYRSKGFDTVKYTOGSGMTGFGVEDLVTIPKGFNTSFLVNIAIT 180
QY 181 FESENFLLPGIKMNGILGLAVATLAKPSSSLBETFFDLSLVTQANIPNVFSQMCGAGLPVA 240
Db 181 FESENFLLPGIKMNGILGLAVATLAKPSSSLBETFFDLSLVTQANIPNVFSQMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKIS 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKIS 360
QY 361 YLRDENSSRSFRITILPOLYIOPMAGALNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIOPMAGALNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
QY 421 RAOKRVGAASPCAEIAGAAVSEISGFSTEDVASNCVPAQSLSEPIIWIYSYALMSVCG 480
Db 421 RAOKRVGAASPCAEIAGAAVSEISGFSTEDVASNCVPAQSLSEPIIWIYSYALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
Db 481 AILLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518

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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:42:44 ; Search time 28 Seconds
(without alignments)
544.324 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 518
Sequence: 1 MGALARALLPLLAQWLRA.....RPRDPEVNDSSLVRRHWK 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 segs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	518	100.0	518	3 US-08-999-723-2	Sequence 2, Appli
2	518	100.0	518	4 US-09-434-427-2	Sequence 2, Appli
3	518	100.0	518	4 US-09-548-372D-2	Sequence 2, Appli
4	518	100.0	518	4 US-09-548-367D-2	Sequence 2, Appli
5	59	11.4	514	4 US-09-717-432-2	Sequence 2, Appli
6	59	11.4	514	4 US-09-912-484-2	Sequence 2, Appli
7	22	4.2	25	4 US-09-548-372D-33	Sequence 33, Appli
8	22	4.2	25	4 US-09-548-367D-33	Sequence 33, Appli
9	12	2.3	425	4 US-09-548-372D-28	Sequence 28, Appli
10	12	2.3	425	4 US-09-548-367D-28	Sequence 28, Appli
11	12	2.3	428	4 US-09-548-372D-51	Sequence 51, Appli
12	12	2.3	428	4 US-09-548-367D-51	Sequence 51, Appli
13	12	2.3	433	4 US-09-548-372D-26	Sequence 26, Appli
14	12	2.3	433	4 US-09-548-367D-26	Sequence 26, Appli
15	12	2.3	434	4 US-09-548-372D-53	Sequence 53, Appli
16	12	2.3	434	4 US-09-548-367D-53	Sequence 53, Appli
17	12	2.3	446	4 US-09-548-372D-22	Sequence 22, Appli
18	12	2.3	446	4 US-09-548-367D-22	Sequence 22, Appli
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251	6	1.2	125	1	US-07-624-742-3	Sequence 3, Appli	324	6	1.2	226	2	US-08-572-447C-15	Sequence 15, Appl
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253	6	1.2	126	3	US-08-513-974B-28	Sequence 28, Appl	326	6	1.2	226	6	5498600-2	Patent No. 5498600
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258	6	1.2	136	4	US-08-905-223-287	Sequence 287, App	331	6	1.2	230	4	US-08-818-111-66	Sequence 66, Appl
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260	6	1.2	144	3	US-08-513-974B-369	Sequence 369, App	333	6	1.2	230	4	US-09-056-556-65	Sequence 65, Appl
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262	6	1.2	144	4	US-08-776-971-109	Sequence 109, App	335	6	1.2	233	4	US-09-214-631-7	Sequence 7, Appli
263	6	1.2	156	4	US-09-064-922-2	Sequence 2, Appli	336	6	1.2	235	1	US-07-940-605A-12	Sequence 12, Appl
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266	6	1.2	164	4	US-08-858-207A-502	Sequence 502, App	339	6	1.2	237	4	US-09-227-357-154	Sequence 154, App
267	6	1.2	169	1	US-08-233-788A-53	Sequence 53, Appl	340	6	1.2	238	4	US-09-149-476-485	Sequence 485, App
268	6	1.2	171	4	US-09-134-001C-5205	Sequence 5205, Ap	341	6	1.2	241	4	US-08-634-475-7	Sequence 7, Appli
269	6	1.2	173	1	US-08-157-005-8	Sequence 8, Appli	342	6	1.2	241	4	US-09-709-791-7	Sequence 7, Appli
270	6	1.2	173	1	US-08-062-472B-6	Sequence 6, Appli	343	6	1.2	241	4	US-09-153-599A-5	Sequence 5, Appli
271	6	1.2	173	2	US-08-799-464A-24	Sequence 24, Appl	344	6	1.2	241	6	5175255-2	Patent No. 5175255
272	6	1.2	173	4	US-08-747-863-8	Sequence 8, Appli	345	6	1.2	241	6	5175255-8	Patent No. 5175255
273	6	1.2	173	4	US-09-565-864-8	Sequence 8, Appli	346	6	1.2	243	1	US-08-021-608D-6	Sequence 6, Appli
274	6	1.2	173	5	PCT-US95-09927-24	Sequence 24, Appl	347	6	1.2	243	1	US-08-726-160-6	Sequence 6, Appli
275	6	1.2	173	5	PCT-US95-10904-24	Sequence 24, Appl	348	6	1.2	243	5	PCT-US94-01782-6	Sequence 6, Appli
276	6	1.2	174	5	US-08-131-625B-14	Sequence 14, Appl	349	6	1.2	244	1	US-08-910-973-22	Sequence 22, Appl
277	6	1.2	174	2	US-08-799-464A-11	Sequence 11, Appl	350	6	1.2	244	3	US-09-003-287-6	Sequence 6, Appli
278	6	1.2	174	4	US-09-113-750A-41	Sequence 41, Appl	351	6	1.2	244	3	US-09-003-287-8	Sequence 8, Appli
279	6	1.2	174	5	PCT-US95-09927-11	Sequence 11, Appl	352	6	1.2	244	4	US-09-518-988-2	Sequence 2, Appli
280	6	1.2	174	5	PCT-US95-10904-17	Sequence 17, Appl	353	6	1.2	244	4	US-09-499-227-22	Sequence 22, Appl
281	6	1.2	174	5	PCT-US95-10904-43	Sequence 43, Appl	354	6	1.2	246	4	US-08-634-475-3	Sequence 3, Appli
282	6	1.2	174	5	PCT-US95-10904-45	Sequence 45, Appl	355	6	1.2	246	4	US-09-709-791-3	Sequence 3, Appli
283	6	1.2	174	5	PCT-US95-10904-47	Sequence 47, Appl	356	6	1.2	247	1	US-08-324-977-44	Sequence 44, Appl
284	6	1.2	174	5	PCT-US95-10904-49	Sequence 49, Appl	357	6	1.2	247	2	US-08-384-616-44	Sequence 44, Appl
285	6	1.2	174	5	PCT-US95-10904-51	Sequence 51, Appl	358	6	1.2	247	2	US-08-904-686A-44	Sequence 44, Appl
286	6	1.2	175	4	US-08-887-534A-14	Sequence 14, Appl	359	6	1.2	247	4	US-09-315-850-44	Sequence 44, Appl
287	6	1.2	177	4	US-09-263-933-25	Sequence 25, Appl	360	6	1.2	247	4	US-09-724-864-49	Sequence 49, Appl
288	6	1.2	179	4	US-09-064-922-5	Sequence 5, Appli	361	6	1.2	249	4	US-09-318-191-34	Sequence 34, Appl
289	6	1.2	181	4	US-09-220-528-40	Sequence 40, Appl	362	6	1.2	254	4	US-09-134-001C-5543	Sequence 5543, Ap
290	6	1.2	184	2	US-08-737-825-10	Sequence 10, Appl	363	6	1.2	258	4	US-09-134-001C-3536	Sequence 3536, Ap
291	6	1.2	184	3	US-08-741-411-7	Sequence 7, Appli	364	6	1.2	259	4	US-09-006-353A-2	Sequence 2, Appli
292	6	1.2	185	3	US-08-984-295-1	Sequence 1, Appli	365	6	1.2	259	4	US-09-632-947B-3	Sequence 3, Appli
293	6	1.2	186	4	US-09-149-476-394	Sequence 394, App	366	6	1.2	259	4	US-09-573-986-2	Sequence 2, Appli
294	6	1.2	188	4	US-08-855-531D-37	Sequence 37, Appl	367	6	1.2	261	4	US-08-163-919A-2	Sequence 2, Appli
295	6	1.2	188	3	US-08-855-526B-37	Sequence 37, Appl	368	6	1.2	261	5	PCT-US94-14073-2	Sequence 2, Appli
296	6	1.2	188	4	US-09-134-001C-3152	Sequence 3152, Ap	369	6	1.2	264	4	US-08-469-260A-76	Sequence 76, Appl
297	6	1.2	192	1	US-08-086-428B-64	Sequence 64, Appl	370	6	1.2	266	4	US-08-904-234-3	Sequence 3, Appli
298	6	1.2	192	2	US-08-468-570-64	Sequence 64, Appl	371	6	1.2	268	4	US-09-403-768-2	Sequence 2, Appli
299	6	1.2	192	2	US-08-290-665A-64	Sequence 64, Appl	372	6	1.2	270	2	US-08-773-368-1	Sequence 1, Appli
300	6	1.2	192	5	PCT-US95-10398-64	Sequence 64, Appl	373	6	1.2	270	3	US-09-199-887-1	Sequence 1, Appli
301	6	1.2	196	3	US-07-998-289B-4	Sequence 4, Appli	374	6	1.2	270	4	US-09-013-881-6	Sequence 6, Appli
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304	6	1.2	205	1	US-08-441-216-2	Sequence 2, Appli	377	6	1.2	271	4	US-09-407-891-2	Sequence 19, Appl
305	6	1.2	205	1	US-08-452-779-1	Sequence 1, Appli	378	6	1.2	274	4	US-09-570-367C-19	Sequence 27, Appl
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308	6	1.2	205	2	US-08-445-065-12	Sequence 12, Appl	381	6	1.2	277	4	US-09-006-353A-10	Sequence 10, Appl
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310	6	1.2	205	3	US-08-959-524-12	Sequence 12, Appl	383	6	1.2	277	4	US-09-573-986-10	Sequence 10, Appl
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314	6	1.2	223	4	US-09-124-238A-34	Sequence 34, Appl	387	6	1.2	281	3	US-08-935-855-9	Sequence 9, Appli
315	6	1.2	223	4	US-09-721-975-34	Sequence 34, Appl	388	6	1.2	282	1	US-08-445-847A-1	Sequence 1, Appli
316	6	1.2	225	1	US-07-991-867B-3	Sequence 3, Appli	389	6	1.2	298	3	US-08-767-942A-25	Sequence 25, Appl
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319	6	1.2	225	3	US-09-248-335-40	Sequence 40, Appl	392	6	1.2	299	4	US-09-134-618-4	Sequence 4, Appli

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503	6	1.2	398	4	US-09-599-661-2	Sequence 2, Appli
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524	6	1.2	408	2	US-08-449-699A-7	Sequence 4, Appli
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538	6	1.2	408	5	PCT-US95-07084-4	Sequence 4, Appli

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540	6	1.2	409	6	5168050-4	Patent No. 5168050	613	6	1.2	453	1	US-08-446-374-12	Sequence 12, Appl
541	6	1.2	412	1	US-08-208-007A-12	Sequence 12, Appl	614	6	1.2	453	1	US-08-446-382-12	Sequence 12, Appl
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543	6	1.2	412	4	US-08-915-095A-12	Sequence 12, Appl	616	6	1.2	453	1	US-08-275-487-12	Sequence 12, Appl
544	6	1.2	412	4	US-08-798-096-12	Sequence 12, Appl	617	6	1.2	453	5	PCT-US95-08919-12	Sequence 12, Appl
545	6	1.2	412	4	US-08-798-095A-12	Sequence 12, Appl	618	6	1.2	454	3	US-08-446-100-26	Sequence 26, Appl
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552	6	1.2	420	4	US-09-705-448-1	Sequence 1, Appli	625	6	1.2	457	4	US-09-124-238A-1	Sequence 10, Appl
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554	6	1.2	424	4	US-09-661-711A-14	Sequence 14, Appli	627	6	1.2	457	4	US-09-134-001C-3838	Sequence 10, Appl
555	6	1.2	425	4	US-09-092-315-6	Sequence 6, Appli	628	6	1.2	457	4	US-09-721-975-1	Sequence 1, Appli
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571	6	1.2	431	1	US-08-469-202-14	Sequence 14, Appl	644	6	1.2	476	4	US-09-092-315-5	Sequence 5, Appli
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608	6	1.2	452	4	US-09-323-872A-15	Sequence 15, Appl	681	6	1.2	529	4	US-09-396-260-5	Sequence 5, Appli
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778	6	1.2	620	4	US-09-232-197-61	Sequence 61, Appl
779	6	1.2	620	4	US-09-232-197-93	Sequence 93, Appl
780	6	1.2	620	4	US-09-232-201-61	Sequence 61, Appl
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836	6	1.2	764	4	US-07-741-453A-60	Sequence 60, Appl
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843	6	1.2	831	2	US-09-097-053-11	Sequence 12, Appl
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845	6	1.2	832	4	US-09-097-053-12	Sequence 12, Appl
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849	6	1.2	834	4	US-09-097-053-10	Sequence 10, Appl
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ALIGNMENTS

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; Sequence 2, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-999-723-2
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; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-434-427-2
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; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-2

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Best Local Similarity 100.0%; Pred. No. 0;
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; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-2

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGAANFLAMVDNLQDSDGRGYLLEMLIGTPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGAANFLAMVDNLQDSDGRGYLLEMLIGTPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTOGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTOGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMWGAGLNIECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMWGAGLNIECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWISYALMSVCG 480
Db 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWISYALMSVCG 480
QY 481 AILLVLIVLLLLPFRCCRRPRDPEVNVNDESSLVRHRWK 518
Db 481 AILLVLIVLLLLPFRCCRRPRDPEVNVNDESSLVRHRWK 518

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RESULT 5
US-09-717-432-2
; Sequence 2, Application US/09717432
; Patent No. 6291223
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: CHRISTIE, GARY
; APPLICANT: POWELL, DAVID J.
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-717-432-2
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Query Match 11.4%; Score 59; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 228 FSMQMGAGLPVAGSGTNGSLVLGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGQ 286
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Db 224 FSMQMGAGLPVAGSGTNGSLVLGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGQ 282
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RESULT 6
US-09-912-484-2
; Sequence 2, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaotong
; APPLICANT: Powell, David J.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/717,432
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-912-484-2
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Query Match 11.4%; Score 59; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 224 FSMQMGAGLPVAGSGTNGSLVLGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGQ 282
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RESULT 7
US-09-548-372D-33
; Sequence 33, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
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; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR APPLICATION DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-33
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Query Match 4.2%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 497 QRRPRDPEVVNDESSLVRHRWK 518
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Db 4 QRRPRDPEVVNDESSLVRHRWK 25
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RESULT 8
US-09-548-367D-33
; Sequence 33, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-33
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Query Match 4.2%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 4 QRRPRDPEVVNDESSLVRHRWK 25
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RESULT 9
US-09-548-372D-28
; Sequence 28, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-372D-28
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Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 107 ILVDTGSSNFAV 118
Db 62 ILVDTGSSNFAV 73
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RESULT 10
US-09-548-367D-28
; Sequence 28, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-367D-28
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Best Local Similarity 100.0%; Pred. No. 0.004;
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Db 62 ILVDTGSSNFAV 73
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US-09-548-372D-51
; Sequence 51, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: THEREOF
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; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
; US-09-548-372D-51
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Best Local Similarity 100.0%; Pred. No. 0.004;
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Db 90 ILVDTGSSNFAV 101
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RESULT 12
US-09-548-367D-51
; Sequence 51, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
; US-09-548-367D-51
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Query Match      2.3%; Score 12; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 90 ILVDTGSSNFAV 101
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RESULT 13
US-09-548-372D-26
; Sequence 26, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
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; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-372D-26
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Query Match          2.3%; Score 12; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 70 ILVDTGSSNFAV 81
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```
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US-09-548-367D-26
; Sequence 26, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-367D-26
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Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 107 ILVDTGSSNFAV 118
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Db 70 ILVDTGSSNFAV 81
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RESULT 15
US-09-548-372D-53
; Sequence 53, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
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; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2 (b) delta TM
; US-09-548-372D-53
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Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 107 ILVDTGSSNFAV 118
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Db 90 ILVDTGSSNFAV 101
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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	518	100.0	518	US-09-886-143-2	Sequence 2, Appli
3	518	100.0	518	US-09-978-697-196	Sequence 196, App
4	518	100.0	518	US-09-978-192A-196	Sequence 196, App
5	518	100.0	518	US-09-999-832A-196	Sequence 196, App
6	518	100.0	518	US-09-978-189-196	Sequence 196, App
7	518	100.0	518	US-10-174-590-72	Sequence 72, Appli
8	518	100.0	518	US-10-176-758-72	Sequence 72, Appli
9	518	100.0	518	US-10-175-737-72	Sequence 72, Appli
10	518	100.0	518	US-10-173-706-72	Sequence 72, Appli
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61	518	100.0	518	US-10-183-010-72	Sequence 72, Appli
62	518	100.0	518	US-10-183-012-72	Sequence 72, Appli
63	518	100.0	518	US-10-184-614-72	Sequence 72, Appli
64	518	100.0	518	US-10-184-623-72	Sequence 72, Appli
65	518	100.0	518	US-10-184-635-72	Sequence 72, Appli
66	518	100.0	518	US-10-184-637-72	Sequence 72, Appli
67	518	100.0	518	US-10-184-646-72	Sequence 72, Appli
68	518	100.0	518	US-10-184-647-72	Sequence 72, Appli
69	518	100.0	518	US-10-184-652-72	Sequence 72, Appli
70	518	100.0	518	US-10-187-594-72	Sequence 72, Appli
71	518	100.0	518	US-10-187-596-72	Sequence 72, Appli
72	518	100.0	518	US-10-187-745-72	Sequence 72, Appli
73	518	100.0	518	US-10-187-885-72	Sequence 72, Appli
74	518	100.0	518	US-10-187-886-72	Sequence 72, Appli
75	518	100.0	518	US-10-199-464-72	Sequence 72, Appli
76	518	100.0	518	US-10-176-751-72	Sequence 72, Appli
77	518	100.0	518	US-10-176-760-72	Sequence 72, Appli
78	518	100.0	518	US-10-176-990-72	Sequence 72, Appli
79	518	100.0	518	US-10-180-541-72	Sequence 72, Appli
80	518	100.0	518	US-10-180-542-72	Sequence 72, Appli
81	518	100.0	518	US-10-180-548-72	Sequence 72, Appli
82	518	100.0	518	US-10-180-551-72	Sequence 72, Appli
83	518	100.0	518	US-10-180-998-72	Sequence 72, Appli
84	518	100.0	518	US-10-180-999-72	Sequence 72, Appli
85	518	100.0	518	US-10-183-013-72	Sequence 72, Appli
86	518	100.0	518	US-10-184-612-72	Sequence 72, Appli
87	518	100.0	518	US-10-184-616-72	Sequence 72, Appli
88	518	100.0	518	US-10-184-617-72	Sequence 72, Appli
89	518	100.0	518	US-10-184-622-72	Sequence 72, Appli
90	518	100.0	518	US-10-184-628-72	Sequence 72, Appli
91	518	100.0	518	US-10-184-629-72	Sequence 72, Appli
92	518	100.0	518	US-10-184-630-72	Sequence 72, Appli

239	518	100.0	518	9	US-10-197-694-72	Sequence 72, Appl	312	12	2.3	446	10	US-09-795-847-22	Sequence 22, Appl
240	518	100.0	518	9	US-10-197-697-72	Sequence 72, Appl	313	12	2.3	446	10	US-09-794-743-22	Sequence 22, Appl
241	518	100.0	518	9	US-10-197-707-72	Sequence 72, Appl	314	12	2.3	446	10	US-09-794-748-22	Sequence 22, Appl
242	518	100.0	518	9	US-10-199-303-72	Sequence 72, Appl	315	12	2.3	446	10	US-09-794-925-22	Sequence 22, Appl
243	518	100.0	518	9	US-10-199-318-72	Sequence 72, Appl	316	12	2.3	446	10	US-09-681-442-22	Sequence 22, Appl
244	518	100.0	518	9	US-10-199-458-72	Sequence 72, Appl	317	12	2.3	453	10	US-09-794-927-30	Sequence 30, Appl
245	518	100.0	518	9	US-10-199-462-72	Sequence 72, Appl	318	12	2.3	453	10	US-09-795-847-30	Sequence 30, Appl
246	518	100.0	518	9	US-10-201-324-72	Sequence 72, Appl	319	12	2.3	453	10	US-09-794-743-30	Sequence 30, Appl
247	518	100.0	518	9	US-10-201-328-72	Sequence 72, Appl	320	12	2.3	453	10	US-09-794-748-30	Sequence 30, Appl
248	518	100.0	518	9	US-10-201-527-72	Sequence 72, Appl	321	12	2.3	453	10	US-09-794-925-30	Sequence 30, Appl
249	518	100.0	518	9	US-10-201-528-72	Sequence 72, Appl	322	12	2.3	453	10	US-09-681-442-30	Sequence 30, Appl
250	518	100.0	518	9	US-10-201-529-72	Sequence 72, Appl	323	12	2.3	459	10	US-09-794-927-24	Sequence 24, Appl
251	518	100.0	518	9	US-10-201-530-72	Sequence 72, Appl	324	12	2.3	459	10	US-09-794-927-32	Sequence 32, Appl
252	518	100.0	518	9	US-10-202-408-72	Sequence 72, Appl	325	12	2.3	459	10	US-09-795-847-24	Sequence 24, Appl
253	518	100.0	518	9	US-10-202-409-72	Sequence 72, Appl	326	12	2.3	459	10	US-09-795-847-32	Sequence 32, Appl
254	518	100.0	518	9	US-10-202-411-72	Sequence 72, Appl	327	12	2.3	459	10	US-09-794-743-24	Sequence 24, Appl
255	518	100.0	518	9	US-10-202-472-72	Sequence 72, Appl	328	12	2.3	459	10	US-09-794-748-24	Sequence 24, Appl
256	518	100.0	518	9	US-10-205-502-72	Sequence 72, Appl	329	12	2.3	459	10	US-09-794-748-32	Sequence 32, Appl
257	518	100.0	518	9	US-10-205-507-72	Sequence 72, Appl	330	12	2.3	459	10	US-09-794-748-32	Sequence 32, Appl
258	518	100.0	518	9	US-10-205-511-72	Sequence 72, Appl	331	12	2.3	459	10	US-09-794-925-24	Sequence 24, Appl
259	518	100.0	518	9	US-10-205-902-72	Sequence 72, Appl	332	12	2.3	459	10	US-09-794-925-32	Sequence 32, Appl
260	518	100.0	518	9	US-10-205-907-72	Sequence 72, Appl	333	12	2.3	459	10	US-09-681-442-24	Sequence 24, Appl
261	518	100.0	518	9	US-09-918-585A-196	Sequence 196, App	334	12	2.3	459	10	US-09-681-442-32	Sequence 32, Appl
262	518	100.0	518	9	US-10-194-456-72	Sequence 72, Appl	335	12	2.3	476	10	US-09-794-927-6	Sequence 6, Appl
263	518	100.0	518	9	US-10-196-758-72	Sequence 72, Appl	336	12	2.3	476	10	US-09-795-847-6	Sequence 6, Appl
264	518	100.0	518	9	US-10-198-770-72	Sequence 72, Appl	337	12	2.3	476	10	US-09-794-743-6	Sequence 6, Appl
265	518	100.0	518	9	US-10-199-308-72	Sequence 72, Appl	338	12	2.3	476	10	US-09-794-748-6	Sequence 6, Appl
266	518	100.0	518	9	US-10-200-617-72	Sequence 72, Appl	339	12	2.3	476	10	US-09-794-925-6	Sequence 6, Appl
267	518	100.0	518	9	US-10-205-893-72	Sequence 72, Appl	340	12	2.3	476	10	US-09-681-442-6	Sequence 6, Appl
268	518	100.0	518	9	US-10-205-897-72	Sequence 72, Appl	341	12	2.3	488	9	US-09-795-903A-2	Sequence 2, Appl
269	518	100.0	518	10	US-09-794-927-2	Sequence 2, Appl	342	12	2.3	488	10	US-09-796-264-2	Sequence 2, Appl
270	518	100.0	518	10	US-09-795-847-2	Sequence 2, Appl	343	12	2.3	488	10	US-09-845-226-2	Sequence 2, Appl
271	518	100.0	518	10	US-09-794-743-2	Sequence 2, Appl	344	12	2.3	501	9	US-09-969-671A-2	Sequence 2, Appl
272	518	100.0	518	10	US-09-794-748-2	Sequence 2, Appl	345	12	2.3	501	10	US-09-794-927-4	Sequence 4, Appl
273	518	100.0	518	10	US-09-794-925-2	Sequence 2, Appl	346	12	2.3	501	10	US-09-794-927-8	Sequence 8, Appl
274	518	100.0	518	10	US-09-215-450-19	Sequence 19, Appl	347	12	2.3	501	10	US-09-795-847-4	Sequence 4, Appl
275	518	100.0	518	10	US-09-681-442-2	Sequence 2, Appl	348	12	2.3	501	10	US-09-795-847-8	Sequence 8, Appl
276	518	100.0	518	12	US-10-052-586-72	Sequence 72, Appl	349	12	2.3	501	10	US-09-794-743-4	Sequence 4, Appl
277	423	81.7	423	9	US-09-470-954A-46	Sequence 46, Appl	350	12	2.3	501	10	US-09-794-748-4	Sequence 4, Appl
278	50	9.7	50	10	US-09-864-761-49075	Sequence 49075, A	351	12	2.3	501	10	US-09-794-748-8	Sequence 8, Appl
279	44	8.5	44	10	US-09-864-761-38089	Sequence 38089, A	352	12	2.3	501	10	US-09-794-748-8	Sequence 8, Appl
280	22	4.2	25	10	US-09-794-927-33	Sequence 33, Appl	353	12	2.3	501	10	US-09-794-925-4	Sequence 4, Appl
281	22	4.2	25	10	US-09-795-847-33	Sequence 33, Appl	354	12	2.3	501	10	US-09-794-925-8	Sequence 8, Appl
282	22	4.2	25	10	US-09-794-743-33	Sequence 33, Appl	355	12	2.3	501	10	US-09-681-442-4	Sequence 4, Appl
283	22	4.2	25	10	US-09-794-748-33	Sequence 33, Appl	356	12	2.3	501	10	US-09-681-442-8	Sequence 8, Appl
284	22	4.2	25	10	US-09-794-925-33	Sequence 33, Appl	357	12	2.3	503	9	US-09-795-903A-3	Sequence 3, Appl
285	22	4.2	25	10	US-09-681-442-33	Sequence 33, Appl	358	12	2.3	503	10	US-09-796-264-3	Sequence 3, Appl
286	16	3.1	16	9	US-09-886-143-6	Sequence 6, Appl	359	12	2.3	503	10	US-09-845-226-3	Sequence 3, Appl
287	12	2.3	425	10	US-09-794-927-28	Sequence 28, Appl	360	12	2.3	774	9	US-09-969-671A-4	Sequence 4, Appl
288	12	2.3	425	10	US-09-795-847-28	Sequence 28, Appl	361	9	1.7	322	9	US-09-470-954A-47	Sequence 47, Appl
289	12	2.3	425	10	US-09-794-743-28	Sequence 28, Appl	362	9	1.7	401	9	US-09-924-340-24	Sequence 24, Appl
290	12	2.3	425	10	US-09-794-748-28	Sequence 28, Appl	363	9	1.7	401	9	US-09-992-600A-24	Sequence 24, Appl
291	12	2.3	425	10	US-09-794-925-28	Sequence 28, Appl	364	8	1.5	458	9	US-09-738-626-3686	Sequence 3686, Ap
292	12	2.3	425	10	US-09-681-442-28	Sequence 28, Appl	365	8	1.5	479	10	US-09-861-400-17	Sequence 17, Appl
293	12	2.3	428	10	US-09-794-927-51	Sequence 51, Appl	366	8	1.5	481	9	US-10-042-431-39	Sequence 39, Appl
294	12	2.3	428	10	US-09-795-847-51	Sequence 51, Appl	367	8	1.5	481	9	US-09-759-130B-409	Sequence 409, App
295	12	2.3	428	10	US-09-794-743-51	Sequence 51, Appl	368	8	1.5	481	10	US-09-731-872-271	Sequence 271, App
296	12	2.3	428	10	US-09-794-925-51	Sequence 51, Appl	369	8	1.5	481	10	US-09-994-185-2	Sequence 2, Appl
297	12	2.3	428	10	US-09-794-925-51	Sequence 51, Appl	370	8	1.5	481	10	US-09-861-400-2	Sequence 2, Appl
298	12	2.3	428	10	US-09-681-442-51	Sequence 51, Appl	371	8	1.5	481	12	US-10-004-139-2	Sequence 2, Appl
299	12	2.3	433	10	US-09-794-927-26	Sequence 26, Appl	372	8	1.5	504	10	US-09-919-497-67	Sequence 67, Appl
300	12	2.3	433	10	US-09-795-847-26	Sequence 26, Appl	373	8	1.5	548	10	US-09-741-669-413	Sequence 413, App
301	12	2.3	433	10	US-09-794-743-26	Sequence 26, Appl	374	8	1.5	692	9	US-09-738-626-6979	Sequence 6979, Ap
302	12	2.3	433	10	US-09-794-748-26	Sequence 26, Appl	375	8	1.5	1246	10	US-09-919-497-85	Sequence 85, Appl
303	12	2.3	433	10	US-09-794-925-26	Sequence 26, Appl	376	7	1.4	13	9	US-10-027-961A-20	Sequence 20, Appl
304	12	2.3	433	10	US-09-681-442-26	Sequence 26, Appl	377	7	1.4	21	9	US-09-974-879-293	Sequence 293, App
305	12	2.3	434	10	US-09-794-927-53	Sequence 53, Appl	378	7	1.4	25	9	US-09-922-199A-19	Sequence 19, Appl
306	12	2.3	434	10	US-09-795-847-53	Sequence 53, Appl	379	7	1.4	25	10	US-09-864-761-45398	Sequence 45398, A
307	12	2.3	434	10	US-09-794-743-53	Sequence 53, Appl	380	7	1.4	28	10	US-09-846-258-8	Sequence 8, Appl
308	12	2.3	434	10	US-09-794-748-53	Sequence 53, Appl	381	7	1.4	30	10	US-09-758-575-3	Sequence 3, Appl
309	12	2.3	434	10	US-09-794-925-53	Sequence 53, Appl	382	7	1.4	34	9	US-09-948-820-94	Sequence 94, Appl
310	12	2.3	434	10	US-09-681-442-53	Sequence 53, Appl	383	7	1.4	50	9	US-09-974-879-291	Sequence 291, App
311	12	2.3	446	10	US-09-794-927-22	Sequence 22, Appl	384	7	1.4	60	8	US-08-914-350-7	Sequence 7, Appl

385	7	1.4	61	9	US-09-852-797-52	Sequence 52, Appl
386	7	1.4	61	10	US-09-853-161-52	Sequence 52, Appl
387	7	1.4	61	10	US-09-852-659A-52	Sequence 52, Appl
388	7	1.4	91	10	US-09-864-761-42428	Sequence 42428, A
389	7	1.4	95	10	US-09-734-569-52	Sequence 52, Appl
390	7	1.4	106	10	US-09-846-258-5	Sequence 5, Appli
391	7	1.4	126	10	US-09-970-518-1	Sequence 1, Appli
392	7	1.4	160	9	US-10-269-781-5	Sequence 5, Appli
393	7	1.4	174	10	US-09-731-872-315	Sequence 315, App
394	7	1.4	175	10	US-09-864-761-46612	Sequence 46612, A
395	7	1.4	185	10	US-09-881-752A-40	Sequence 40, Appl
396	7	1.4	193	10	US-09-764-898-214	Sequence 214, App
397	7	1.4	194	9	US-09-925-299-1005	Sequence 1005, Ap
398	7	1.4	194	10	US-09-925-299-1005	Sequence 1005, Ap
399	7	1.4	231	10	US-09-768-826-56	Sequence 56, Appl
400	7	1.4	238	10	US-09-904-954-2	Sequence 2, Appli
401	7	1.4	262	10	US-09-925-302-522	Sequence 522, App
402	7	1.4	265	9	US-09-866-050A-655	Sequence 655, App
403	7	1.4	270	10	US-09-758-575-9	Sequence 9, Appli
404	7	1.4	273	10	US-09-758-575-2	Sequence 9, Appli
405	7	1.4	273	10	US-09-758-575-6	Sequence 6, Appli
406	7	1.4	273	10	US-09-893-737-228	Sequence 228, App
407	7	1.4	279	10	US-09-820-893-138	Sequence 138, App
408	7	1.4	280	10	US-09-731-872-314	Sequence 314, App
409	7	1.4	306	10	US-09-741-669-456	Sequence 456, App
410	7	1.4	320	8	US-08-914-350-2	Sequence 2, Appli
411	7	1.4	323	9	US-09-948-820-85	Sequence 85, Appl
412	7	1.4	326	9	US-09-795-903A-31	Sequence 31, Appl
413	7	1.4	326	10	US-09-796-264-31	Sequence 31, Appl
414	7	1.4	326	10	US-09-845-226-31	Sequence 31, Appl
415	7	1.4	327	10	US-09-734-569-156	Sequence 156, App
416	7	1.4	363	10	US-09-905-173-36	Sequence 36, Appl
417	7	1.4	388	10	US-09-215-450-23	Sequence 23, Appl
418	7	1.4	451	9	US-10-042-431-43	Sequence 43, Appl
419	7	1.4	451	9	US-09-759-130B-413	Sequence 413, App
420	7	1.4	453	9	US-09-443-745-27	Sequence 27, Appl
421	7	1.4	470	9	US-10-042-431-69	Sequence 69, Appl
422	7	1.4	470	9	US-09-759-130B-439	Sequence 439, App
423	7	1.4	491	9	US-09-712-363-152	Sequence 152, App
424	7	1.4	517	9	US-09-972-268-20	Sequence 20, Appl
425	7	1.4	518	10	US-09-919-172-20	Sequence 20, Appl
426	7	1.4	537	9	US-10-047-542-74	Sequence 74, Appl
427	7	1.4	550	9	US-09-738-626-6950	Sequence 6950, Ap
428	7	1.4	550	9	US-10-226-136-19	Sequence 19, Appl
429	7	1.4	569	10	US-09-815-242-10503	Sequence 10503, A
430	7	1.4	604	9	US-10-027-961A-18	Sequence 18, Appl
431	7	1.4	615	10	US-09-862-027-49	Sequence 49, Appl
432	7	1.4	638	10	US-09-851-859A-6	Sequence 6, Appli
433	7	1.4	654	10	US-09-969-528-10	Sequence 10, Appl
434	7	1.4	667	9	US-09-874-503-16	Sequence 16, Appl
435	7	1.4	667	9	US-10-000-157-16	Sequence 16, Appl
436	7	1.4	667	9	US-09-816-744-16	Sequence 16, Appl
437	7	1.4	667	9	US-09-747-259-16	Sequence 16, Appl
438	7	1.4	667	9	US-10-227-884-20	Sequence 20, Appl
439	7	1.4	667	9	US-10-230-163-20	Sequence 20, Appl
440	7	1.4	667	9	US-10-218-631-20	Sequence 20, Appl
441	7	1.4	667	9	US-10-230-338-20	Sequence 20, Appl
442	7	1.4	667	9	US-10-230-414-20	Sequence 20, Appl
443	7	1.4	667	9	US-09-908-827-16	Sequence 16, Appl
444	7	1.4	704	10	US-09-912-020-248	Sequence 248, App
445	7	1.4	704	10	US-09-815-242-10363	Sequence 10363, A
446	7	1.4	704	10	US-09-815-242-13965	Sequence 13965, A
447	7	1.4	760	10	US-09-833-017-26	Sequence 26, Appl
448	7	1.4	862	9	US-09-738-626-3956	Sequence 3956, Ap
449	7	1.4	942	9	US-10-101-464A-911	Sequence 911, App
450	7	1.4	1429	9	US-09-953-407-1	Sequence 1, Appli
451	7	1.4	1520	9	US-09-738-626-4444	Sequence 4444, Ap
452	7	1.4	2047	9	US-09-736-968A-2	Sequence 2, Appli
453	6	1.2	12	8	US-08-424-550B-446	Sequence 446, App
454	6	1.2	14	10	US-09-918-171A-28	Sequence 28, Appl
455	6	1.2	19	10	US-09-918-171A-24	Sequence 24, Appl
456	6	1.2	21	12	US-10-096-241-24	Sequence 24, Appl
457	6	1.2	22	9	US-09-832-355A-58	Sequence 58, Appl
458	6	1.2	22	10	US-09-847-185-6	Sequence 6, Appli
459	6	1.2	23	9	US-10-057-558-2	Sequence 2, Appli
460	6	1.2	26	12	US-10-016-481-10	Sequence 10, Appl
461	6	1.2	27	8	US-08-873-601-31	Sequence 31, Appl
462	6	1.2	27	9	US-09-792-630-84	Sequence 84, Appl
463	6	1.2	27	9	US-10-080-376-84	Sequence 84, Appl
464	6	1.2	27	9	US-10-061-395-32	Sequence 32, Appl
465	6	1.2	27	9	US-10-096-339-30	Sequence 30, Appl
466	6	1.2	27	10	US-09-157-748-35	Sequence 35, Appl
467	6	1.2	27	10	US-09-916-940-35	Sequence 35, Appl
468	6	1.2	29	9	US-09-832-355A-53	Sequence 53, Appl
469	6	1.2	31	9	US-10-057-558-6	Sequence 6, Appli
470	6	1.2	31	9	US-09-996-069-12	Sequence 12, Appl
471	6	1.2	32	9	US-10-057-558-12	Sequence 12, Appl
472	6	1.2	32	9	US-09-755-109-18	Sequence 18, Appl
473	6	1.2	32	9	US-10-012-542-478	Sequence 478, App
474	6	1.2	32	10	US-09-864-761-41359	Sequence 41359, A
475	6	1.2	33	9	US-10-057-558-4	Sequence 4, Appli
476	6	1.2	34	9	US-09-759-130B-74	Sequence 74, Appl
477	6	1.2	35	10	US-09-864-761-36036	Sequence 36036, A
478	6	1.2	35	10	US-09-864-761-39580	Sequence 39580, A
479	6	1.2	35	8	US-08-873-601-18	Sequence 18, Appl
480	6	1.2	36	9	US-09-792-630-71	Sequence 71, Appl
481	6	1.2	36	9	US-10-080-376-71	Sequence 71, Appl
482	6	1.2	36	9	US-10-061-395-19	Sequence 19, Appl
483	6	1.2	36	9	US-10-096-339-18	Sequence 18, Appl
484	6	1.2	36	10	US-09-157-748-24	Sequence 24, Appl
485	6	1.2	36	10	US-09-916-940-22	Sequence 22, Appl
486	6	1.2	36	10	US-09-916-940-22	Sequence 22, Appl
487	6	1.2	38	9	US-09-908-153B-51	Sequence 51, Appl
488	6	1.2	38	10	US-09-864-761-40768	Sequence 40768, A
489	6	1.2	38	10	US-09-864-761-43013	Sequence 43013, A
490	6	1.2	40	9	US-10-057-558-10	Sequence 10, Appl
491	6	1.2	41	10	US-09-864-761-47936	Sequence 47936, A
492	6	1.2	42	9	US-09-983-802-221	Sequence 221, App
493	6	1.2	43	9	US-09-809-391-524	Sequence 524, App
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496	6	1.2	48	10	US-09-864-761-48227	Sequence 48227, A
497	6	1.2	49	10	US-09-864-761-35522	Sequence 35522, A
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506	6	1.2	54	10	US-09-764-877-1326	Sequence 1326, Ap
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508	6	1.2	55	10	US-09-864-761-39275	Sequence 39275, A
509	6	1.2	55	10	US-09-864-761-40066	Sequence 40066, A
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518	6	1.2	61	9	US-10-125-258-16	Sequence 16, Appl
519	6	1.2	62	9	US-10-012-542-191	Sequence 191, App
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524	6	1.2	68	10	US-09-864-761-37739	Sequence 37739, A
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ALIGNMENTS

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; GENERAL INFORMATION:
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWILRAAPELAPFTLPLRYAAATNRVAPTGPCTPAERHADGL 60
Db 1 MGALARALLPLLAQWILRAAPELAPFTLPLRYAAATNRVAPTGPCTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAVNDNLQDSDGRGYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAVNDNLQDSDGRGYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTOGSWTGVGEDLVITPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTOGSWTGVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENEFLPGIKWNGILGLAYATLAKPSSSLETFRDSLVTQANIPNVFSMOCAGLPVA 240
Db 181 FESENEFLPGIKWNGILGLAYATLAKPSSSLETFRDSLVTQANIPNVFSMOCAGLPVA 240
QY 241 GSGTNGGSLVLGIEPSLYKGDIMWYTPIKEEMYYOIEILKLEIGGOSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGIEPSLYKGDIMWYTPIKEEMYYOIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVDVAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYEPKISI 360
Db 301 IVDSGTTLLRLPQKVDVAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYEPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNEYCYRFGISPSSTNALVIGATWEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNEYCYRFGISPSSTNALVIGATWEGFYVIFD 420
QY 421 RAQKRVGAASPCAEIAGAAVSEISGPFSTEDVANSVCVPAQSLSEPIILWISYALMSVCG 480
Db 421 RAQKRVGAASPCAEIAGAAVSEISGPFSTEDVANSVCVPAQSLSEPIILWISYALMSVCG 480
QY 481 ALLVLIVLLLPFCORRRPRDPEVNVNDESSLVHRWK 518
Db 481 ALLVLIVLLLPFCORRRPRDPEVNVNDESSLVHRWK 518

RESULT 2
US-09-886-143-2
; Sequence 2, Application US/09886143
; Patent No. US2002015991A1
; GENERAL INFORMATION:
; APPLICANT: Cordell, Barbara
; APPLICANT: Schimmoller, Frauke
; APPLICANT: Liu, Yu-Wang
; APPLICANT: Quon, Diana Hom
; TITLE OF INVENTION: Modulation of A levels by
; TITLE OF INVENTION: Secretase BACE2

FILE REFERENCE: SCIOS.022A
CURRENT APPLICATION NUMBER: US/09/886,143
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/215,729
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 518
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-143-2

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
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DB 61 ALALEPALASPAGANFLAVDNLQDSDGRGYLLEMLIGTFPPQKLQILVDTGSSNFAVAG 120
QY 121 TPFSYIDTYFDTERSSSTYRSKGDVTVKYTGSGSWTGFGEDLVTIPKGFTSFLVNIATI 180
DB 121 TPFSYIDTYFDTERSSSTYRSKGDVTVKYTGSGSWTGFGEDLVTIPKGFTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGLPVA 240
DB 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKEIGGQSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQLA CWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQLA CWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVFD 420
DB 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVFD 420
QY 421 RAQKRVGFASPACAEIAGAASEISGPFSTEDVASNCVPAQSISEPILMIVSYALMSVCG 480
DB 421 RAQKRVGFASPACAEIAGAASEISGPFSTEDVASNCVPAQSISEPILMIVSYALMSVCG 480
QY 481 AILLVLIVLLLPFCQRRPRDPEVNVNDESSLVRHRWK 518
DB 481 AILLVLIVLLLPFCQRRPRDPEVNVNDESSLVRHRWK 518

RESULT 3

US-09-978-697-196
Sequence 196, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAPELAPAPFTPLRVAATNRVAPPTPGPTPAERHADGL 60
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QY 61 ALALEPALASPAGANFLAMVDNLQDGSRGYLEMLIGTPPKQLQILVDTGSSNFAVAG 120
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DB 121 TPHSYIDTYFDTERRSSTYRSKGFVDYTVKTYQGSWTGFVGEDLVITPKGNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
DB 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGSLVLGTEPSLYKGDIMWYTPIKEMWYQIEILKEIGGOSLNDCREYNADKA 300
DB 241 GSGTNGSLVLGTEPSLYKGDIMWYTPIKEMWYQIEILKEIGGOSLNDCREYNADKA 300
QY 301 IVDSGTTLLRLPKQYFDVAVEAVARASLIPEPSDGFWTGSQACWNTSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPKQYFDVAVEAVARASLIPEPSDGFWTGSQACWNTSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
DB 361 YLRDENSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAASPCAEIAGAAVSEISGPSTEDVANSNCVPAQSLSEPLIMIVSYALMSVCG 480
DB 421 RAQKRVGFAASPCAEIAGAAVSEISGPSTEDVANSNCVPAQSLSEPLIMIVSYALMSVCG 480

QY 481 ALLVLIVLLLPFCQRRPRDEVVNDESSLVRHRWK 518
DB 481 ALLVLIVLLLPFCQRRPRDEVVNDESSLVRHRWK 518

RESULT 4

US-09-978-192A-196
; Sequence 196, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
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; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
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; PRIOR APPLICATION NUMBER: 60/084366
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALARALLPLAQWLLRAABELAPAFPTLPLRVAATNRVVAPTPGGTPAERHADGL 60
Db 1 MGAALARALLPLAQWLLRAABELAPAFPTLPLRVAATNRVVAPTPGGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQGDSSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120

Db 61 ALALEPALASPAGANFLAMVDNLQGDSSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFVDVTKYTQGSWTGFVEDLVTPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFVDVTKYTQGSWTGFVEDLVTPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQCGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQCGAGLPVA 240
QY 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKA 300
Db 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKA 300
QY 301 IVDSGTTLLRLPOKVPDVAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLLRLPOKVPDVAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITIPOLYIQPMGAGLNEYECYRFGISPSSTNALVIGATVMEGFYIFD 420
Db 361 YLRDENSRSFRITIPOLYIQPMGAGLNEYECYRFGISPSSTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIMLVSYALMSVCG 480
Db 421 RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIMLVSYALMSVCG 480
QY 481 ALLVLIVLLLPFCORRPRDPEVVNDESSLVHRWK 518
Db 481 ALLVLIVLLLPFCORRPRDPEVVNDESSLVHRWK 518

RESULT 5
US-09-999-832A-196
; Sequence 196, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYEDTERSTYRSKGFVTVKYTGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYEDTERSTYRSKGFVTVKYTGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAYATIAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAYATIAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGIEPSLYKGDIMYTPRIKEWYYQIEILKEIGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGIEPSLYKGDIMYTPRIKEWYYQIEILKEIGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQLA CWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQLA CWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSRFRITILPOLYIQPMWAGLNYECYRFGISPTNALVIGATVMEGFYIIFD 420
Db 361 YLRDENSRSRFRITILPOLYIQPMWAGLNYECYRFGISPTNALVIGATVMEGFYIIFD 420
QY 421 RAQKRVGFAASPCAIEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSYCG 480
Db 421 RAQKRVGFAASPCAIEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSYCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
Db 481 AILLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 6
US-09-978-189-196
; Sequence 196, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/084627
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAWDNLQDSDGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAWDNLQDSDGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTFVGEDLVTI PKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTFVGEDLVTI PKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPIKEWYQIETILKLEIGGOSLNLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPIKEWYQIETILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDVAVAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVFDVAVAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFASPCAEIAGAVSEISGPFSTEDVASNCVPAQSLSEPILMWISYALMSVCG 480

Db 421 RAQKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILMIVSYALMSVCG 480
QY 481 AILLVIVLVLPLPFCQRRPRDPEVNDSSLVRHRWK 518
Db 481 AILLVIVLVLPLPFCQRRPRDPEVNDSSLVRHRWK 518

RESULT 7

US-10-174-590-72
; Sequence 72, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-72

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRLRAABELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLRLRAABELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQOLACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFD 420
QY 421 RAQKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILMIVSYALMSVCG 480

QY 481 AILLVIVLVLPLPFCQRRPRDPEVNDSSLVRHRWK 518
Db 481 AILLVIVLVLPLPFCQRRPRDPEVNDSSLVRHRWK 518

RESULT 8

US-10-176-758-72
; Sequence 72, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-72

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRLRAABELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLRLRAABELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQOLACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFD 420
QY 421 RAQKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILMIVSYALMSVCG 480
QY 481 AILLVIVLVLPLPFCQRRPRDPEVNDSSLVRHRWK 518
Db 481 AILLVIVLVLPLPFCQRRPRDPEVNDSSLVRHRWK 518

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RESULT 9
US-10-175-737-72
; Sequence 72, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-72
```

```
Query Match      100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVAPTPGPGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVAPTPGPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFVDVTKYTGSGWTGFGEDLVTPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFVDVTKYTGSGWTGFGEDLVTPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMCGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQQLACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQQLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASCNCPAQSLSEPIIWIYSALMSVCG 480
Db 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASCNCPAQSLSEPIIWIYSALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSSLVRHRWK 518
Db 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSSLVRHRWK 518
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RESULT 10

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US-10-173-706-72
; Sequence 72, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-72
```

```
Query Match      100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVAPTPGPGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVAPTPGPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFVDVTKYTGSGWTGFGEDLVTPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFVDVTKYTGSGWTGFGEDLVTPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMCGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQQLACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQQLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASCNCPAQSLSEPIIWIYSALMSVCG 480
Db 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASCNCPAQSLSEPIIWIYSALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSSLVRHRWK 518
Db 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSSLVRHRWK 518
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RESULT 11
US-10-175-738-72
; Sequence 72, Application US/10175738
; Publication No. US20030022294A1

```
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C45
; CURRENT FILING DATE: 2002-06-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-72
```

```
Query Match          100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQGDSSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQGDSSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSTYRSKGFDTVTKYTQGSWTGFGVEDLVTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSTYRSKGFDTVTKYTQGSWTGFGVEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGLPVA 240
DB 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPOKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPOKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
DB 361 YLRDENSRSFRITILLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAPASPACAEIAGAASEISGPFSTEDVASNVCVPAQSLSEPIIIVSYALMSVCG 480
DB 421 RAQKRVGFAPASPACAEIAGAASEISGPFSTEDVASNVCVPAQSLSEPIIIVSYALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
DB 481 AILLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
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```
RESULT 12
US-10-175-752-72
; Sequence 72, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
```

```
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT FILING DATE: 2002-06-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-72
```

```
Query Match          100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQGDSSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQGDSSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSTYRSKGFDTVTKYTQGSWTGFGVEDLVTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSTYRSKGFDTVTKYTQGSWTGFGVEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGLPVA 240
DB 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPOKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPOKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
DB 361 YLRDENSRSFRITILLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAPASPACAEIAGAASEISGPFSTEDVASNVCVPAQSLSEPIIIVSYALMSVCG 480
DB 421 RAQKRVGFAPASPACAEIAGAASEISGPFSTEDVASNVCVPAQSLSEPIIIVSYALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
DB 481 AILLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
```

```
RESULT 13
US-10-176-482-72
; Sequence 72, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```


; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT FILING DATE: 2002-06-20
; CURRENT APPLICATION NUMBER: US/10/176,482
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-72

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLIRAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLIRAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQACWTNSETPMSYFPKISI 360
Db 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQACWTNSETPMSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFASPACAEIAGAAVSEISGPSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPACAEIAGAAVSEISGPSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 ALLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
Db 481 ALLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 14

US-10-176-757-72
; Sequence 72, Application US/10176757
; Publication No. US20030022297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C86
; CURRENT FILING DATE: 2002-06-20
; CURRENT APPLICATION NUMBER: US/10/176,757
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-757-72

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLIRAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLIRAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQACWTNSETPMSYFPKISI 360
Db 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQACWTNSETPMSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFASPACAEIAGAAVSEISGPSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPACAEIAGAAVSEISGPSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 ALLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
Db 481 ALLVLIIVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 15

US-10-176-913-72
; Sequence 72, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C66
; CURRENT APPLICATION NUMBER: US/10/176,913
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-913-72

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLRAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTRSKGFDVTVKYTGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSSTRSKGFDVTVKYTGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDLSLTQANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDLSLTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGGOSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVAVARASLIPEFSDGFWTGSQACWTNSETPWSYPPKISI 360
DB 301 IVDSGTTLRLPQKVFDAVVAVARASLIPEFSDGFWTGSQACWTNSETPWSYPPKISI 360
QY 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATMEGFYVIFD 420
DB 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATMEGFYVIFD 420
QY 421 RAQKRVGFAPASPCAETIAGAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
DB 421 RAQKRVGFAPASPCAETIAGAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 ALLVLIVLILLPFRCCQRRPRDPEVNVDESSLVRHRWK 518
DB 481 ALLVLIVLILLPFRCCQRRPRDPEVNVDESSLVRHRWK 518

Search completed: April 1, 2003, 11:50:44
Job time : 36 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:41:59 ; Search time 46 Seconds
(without alignments)
1082.557 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 518
Sequence: 1 MGALARALLPLLAQWLRA.....RRPDEVVNDESSLVRHRWK 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	2.3	501	2 A59090	aspartic proteinas
2	9	1.7	319	2 D87087	hypothetical prote
3	9	1.7	863	2 E82654	conserved hypothet
4	8	1.5	166	2 H64131	transcription regu
5	8	1.5	178	2 T09585	high mobility grou
6	8	1.5	202	2 A71935	hypothetical prote
7	8	1.5	205	2 G64646	hypothetical prote
8	8	1.5	237	2 JQ0729	60K inner-membrane
9	8	1.5	257	2 JQ2332	AR1 protein - cass
10	8	1.5	287	2 G96659	protein F2K11.24 f
11	8	1.5	303	2 H75528	conserved hypothet
12	8	1.5	318	2 B95844	probable sugar ABC
13	8	1.5	319	2 AG0742	high-affinity zinc
14	8	1.5	323	1 PRLJHD	proteinase (EC 3.4
15	8	1.5	327	2 T42999	ethanolamine-phosp
16	8	1.5	340	1 PEIKL	polyporopepsin (EC
17	8	1.5	352	2 C72748	probable sun prote
18	8	1.5	364	2 D96973	spore germination
19	8	1.5	365	2 T37720	ethanolamine-phosp
20	8	1.5	368	2 G65119	hypothetical 40.4
21	8	1.5	393	2 B85992	probable transport
22	8	1.5	399	2 F91146	probable transport
23	8	1.5	449	2 E96676	hypothetical prote
24	8	1.5	472	2 JC7626	amino acid transpo
25	8	1.5	477	2 A35843	lipopolysaccharide
26	8	1.5	548	1 B65173	probable 60K inner
27	8	1.5	548	2 H91208	60 KD inner-membra
28	8	1.5	548	2 B86055	60 KD inner-membra
29	8	1.5	548	2 AF0957	probable membrane

30	8	1.5	580	2 C71182	probable ABC trans
31	8	1.5	637	2 T01961	hypothetical prote
32	8	1.5	904	2 C83030	exoribonuclease RN
33	8	1.5	1247	1 MHHUND	nidogen precursor
34	8	1.5	1622	2 JE0378	DNA (cytosine-5-)-
35	7	1.4	88	2 PN0135	pepsin (EC 3.4.23.
36	7	1.4	96	2 D83228	hypothetical prote
37	7	1.4	97	4 S26485	cytochrome P450 21
38	7	1.4	104	2 AH1551	hypothetical prote
39	7	1.4	106	2 H84370	hypothetical prote
40	7	1.4	115	2 T51324	nickel-insertion a
41	7	1.4	119	2 D86800	prophage p13 prote
42	7	1.4	128	1 UODOR	ubiquitin / riboso
43	7	1.4	131	2 B90553	50S ribosomal prot
44	7	1.4	132	2 AE3445	ATP synthase BME11
45	7	1.4	136	2 E69376	hypothetical prote
46	7	1.4	141	2 D83834	flagellar biosynth
47	7	1.4	149	2 C90885	hypothetical prote
48	7	1.4	149	2 D85733	hypothetical prote
49	7	1.4	149	2 B64897	probable membrane
50	7	1.4	160	2 S58214	apoptosis inducer
51	7	1.4	161	2 D81940	probable membrane
52	7	1.4	161	2 E81166	hypothetical prote
53	7	1.4	168	2 C71828	hypothetical prote
54	7	1.4	168	2 F64689	hypothetical prote
55	7	1.4	170	2 AE1391	H+-transporting AT
56	7	1.4	170	2 AG1766	H+-transporting AT
57	7	1.4	180	2 G70912	hypothetical prote
58	7	1.4	185	2 B64615	hypothetical prote
59	7	1.4	186	2 AE1450	hypothetical prote
60	7	1.4	192	2 AI0268	anthranilate synth
61	7	1.4	200	2 T36305	probable anthranil
62	7	1.4	203	2 AB2285	hypothetical prote
63	7	1.4	206	2 B97594	50S ribosomal prot
64	7	1.4	206	2 AG2815	50S ribosomal prot
65	7	1.4	212	2 C65165	tkk protein - Esch
66	7	1.4	212	2 D91193	probable transcrip
67	7	1.4	212	2 E86040	probable transcrip
68	7	1.4	219	2 H85358	hypothetical prote
69	7	1.4	222	2 S61241	hypothetical prote
70	7	1.4	227	2 G75269	conserved hypothet
71	7	1.4	235	2 F86598	pseudouridine synt
72	7	1.4	235	2 H72025	probable pseudouri
73	7	1.4	235	2 G81515	ribosomal large ch
74	7	1.4	238	2 I38849	LERK-3 - human
75	7	1.4	241	2 F71478	probable pseudouri
76	7	1.4	241	2 E81741	ribosomal large ch
77	7	1.4	244	2 AD3266	asparagine transpo
78	7	1.4	245	2 E87719	protein R119.3 lim
79	7	1.4	249	2 T35589	probable secreted
80	7	1.4	251	2 A83660	hypothetical prote
81	7	1.4	254	2 B87630	hypothetical prote
82	7	1.4	257	2 T44278	conserved hypothet
83	7	1.4	265	2 T46853	yibQ protein limpo
84	7	1.4	267	2 T00114	exodeoxyribonuclea
85	7	1.4	267	2 H64044	exodeoxyribonuclea
86	7	1.4	267	2 B83109	probable transcrip
87	7	1.4	268	1 NCECX3	exodeoxyribonuclea
88	7	1.4	268	2 G90935	exonuclease III [i
89	7	1.4	268	2 C85784	exonuclease III [i
90	7	1.4	270	2 H70690	hypothetical prote
91	7	1.4	276	2 G01564	proteasome chain L
92	7	1.4	276	2 C44324	hypothetical endope
93	7	1.4	276	2 T35483	hypothetical prote
94	7	1.4	284	2 S58650	hypothetical prote
95	7	1.4	289	2 H83433	hypothetical prote
96	7	1.4	289	2 AC0555	probable membrane
97	7	1.4	290	2 AH3448	xhc protein (assi
98	7	1.4	291	2 D82491	hypothetical prote
99	7	1.4	294	2 S36932	chitinase (EC 3.2.
100	7	1.4	296	2 JC6050	homoserine kinase
101	7	1.4	297	2 F69054	cobalamin biosynth
102	7	1.4	298	2 S53483	probable membrane

103	7	1.4	299	2	AC3185	transcription regu	176	7	1.4	392	2	E75042	transporter (major
104	7	1.4	302	2	S61836	cher protein - Rhi	177	7	1.4	394	2	D82725	nicotinate phospho
105	7	1.4	302	2	C64311	Na+/Ca2+-exchangin	178	7	1.4	394	2	S74643	proteinase phoA (E
106	7	1.4	306	1	CEECDL	D-alanine-D-alanin	179	7	1.4	398	2	I51185	cathepsin D (EC 3.
107	7	1.4	306	2	H90640	D-alanine-D-alanin	180	7	1.4	398	2	B75475	glucose-fructose o
108	7	1.4	306	2	H85491	D-alanine-D-alanin	181	7	1.4	408	2	A46712	glycoprotein IIA -
109	7	1.4	306	2	AG0518	D-alanine,D-alanin	182	7	1.4	411	2	S40064	3-deoxy-manno-octu
110	7	1.4	308	2	T14739	hypothetical prote	183	7	1.4	416	2	AG0125	N-acetylmuramoyl-l
111	7	1.4	314	2	TS0871	hypothetical prote	184	7	1.4	416	2	F83010	probable oxidoredu
112	7	1.4	316	2	B82485	iron(III) ABC tran	185	7	1.4	428	2	S47096	cynarase (EC 3.4.2
113	7	1.4	319	2	AH3527	D-xylose-binding p	186	7	1.4	428	2	B90636	survival protein l
114	7	1.4	320	2	C81972	probable 3-oxoacyl	187	7	1.4	428	2	B85487	probable peptidylp
115	7	1.4	320	2	C81029	3-oxoacyl- (acyl-ca	188	7	1.4	428	2	E64726	hypothetical prote
116	7	1.4	320	2	A40660	outer membrane pro	189	7	1.4	433	2	E96649	sensor histidine k
117	7	1.4	325	2	H96032	probable thiamine	190	7	1.4	433	2	B75376	peptidylprolyl iso
118	7	1.4	326	2	JQ0855	hypothetical 36.8K	191	7	1.4	434	2	AD0061	membrane protein l
119	7	1.4	326	2	T34594	probable oxidoredu	192	7	1.4	436	2	C95236	probable cell-surf
120	7	1.4	327	1	A41720	acid phosphatase (193	7	1.4	436	2	G96009	conserved hypothet
121	7	1.4	327	1	HLHUCD	T-cell surface gly	194	7	1.4	436	2	D98100	aspartic hemoglobi
122	7	1.4	327	2	F95889	probable dehydroge	195	7	1.4	444	2	T26229	hypothetical prote
123	7	1.4	328	2	H81996	probable integral	196	7	1.4	452	2	S41717	gastirin receptor -
124	7	1.4	328	2	E81225	hypothetical prote	197	7	1.4	453	2	S32817	hypothetical prote
125	7	1.4	331	2	A83534	probable C4-dicarb	198	7	1.4	460	2	T43224	probable heml prot
126	7	1.4	331	2	F75268	hypothetical prote	199	7	1.4	462	2	G70544	ammonium transport
127	7	1.4	333	2	D70855	probable ilvC prot	200	7	1.4	468	2	A69468	cyprosin (EC 3.4.2
128	7	1.4	333	2	AH0268	anthranilate phosp	201	7	1.4	474	2	T12049	probable penicilli
129	7	1.4	334	2	JC4870	pepsin A (EC 3.4.2	202	7	1.4	474	2	T10011	hypothetical prote
130	7	1.4	335	2	H81453	probable nucleosid	203	7	1.4	475	2	T45766	IMF dehydrogenase
131	7	1.4	336	2	T49112	aspartic proteinas	204	7	1.4	484	1	B69056	probable protein k
132	7	1.4	336	2	T41118	hypothetical prote	205	7	1.4	486	2	F84682	conserved hypothet
133	7	1.4	337	2	G95915	probable sugar ABC	206	7	1.4	488	2	G81213	conserved hypothet
134	7	1.4	337	2	F70071	hypothetical prote	207	7	1.4	490	2	C81790	polyketide synthas
135	7	1.4	339	2	A83358	hypothetical prote	208	7	1.4	491	2	C98275	stomelysin 3 (EC
136	7	1.4	341	2	JC5663	major histocompati	209	7	1.4	491	2	AC3009	4-hydroxybutyrate
137	7	1.4	345	2	AG3186	hypothetical prote	210	7	1.4	491	2	JC6197	probable pbpA prot
138	7	1.4	345	2	AI0926	probable capsid po	211	7	1.4	491	2	H84379	steroid 21-monooxy
139	7	1.4	345	2	B75274	conserved hypothet	212	7	1.4	491	2	F70699	aspartic proteinas
140	7	1.4	346	2	E86715	transcription regu	213	7	1.4	492	2	B86911	hypothetical prote
141	7	1.4	346	2	A83686	hypothetical prote	214	7	1.4	494	2	O4HUC2	aspartic proteinas
142	7	1.4	347	2	AG1817	rod shape-determin	215	7	1.4	496	2	JS0732	hypothetical prote
143	7	1.4	350	2	B82777	conserved hypothet	216	7	1.4	496	2	B83160	hypothetical prote
144	7	1.4	354	2	C71368	probable UDP-N-ace	217	7	1.4	504	2	F70813	probable aspartic
145	7	1.4	354	2	S60967	YGP1 protein precu	218	7	1.4	506	2	T07915	aspartic proteinas
146	7	1.4	356	1	S55437	translation releas	219	7	1.4	506	2	S71591	hypothetical prote
147	7	1.4	365	2	T49733	probable homoserin	220	7	1.4	506	2	F86253	probable aspartic
148	7	1.4	368	2	B97623	cpaA protein (AU00	221	7	1.4	508	2	D85056	hypothetical prote
149	7	1.4	368	2	AB2846	Ca2+/H+ antiporter	222	7	1.4	509	2	JC7272	aspartic proteinas
150	7	1.4	372	2	D98164	hypothetical prote	223	7	1.4	510	2	D89796	hypothetical prote
151	7	1.4	372	2	AC3123	sugar acetylase [i	224	7	1.4	511	2	JC7682	spermatogenesis as
152	7	1.4	373	2	T45747	GDP-D-mannose-4,6-	225	7	1.4	513	2	T09739	hypothetical prote
153	7	1.4	374	2	AB1765	B. subtilis O-succ	226	7	1.4	517	2	SI2227	hypothetical prote
154	7	1.4	376	2	E70918	hypothetical prote	227	7	1.4	518	2	JC4024	poliovirus recepto
155	7	1.4	379	2	B71331	conserved hypothet	228	7	1.4	519	2	T45764	hypothetical prote
156	7	1.4	380	2	S03433	candidapepsin (EC	229	7	1.4	527	2	H85135	hypothetical prote
157	7	1.4	381	2	JC7247	prochymosin - comm	230	7	1.4	527	2	G89999	conserved hypothet
158	7	1.4	382	1	PECH	pepsin A (EC 3.4.2	231	7	1.4	541	2	D97930	conserved hypothet
159	7	1.4	383	2	JC7573	pepsinogen C - Afr	232	7	1.4	547	2	H87679	sensor histidine k
160	7	1.4	384	2	A39314	gastricsin (EC 3.4	233	7	1.4	550	1	A49936	arginine-tRNA liga
161	7	1.4	385	2	C64251	hypothetical prote	234	7	1.4	551	2	T16426	hypothetical prote
162	7	1.4	386	1	PEPG	pepsin A (EC 3.4.2	235	7	1.4	551	2	AI2964	hypothetical prote
163	7	1.4	387	2	D38302	pepsin (EC 3.4.23.	236	7	1.4	554	2	G82538	conserved hypothet
164	7	1.4	387	2	C38302	pepsin (EC 3.4.23.	237	7	1.4	555	2	F86487	unknown protein [i
165	7	1.4	387	2	B38302	pepsin (EC 3.4.23.	238	7	1.4	555	2	T43357	potassium channel
166	7	1.4	387	2	E38302	pepsin (EC 3.4.23.	239	7	1.4	556	2	F82342	methyl-accepting C
167	7	1.4	387	2	I46617	pregnancy-associat	240	7	1.4	558	2	E70756	hypothetical glyci
168	7	1.4	387	2	JC7245	pepsinogen A - com	241	7	1.4	562	2	T05758	hypothetical prote
169	7	1.4	388	1	PEHU	pepsin A (EC 3.4.2	242	7	1.4	569	2	S64957	asparglylloepsin I
170	7	1.4	388	1	PEMOAR	pepsin A (EC 3.4.2	243	7	1.4	570	2	A83118	probable ATP-bindi
171	7	1.4	388	1	PEMQAJ	pepsin A (EC 3.4.2	244	7	1.4	589	2	A34341	poly(3-hydroxybuty
172	7	1.4	388	1	S19684	pepsin A (EC 3.4.2	245	7	1.4	596	2	S57971	aspartic proteinas
173	7	1.4	388	1	S19682	pepsin A (EC 3.4.2	246	7	1.4	601	2	T02581	nodulin-like prote
174	7	1.4	388	2	A30142	pepsin A (EC 3.4.2	247	7	1.4	603	2	JC5063	prostaglandin-endo
175	7	1.4	388	2	B30142	pepsin A (EC 3.4.2	248	7	1.4	604	2	A46150	prostaglandin-endo

249	7	1.4	625	2	E83127	transcription regu	322	7	1.4	1513	2	A70982	probable ATP-depen
250	7	1.4	626	2	H82147	methy1-accepting c	323	7	1.4	1533	2	A46221	abdominal segment
251	7	1.4	638	2	E71018	hypothetical prote	324	7	1.4	1632	2	C70752	probable ctgPI prot
252	7	1.4	644	2	T34879	probable integral	325	7	1.4	1690	2	T35694	ATP dependent DNA
253	7	1.4	646	2	T28868	hypothetical prote	326	7	1.4	1875	2	A36429	integrin beta-4 ch
254	7	1.4	646	2	T38171	probable serine/th	327	7	1.4	2014	2	T21560	hypothetical prote
255	7	1.4	660	1	UYPVFP	noncapsid protein	328	7	1.4	2025	2	D86201	hypothetical prote
256	7	1.4	662	1	UYPVNA	noncapsid protein	329	7	1.4	2894	2	C64474	hypothetical prote
257	7	1.4	682	2	AE0033	secretion system a	330	7	1.4	6486	2	T31076	tyrocidine synthet
258	7	1.4	689	2	T11917	NADH2 dehydrogenas	331	7	1.4	8243	2	T31307	type I fatty acid
259	7	1.4	690	2	B82409	alpha-amylase VCA0	332	6	1.2	9	2	PT0326	ig heavy chain CRD
260	7	1.4	690	2	D98318	ABC protein AGR_L_	333	6	1.2	16	2	A44352	candidapepsin (EC
261	7	1.4	697	2	T37827	hypothetical prote	334	6	1.2	23	2	PH1364	ig heavy chain DJ
262	7	1.4	699	2	E84565	hypothetical prote	335	6	1.2	31	2	T46840	hypothetical prote
263	7	1.4	704	1	EFECEG	translation elonga	336	6	1.2	33	2	I68894	gene TAP1 protein
264	7	1.4	704	2	JC1424	translation elonga	337	6	1.2	39	2	S35325	protein kinase sgg
265	7	1.4	704	2	G91152	translation elonga	338	6	1.2	40	2	D96733	hypothetical prote
266	7	1.4	704	2	C85998	translation elonga	339	6	1.2	48	2	JV0019	hypothetical prote
267	7	1.4	704	2	AC1005	elongation factor	340	6	1.2	49	2	S55324	endo-beta-1,6-gluc
268	7	1.4	707	2	F86925	probable acyl-CoA	341	6	1.2	52	1	S07502	gene 5.9 protein -
269	7	1.4	709	2	T29692	hypothetical prote	342	6	1.2	52	1	S42315	gene 5.9 protein -
270	7	1.4	715	2	G86634	hypothetical prote	343	6	1.2	52	2	A34657	cathepsin E (EC 3.
271	7	1.4	715	2	B43943	ATP-dependent memb	344	6	1.2	59	2	B87614	pilus subunit prot
272	7	1.4	717	2	A39203	comA protein - Str	345	6	1.2	64	2	E98056	hypothetical prote
273	7	1.4	717	2	C97877	transport ATP-bind	346	6	1.2	65	2	F81607	hypothetical prote
274	7	1.4	717	2	F95004	hypothetical prote	347	6	1.2	67	2	AB1771	hypothetical prote
275	7	1.4	721	2	F82198	probable toxin sec	348	6	1.2	67	2	AF1487	probable transcrip
276	7	1.4	722	2	T46560	swi2 protein - fis	349	6	1.2	67	2	AI1126	probable transcrip
277	7	1.4	725	2	T03514	probable secretion	350	6	1.2	68	2	E86772	hypothetical prote
278	7	1.4	754	1	S62512	probable cysteinyl	351	6	1.2	69	2	B83632	hypothetical prote
279	7	1.4	773	2	JH0609	protein-tyrosine-p	352	6	1.2	71	2	T07731	1-aminocyclopropan
280	7	1.4	775	2	S55345	protein-tyrosine-p	353	6	1.2	71	2	S22905	lysis protein S -
281	7	1.4	784	2	AC1091	5'-nucleotidase, p	354	6	1.2	72	2	S01799	pepsin (EC 3.4.23.
282	7	1.4	788	2	G82764	membrane protein X	355	6	1.2	73	1	F2NT0P	photosystem II pho
283	7	1.4	802	2	D85035	ent-kaurene synthe	356	6	1.2	73	2	S21754	gastricsin (EC 3.4
284	7	1.4	830	2	C69011	conserved hypothet	357	6	1.2	73	2	A87686	collagen alpha 1(X
285	7	1.4	831	2	A48489	nitrate reductase	358	6	1.2	74	2	B40020	aspartic proteinas
286	7	1.4	832	2	C86431	T518.5 protein - A	359	6	1.2	79	2	S03266	hypothetical prote
287	7	1.4	843	1	JDVLVR	DNA-directed DNA p	360	6	1.2	79	2	D64596	E5 protein - human
288	7	1.4	843	2	T16906	hypothetical prote	361	6	1.2	81	1	WSWL35	mitochondrial prot
289	7	1.4	881	2	F83530	hypothetical prote	362	6	1.2	81	2	A24522	hypothetical prote
290	7	1.4	887	2	T20866	hypothetical prote	363	6	1.2	81	2	H82515	hypothetical prote
291	7	1.4	899	2	S62428	probable coiled co	364	6	1.2	83	2	C69440	hypothetical prote
292	7	1.4	933	1	BVECCC	sensor protein rcs	365	6	1.2	87	2	JQ1135	hypothetical prote
293	7	1.4	933	2	C91017	sensor for ctr cap	366	6	1.2	88	2	A28056	levitide precursor
294	7	1.4	933	2	E85861	hypothetical prote	367	6	1.2	88	2	D64562	hypothetical prote
295	7	1.4	939	2	AE2275	hypothetical prote	368	6	1.2	88	2	T31230	hypothetical prote
296	7	1.4	958	2	S47179	integrin beta-4 pr	369	6	1.2	89	2	T14135	NADH2 dehydrogenas
297	7	1.4	964	2	JC5545	diguanylate cyclas	370	6	1.2	89	2	A33542	islet amyloid poly
298	7	1.4	964	2	AG3433	lantibiotic Peps b	371	6	1.2	89	2	F86706	hypothetical prote
299	7	1.4	967	2	S58360	hypothetical prote	372	6	1.2	90	2	S56455	probable ATP-bindi
300	7	1.4	971	2	H97454	conserved hypothet	373	6	1.2	90	2	D70678	hypothetical prote
301	7	1.4	971	2	AB2673	beta-galactosidase	374	6	1.2	91	1	S00060	phospholipid trans
302	7	1.4	1015	2	I39697	type II CAMP-depen	375	6	1.2	91	2	T42907	hypothetical prote
303	7	1.4	1015	2	A42915	alpha-mannosidase	376	6	1.2	92	2	S06034	hypothetical prote
304	7	1.4	1039	2	G83748	acid trehalase hom	377	6	1.2	92	2	S06033	hypothetical prote
305	7	1.4	1054	2	T18304	hypothetical prote	378	6	1.2	92	2	AG3634	noirF [imported] -
306	7	1.4	1062	2	T46444	hypothetical prote	379	6	1.2	94	2	S03380	major fecal allerg
307	7	1.4	1073	2	S56220	probable membrane	380	6	1.2	96	2	A87110	conserved hypothet
308	7	1.4	1121	2	C87973	protein Y43F8C.12	381	6	1.2	98	2	PQ0496	hypothetical prote
309	7	1.4	1131	2	AD2166	two-component sens	382	6	1.2	99	2	B95393	hypothetical prote
310	7	1.4	1142	2	C97080	levanase/invertase	383	6	1.2	99	2	AI1907	hypothetical prote
311	7	1.4	1153	2	T26883	hypothetical prote	384	6	1.2	100	2	A38685	apolipoprotein C-I
312	7	1.4	1172	2	T36053	probable ABC-type	385	6	1.2	100	2	F95369	hypothetical prote
313	7	1.4	1194	1	G70837	probable ABC trans	386	6	1.2	100	2	B71410	hypothetical prote
314	7	1.4	1236	2	T50904	Mg protoporphyrin	387	6	1.2	100	2	D98044	ABC transporter, t
315	7	1.4	1238	2	T03465	probable exonuclea	388	6	1.2	101	2	A33351	H+-transporting tw
316	7	1.4	1246	2	G89287	protein H39E23.1 l	389	6	1.2	101	2	T17689	hypothetical prote
317	7	1.4	1253	2	F86436	hypothetical prote	390	6	1.2	101	2	G72450	hypothetical prote
318	7	1.4	1269	2	T14476	psIA protein - sli	391	6	1.2	101	2	AD3542	hypothetical prote
319	7	1.4	1336	2	T39978	M-factor ABC-type	392	6	1.2	101	2	B83061	conserved hypothet
320	7	1.4	1379	2	T13718	pollux gene protei	393	6	1.2	102	2	B34770	ORF2 protein - sal
321	7	1.4	1433	2	A46053	bullous pemphigoid	394	6	1.2	102	2	AH3257	bolA protein [impo

395	6	1.2	102	2	D90915	hypothetical prote
396	6	1.2	102	2	A85764	hypothetical prote
397	6	1.2	102	2	A12693	conserved hypothet
398	6	1.2	103	2	T03013	hypothetical prote
399	6	1.2	103	2	G75513	conserved hypothet
400	6	1.2	104	2	G75090	hypothetical prote
401	6	1.2	105	2	S62844	H+-transporting tw
402	6	1.2	105	2	B69857	chaperonin homolog
403	6	1.2	105	2	T49332	hypothetical prote
404	6	1.2	105	2	G90023	hypothetical prote
405	6	1.2	105	2	AD3365	hypothetical prote
406	6	1.2	106	2	S72815	hypothetical prote
407	6	1.2	107	2	JQ2035	hypothetical 11.7K
408	6	1.2	107	2	T25670	hypothetical prote
409	6	1.2	108	2	S09278	insulin precursor
410	6	1.2	108	2	A39883	insulin precursor
411	6	1.2	109	2	A45887	leukocyte differen
412	6	1.2	109	2	S53546	hypothetical prote
413	6	1.2	109	2	H72641	hypothetical prote
414	6	1.2	110	1	PEBO	pepsin A (EC 3.4.2
415	6	1.2	110	1	IPHU	insulin precursor
416	6	1.2	110	1	INRB	insulin precursor
417	6	1.2	110	1	IPDG	insulin precursor
418	6	1.2	110	2	B42179	insulin precursor
419	6	1.2	110	2	JQ0178	insulin precursor
420	6	1.2	110	2	E69607	protein secretion
421	6	1.2	110	2	D95267	hypothetical prote
422	6	1.2	112	2	T44986	probable sulfate/t
423	6	1.2	112	2	T48324	DNAJ protein-like
424	6	1.2	112	2	G95961	hypothetical membr
425	6	1.2	112	2	AB0687	probable membrane
426	6	1.2	113	2	A70553	hypothetical prote
427	6	1.2	113	2	T42985	hypothetical prote
428	6	1.2	113	2	C83893	hypothetical prote
429	6	1.2	114	2	D46516	Ig lambda chain V
430	6	1.2	114	2	F83735	chaperonin BH0686
431	6	1.2	114	2	E72724	hypothetical prote
432	6	1.2	114	2	AE2761	hypothetical prote
433	6	1.2	115	1	DNHUN3	NADH2 dehydrogenas
434	6	1.2	115	1	QXBO3M	NADH2 dehydrogenas
435	6	1.2	115	1	QXMS3M	NADH2 dehydrogenas
436	6	1.2	115	2	S04754	NADH2 dehydrogenas
437	6	1.2	115	2	S26158	NADH2 dehydrogenas
438	6	1.2	115	2	A55746	NADH2 dehydrogenas
439	6	1.2	115	2	S41842	NADH2 dehydrogenas
440	6	1.2	115	2	S41827	NADH2 dehydrogenas
441	6	1.2	115	2	C55746	NADH2 dehydrogenas
442	6	1.2	115	2	S65745	NADH2 dehydrogenas
443	6	1.2	115	2	H58850	NADH2 dehydrogenas
444	6	1.2	115	2	T17139	NADH2 dehydrogenas
445	6	1.2	115	2	T17176	NADH2 dehydrogenas
446	6	1.2	115	2	T17182	NADH2 dehydrogenas
447	6	1.2	115	2	T17347	NADH2 dehydrogenas
448	6	1.2	115	2	T17359	NADH2 dehydrogenas
449	6	1.2	115	2	T17362	NADH2 dehydrogenas
450	6	1.2	115	2	T17135	NADH2 dehydrogenas
451	6	1.2	115	2	T17142	NADH2 dehydrogenas
452	6	1.2	115	2	T17173	NADH2 dehydrogenas
453	6	1.2	115	2	T17085	NADH2 dehydrogenas
454	6	1.2	115	2	T17094	NADH2 dehydrogenas
455	6	1.2	115	2	T17082	NADH2 dehydrogenas
456	6	1.2	115	2	T17098	NADH2 dehydrogenas
457	6	1.2	115	2	T17090	NADH2 dehydrogenas
458	6	1.2	115	2	T11448	NADH2 dehydrogenas
459	6	1.2	115	2	T11500	NADH2 dehydrogenas
460	6	1.2	115	2	T11396	NADH2 dehydrogenas
461	6	1.2	115	2	T11461	NADH2 dehydrogenas
462	6	1.2	115	2	T11840	NADH2 dehydrogenas
463	6	1.2	115	2	T11864	NADH2 dehydrogenas
464	6	1.2	115	2	T10979	NADH2 dehydrogenas
465	6	1.2	115	2	T11057	NADH2 dehydrogenas
466	6	1.2	115	2	T11487	NADH2 dehydrogenas
467	6	1.2	115	2	T11147	NADH2 dehydrogenas
468	6	1.2	115	2	T11254	NADH2 dehydrogenas
469	6	1.2	115	2	T11344	NADH2 dehydrogenas
470	6	1.2	115	2	T11370	NADH2 dehydrogenas
471	6	1.2	115	2	T11409	NADH2 dehydrogenas
472	6	1.2	115	2	H59153	NADH2 dehydrogenas
473	6	1.2	115	2	T17350	NADH2 dehydrogenas
474	6	1.2	115	2	D64914	hypothetical prote
475	6	1.2	116	2	S08425	NADH2 dehydrogenas
476	6	1.2	116	2	S10194	NADH2 dehydrogenas
477	6	1.2	116	2	A30401	NADH2 dehydrogenas
478	6	1.2	116	2	B30401	NADH2 dehydrogenas
479	6	1.2	116	2	E30396	NADH2 dehydrogenas
480	6	1.2	116	2	F30396	NADH2 dehydrogenas
481	6	1.2	116	2	G30396	NADH2 dehydrogenas
482	6	1.2	116	2	H30396	NADH2 dehydrogenas
483	6	1.2	116	2	S36004	NADH2 dehydrogenas
484	6	1.2	116	2	H58892	NADH2 dehydrogenas
485	6	1.2	116	2	T11174	NADH2 dehydrogenas
486	6	1.2	116	2	S47877	NADH2 dehydrogenas
487	6	1.2	116	2	H90612	NADH dehydrogenase
488	6	1.2	116	2	H90614	NADH dehydrogenase
489	6	1.2	116	2	H90616	NADH dehydrogenase
490	6	1.2	116	2	H90618	NADH dehydrogenase
491	6	1.2	116	2	H90620	NADH dehydrogenase
492	6	1.2	116	2	H90622	NADH dehydrogenase
493	6	1.2	116	2	H90624	NADH dehydrogenase
494	6	1.2	116	2	H90626	NADH dehydrogenase
495	6	1.2	116	2	T10993	NADH2 dehydrogenas
496	6	1.2	116	2	T11200	NADH2 dehydrogenas
497	6	1.2	116	2	T11294	NADH2 dehydrogenas
498	6	1.2	116	2	T11541	NADH2 dehydrogenas
499	6	1.2	116	2	T11082	NADH2 dehydrogenas
500	6	1.2	116	2	T11108	NADH2 dehydrogenas
501	6	1.2	116	2	T11187	NADH2 dehydrogenas
502	6	1.2	116	2	T11331	NADH2 dehydrogenas
503	6	1.2	116	2	T11771	NADH2 dehydrogenas
504	6	1.2	116	2	T09954	NADH2 dehydrogenas
505	6	1.2	116	2	T11029	NADH2 dehydrogenas
506	6	1.2	116	2	T11307	NADH2 dehydrogenas
507	6	1.2	116	2	T11435	NADH2 dehydrogenas
508	6	1.2	117	2	T45557	NADH2 dehydrogenas
509	6	1.2	117	2	T09155	NADH2 dehydrogenas
510	6	1.2	119	2	S24294	lipid transfer pro
511	6	1.2	119	2	S24291	chorion protein -
512	6	1.2	119	2	B45937	early chorion prot
513	6	1.2	120	2	D95980	hypothetical prote
514	6	1.2	121	2	S24293	chorion class CA p
515	6	1.2	121	2	B97446	hypothetical prote
516	6	1.2	121	2	AC2664	ATP synthase, subu
517	6	1.2	121	2	T18126	hypothetical prote
518	6	1.2	121	2	G90170	hypothetical prote
519	6	1.2	121	2	F72580	hypothetical prote
520	6	1.2	122	1	A55115	uterine plasmin/tr
521	6	1.2	122	2	JQ0150	hypothetical 13K p
522	6	1.2	123	2	D84383	hypothetical prote
523	6	1.2	124	1	NRCB	pancreatic ribonuc
524	6	1.2	124	1	GCAF	glucagon 1 precurs
525	6	1.2	125	2	TN0470	interferon gamma-i
526	6	1.2	125	2	F84604	hypothetical prote
527	6	1.2	125	2	B97470	hypothetical prote
528	6	1.2	125	2	AG2688	Na+/H+ antiporter
529	6	1.2	125	2	H70101	glpE protein (glpE
530	6	1.2	125	2	F83072	hypothetical prote
531	6	1.2	125	2	F70106	hypothetical prote
532	6	1.2	125	2	S74723	hypothetical prote
533	6	1.2	126	2	B83265	hypothetical prote
534	6	1.2	126	2	H86347	hypothetical prote
535	6	1.2	128	2	H82060	ribosomal protein
536	6	1.2	128	2	H72500	hypothetical prote
537	6	1.2	128	2	H82267	conserved hypothet
538	6	1.2	128	2	T30714	hypothetical prote
539	6	1.2	129	2	E90535	hypothetical prote
540	6	1.2	129	2	I56195	gene Tap-1 protein

541	6	1.2	129	2	AB3459	hypothetical prote
542	6	1.2	130	2	T36788	hypothetical prote
543	6	1.2	130	2	T12478	hypothetical prote
544	6	1.2	131	2	S24285	RNA-directed RNA p
545	6	1.2	131	2	S06479	fatty acid-binding
546	6	1.2	131	2	D90419	transcriptional re
547	6	1.2	131	2	B84598	hypothetical prote
548	6	1.2	132	2	F70650	hypothetical prote
549	6	1.2	132	2	D69520	hypothetical prote
550	6	1.2	132	2	T35141	hypothetical prote
551	6	1.2	132	2	H75548	hypothetical prote
552	6	1.2	132	2	AB1767	ATP synthase chain
553	6	1.2	132	2	AB1391	ATP synthase chain
554	6	1.2	133	2	D87690	hypothetical prote
555	6	1.2	133	2	S69803	hypothetical prote
556	6	1.2	134	2	B72101	ribosomal protein
557	6	1.2	134	2	F86521	ribosomal protein
558	6	1.2	134	2	F72802	gp24 protein - Myc
559	6	1.2	134	2	F75543	hypothetical prote
560	6	1.2	134	2	F97475	id894 (AF322013) [
561	6	1.2	134	2	AC3234	conserved hypotet
562	6	1.2	135	2	D71228	hypothetical prote
563	6	1.2	136	2	T07975	probable arabinoga
564	6	1.2	136	2	T07945	probable arabinoga
565	6	1.2	136	2	H82763	hypothetical prote
566	6	1.2	137	2	S53025	photosystem II pro
567	6	1.2	138	2	G65096	hypothetical prote
568	6	1.2	138	2	D91124	hypothetical prote
569	6	1.2	138	2	C85969	hypothetical prote
570	6	1.2	138	2	H75333	hypothetical prote
571	6	1.2	138	2	S20087	homeotic protein b
572	6	1.2	138	2	H83299	hypothetical prote
573	6	1.2	139	2	D72539	hypothetical prote
574	6	1.2	139	2	G69543	conserved hypotet
575	6	1.2	139	2	D82296	transcription regu
576	6	1.2	140	2	S75420	ribosomal protein
577	6	1.2	140	2	E75518	probable biopolyme
578	6	1.2	140	2	F69389	hypothetical prote
579	6	1.2	141	2	A91249	probable transcrip
580	6	1.2	141	2	A90130	hypothetical prote
581	6	1.2	141	2	F97978	alanine dehydrogen
582	6	1.2	141	2	AC3590	3-oxoadipate CoA-t
583	6	1.2	142	2	T40837	DNA-directed RNA p
584	6	1.2	142	2	S27050	hemoglobin alpha-2
585	6	1.2	142	2	A60514	hemoglobin alpha-2
586	6	1.2	142	2	AC3345	LSU ribosomal prot
587	6	1.2	142	2	T49256	hypothetical prote
588	6	1.2	143	2	T13214	minor capsid prote
589	6	1.2	143	2	T41630	very hypothetical
590	6	1.2	143	2	B70010	Na+/H+ antiporter
591	6	1.2	144	2	B82556	C-type cytochrome
592	6	1.2	144	2	C70455	hypothetical prote
593	6	1.2	144	2	T49706	hypothetical prote
594	6	1.2	145	2	T34303	hypothetical prote
595	6	1.2	145	2	D83424	hypothetical prote
596	6	1.2	146	2	A72115	conserved hypotet
597	6	1.2	146	2	D86508	hypothetical prote
598	6	1.2	146	2	G90337	hypothetical prote
599	6	1.2	147	2	A26697	hypothetical prote
600	6	1.2	147	2	S05320	echinoidin - sea u
601	6	1.2	147	2	G72384	transhyretin prec
602	6	1.2	148	2	C70451	conserved hypotet
603	6	1.2	148	2	E75283	biopolymer transpo
604	6	1.2	148	2	F86701	conserved hypotet
605	6	1.2	148	2	C72422	hypothetical prote
606	6	1.2	148	2	H95849	hypothetical prote
607	6	1.2	149	2	D98196	hypothetical prote
608	6	1.2	149	2	AF3090	conserved hypotet
609	6	1.2	151	2	A86705	transcriptional re
610	6	1.2	151	2	D87683	conserved hypotet
611	6	1.2	151	2	A82978	hypothetical prote
612	6	1.2	151	2	G84165	hypothetical prote
613	6	1.2	151	2	T18478	hypothetical prote
614	6	1.2	152	2	B75042	aspartate carbamoy
615	6	1.2	152	2	F72702	hypothetical prote
616	6	1.2	152	2	D75367	hypothetical prote
617	6	1.2	152	2	B72754	hypothetical prote
618	6	1.2	153	2	S12206	hypothetical prote
619	6	1.2	153	2	D83012	hypothetical prote
620	6	1.2	153	2	AF3648	hypothetical prote
621	6	1.2	154	2	AB0163	probable membrane
622	6	1.2	155	2	E64105	acetyl-CoA carboxy
623	6	1.2	155	2	AB3512	nodulation protein
624	6	1.2	155	2	E72661	hypothetical prote
625	6	1.2	155	2	AB1226	hypothetical prote
626	6	1.2	155	2	AD1579	hypothetical prote
627	6	1.2	157	2	H83082	probable transcrip
628	6	1.2	157	2	C82121	phosphohistidine p
629	6	1.2	157	2	H72673	hypothetical prote
630	6	1.2	158	2	D72017	conserved hypotet
631	6	1.2	158	2	H86607	hypothetical prote
632	6	1.2	158	2	B75141	hypothetical prote
633	6	1.2	158	2	D83382	hypothetical prote
634	6	1.2	159	2	G70841	hypothetical prote
635	6	1.2	159	2	H86997	conserved hypotet
636	6	1.2	159	2	T35623	probable protein p
637	6	1.2	159	2	B71423	hypothetical prote
638	6	1.2	160	2	B70718	hypothetical prote
639	6	1.2	160	2	C70947	hypothetical prote
640	6	1.2	160	2	H70889	hypothetical prote
641	6	1.2	161	1	VCTMSH	coat protein - cuc
642	6	1.2	161	2	S54434	phosphoribosylamin
643	6	1.2	161	2	S27127	tropomyosin homolo
644	6	1.2	161	2	H69184	conserved hypotet
645	6	1.2	161	2	S52600	probable membrane
646	6	1.2	161	2	S53473	probable membrane
647	6	1.2	161	2	E71099	hypothetical prote
648	6	1.2	161	2	AD2606	hypothetical prote
649	6	1.2	162	1	D71206	hypothetical prote
650	6	1.2	162	2	H75019	hypothetical prote
651	6	1.2	162	2	C82765	conserved hypotet
652	6	1.2	162	2	C69495	conserved hypotet
653	6	1.2	162	2	D97467	hypothetical prote
654	6	1.2	162	2	AG2685	acetyltransferase
655	6	1.2	163	2	H72759	probable dCTP deam
656	6	1.2	164	1	RGECLR	leucine-responsive
657	6	1.2	164	1	S22196	MJ0653 homolog - D
658	6	1.2	164	2	G64132	phosphoribosylamin
659	6	1.2	164	2	S59991	transcription regu
660	6	1.2	164	2	S59993	transcription regu
661	6	1.2	164	2	S59992	transcription regu
662	6	1.2	164	2	B82142	leucine-responsive
663	6	1.2	164	2	AI0167	leucine-responsive
664	6	1.2	164	2	F90750	leucine-responsive
665	6	1.2	164	2	D85614	leucine-responsive
666	6	1.2	164	2	AE0611	leucine-responsive
667	6	1.2	165	1	A54184	destrin [validated
668	6	1.2	165	1	A35179	destrin - pig
669	6	1.2	165	2	H75284	hypothetical prote
670	6	1.2	165	2	AI2904	hypothetical prote
671	6	1.2	165	2	S61602	probable membrane
672	6	1.2	166	2	D69695	ribosomal protein
673	6	1.2	166	2	H72579	hypothetical prote
674	6	1.2	167	2	C97542	hypothetical prote
675	6	1.2	167	2	B43755	vasopressin / neur
676	6	1.2	168	2	D29016	cell division inhi
677	6	1.2	168	2	AE0175	probable cell divi
678	6	1.2	168	2	D75259	hypothetical prote
679	6	1.2	168	2	A72226	conserved hypotet
680	6	1.2	168	2	G83428	hypothetical prote
681	6	1.2	169	1	QOECAl	cell division inhi
682	6	1.2	169	2	B29016	cell division inhi
683	6	1.2	169	2	C29016	cell division inhi
684	6	1.2	169	2	B90759	suppressor of lon
685	6	1.2	169	2	H85622	hypothetical prote
686	6	1.2	169	2	AB0627	cell division inhi

687	6	1.2	169	2	A89912	hypothetical prote	760	6	1.2	192	2	H70375	conserved hypothet
688	6	1.2	169	2	D90857	hypothetical prote	761	6	1.2	192	2	G71089	hypothetical prote
689	6	1.2	169	2	B75490	hypothetical prote	762	6	1.2	194	2	E84097	imidazoleglycerol-
690	6	1.2	169	2	F85762	hypothetical prote	763	6	1.2	194	2	H82520	hypothetical prote
691	6	1.2	170	2	B90214	NADH dehydrogenase	764	6	1.2	194	2	T14746	hypothetical prote
692	6	1.2	171	2	C87418	hypothetical prote	765	6	1.2	195	2	B40635	anthranilate synth
693	6	1.2	171	2	E87459	cytochrome c famil	766	6	1.2	195	2	A99240	anthranilate synth
694	6	1.2	171	2	G84421	probable auxin-ind	767	6	1.2	195	2	H97288	para-aminobenzoate
695	6	1.2	171	2	A84561	probable bZIP tran	768	6	1.2	195	2	G70211	hypothetical prote
696	6	1.2	172	2	A91070	hypothetical prote	769	6	1.2	195	2	A96998	CDP-diglyceride sy
697	6	1.2	172	2	D85914	hypothetical prote	770	6	1.2	196	2	D87712	imidazoleglycerol-
698	6	1.2	172	2	T02229	protein BYJ15 - co	771	6	1.2	196	2	A71325	hypothetical prote
699	6	1.2	172	2	B86439	protein T19E23.11	772	6	1.2	196	2	F88382	hypothetical prote
700	6	1.2	173	2	S34767	neuropeptides prec	773	6	1.2	196	2	D81696	acetyltransferase
701	6	1.2	173	2	AF3293	crossover junction	774	6	1.2	196	2	AD2949	imidazoleglycerol-
702	6	1.2	173	2	F45392	orf6 protein - por	775	6	1.2	197	2	JQ0638	hypothetical prote
703	6	1.2	173	2	A44281	envelope protein -	776	6	1.2	197	2	S25106	capsid protein - b
704	6	1.2	173	2	A75512	conserved hypothet	777	6	1.2	197	2	S70678	membrane protein l
705	6	1.2	173	2	D83464	glucuronosyltransf	778	6	1.2	197	2	S51372	T-cell surface gly
706	6	1.2	174	2	A47113	hypothetical prote	779	6	1.2	198	2	S25656	hypothetical prote
707	6	1.2	174	2	E65046	hypothetical prote	780	6	1.2	198	2	T29135	N-(5'-phosphoribos
708	6	1.2	174	2	B72712	probable membrane	781	6	1.2	199	2	E95211	coat protein - bee
709	6	1.2	174	2	S64440	hypothetical prote	782	6	1.2	199	2	S41316	molYdendum transpo
710	6	1.2	174	2	S73052	hypothetical prote	783	6	1.2	199	2	AE3509	lipoprotein signal
711	6	1.2	174	2	H87617	hypothetical prote	784	6	1.2	199	2	I64125	probable lppc prot
712	6	1.2	175	2	D86787	hypothetical prote	785	6	1.2	199	2	F86832	coat protein - bee
713	6	1.2	175	2	B44102	di-N-acetylchitobi	786	6	1.2	200	2	T18479	coat protein - bee
714	6	1.2	176	2	I48752	gene RXRbeta1 prot	787	6	1.2	201	1	VCVQGB	molYdendum transpo
715	6	1.2	176	2	T18921	hypothetical prote	788	6	1.2	201	2	H90025	lipoprotein signal
716	6	1.2	176	2	B70445	heat shock protein	789	6	1.2	201	2	A87059	probable heme expo
717	6	1.2	177	2	I39709	fixr homolog - Agr	790	6	1.2	201	2	D70519	hypothetical prote
718	6	1.2	178	2	D86696	pantothenate metab	791	6	1.2	202	1	VCVQFL	hypothetical prote
719	6	1.2	178	2	I40124	outer surface prot	792	6	1.2	202	2	C72701	hypothetical prote
720	6	1.2	178	2	S03629	neurogenic gene co	793	6	1.2	202	2	B83375	hypothetical prote
721	6	1.2	178	2	T08444	hypothetical prote	794	6	1.2	202	2	AC2875	hypothetical prote
722	6	1.2	178	2	E88637	protein W09G12.6 l	795	6	1.2	202	2	C70650	probable lipoprote
723	6	1.2	179	2	S39078	auxin-induced prot	796	6	1.2	202	2	H70760	nef protein (clone
724	6	1.2	179	2	C75469	hypothetical prote	797	6	1.2	204	2	S03246	conserved hypothet
725	6	1.2	180	2	T16445	hypothetical prote	798	6	1.2	204	2	H72256	hypothetical prote
726	6	1.2	180	2	D83254	probable transcrip	799	6	1.2	204	2	C97389	conserved hypothet
727	6	1.2	182	2	S70689	adenine phosphorib	800	6	1.2	204	2	AD2607	nef protein - huma
728	6	1.2	182	2	A71688	heat shock protein	801	6	1.2	205	1	B44963	guanylate kinase (
729	6	1.2	182	2	A97754	heat shock protein	802	6	1.2	205	2	C86862	D-alanine-D-alanin
730	6	1.2	183	2	A72657	VPS29-like phospho	803	6	1.2	205	2	PQ0272	heme exporter prot
731	6	1.2	183	2	T22183	hypothetical prote	804	6	1.2	205	2	G64989	ATP binding protei
732	6	1.2	184	2	S10125	alpha-2u-globulin	805	6	1.2	205	2	B91015	ATP binding protei
733	6	1.2	185	2	AF0787	thiol, disulfide in	806	6	1.2	205	2	D85859	heme exporter prot
734	6	1.2	185	2	AI0960	CD45-associated 30	807	6	1.2	205	2	AC0960	heme exporter prot
735	6	1.2	185	2	A49957	conserved hypothet	808	6	1.2	205	2	AD0788	hypothetical prote
736	6	1.2	185	2	B70072	probable CDP-alcoh	809	6	1.2	205	2	A36377	B61 protein precur
737	6	1.2	186	2	D75005	SSU ribosomal prot	810	6	1.2	205	2	S37804	hypothetical prote
738	6	1.2	186	2	AH3348	hypothetical prote	811	6	1.2	205	2	T34724	probable transcrip
739	6	1.2	186	2	AB2408	hypothetical prote	812	6	1.2	206	2	JC4268	hypothetical prote
740	6	1.2	186	2	T32656	hypothetical prote	813	6	1.2	206	2	AF2299	probable membrane
741	6	1.2	186	2	AF2556	hypothetical prote	814	6	1.2	206	2	AE0891	fibroblast growth
742	6	1.2	187	2	S69315	hypothetical prote	815	6	1.2	206	2	T48149	cobalt transport A
743	6	1.2	187	2	T38452	hypothetical prote	816	6	1.2	206	2	F72670	probable membrane
744	6	1.2	187	2	T08912	hypothetical prote	817	6	1.2	206	2	H89828	hypothetical prote
745	6	1.2	188	2	E71157	probable CDP-alcoh	818	6	1.2	207	2	B86498	conserved hypothet
746	6	1.2	188	2	F83855	GTP cyclohydrolase	819	6	1.2	207	2	B72124	superoxide dismuta
747	6	1.2	188	2	T02781	probable conjugal	820	6	1.2	207	2	JE0045	imidazoleglycerol-
748	6	1.2	188	2	B84719	hypothetical prote	821	6	1.2	207	2	B84151	hypothetical prote
749	6	1.2	188	2	AF3559	hypothetical prote	822	6	1.2	207	2	T36937	hypothetical prote
750	6	1.2	188	2	B70736	hypothetical prote	823	6	1.2	208	2	T09901	hydrogenase matura
751	6	1.2	189	2	A71569	hypothetical prote	824	6	1.2	209	1	S53657	phosphoribosylanth
752	6	1.2	189	2	JC7262	receptor activity	825	6	1.2	209	2	G98075	prolactin precursor
753	6	1.2	189	2	F98333	hypothetical prote	826	6	1.2	209	2	S30541	hypothetical prote
754	6	1.2	189	2	T18480	hypothetical prote	827	6	1.2	209	2	G72528	hypothetical prote
755	6	1.2	190	2	T10740	carbonate dehydrat	828	6	1.2	210	2	F69510	hypothetical prote
756	6	1.2	191	2	I45716	GTP-binding protei	829	6	1.2	210	2	B71527	micrococcal nuclea
757	6	1.2	191	2	C40364	hypothetical prote	830	6	1.2	211	2	D69888	deoxyribose-phosph
758	6	1.2	191	2	E75132	molybdopterin-guan	831	6	1.2	211	2	A69619	conserved hypothet
759	6	1.2	192	1	NNSE2	anthranilate synth	832	6	1.2	211	2	A81700	conserved hypothet

833	6	1.2	212	1	R5HSLH	ribosomal protein	906	6	1.2	230	2	H72244	conserved hypothet
834	6	1.2	212	2	T36720	probable glutamine	907	6	1.2	230	2	G83680	ABC transporter (A
835	6	1.2	212	2	H84266	50S ribosomal prot	908	6	1.2	230	2	E87578	hypothetical prote
836	6	1.2	212	2	T05721	germin-like protei	909	6	1.2	231	2	H81698	conserved hypothet
837	6	1.2	212	2	T44970	gas-vesicle operon	910	6	1.2	231	2	G69403	hypothetical prote
838	6	1.2	213	2	F98019	hypothetical prote	911	6	1.2	231	2	S48966	hypothetical prote
839	6	1.2	213	2	B87694	cytidylate kinase	912	6	1.2	232	2	T10008	probable p-aminobe
840	6	1.2	213	2	T27841	hypothetical prote	913	6	1.2	232	2	S58353	CD1b protein - she
841	6	1.2	214	2	S59149	H+-transporting tw	914	6	1.2	232	2	T12740	hypothetical prote
842	6	1.2	214	2	B87424	outer membrane pro	915	6	1.2	232	2	T12740	hypothetical prote
843	6	1.2	215	2	B35534	hypothetical 23K p	916	6	1.2	232	2	G87629	6-phospho-glucono-
844	6	1.2	215	2	F97825	50S ribosomal prot	917	6	1.2	232	2	AG1452	hypothetical prote
845	6	1.2	215	2	C72635	triose-phosphate i	918	6	1.2	232	2	A87504	hypothetical prote
846	6	1.2	215	2	AH3389	transporter BME111	919	6	1.2	232	2	G84382	cobalt transport A
847	6	1.2	216	2	A71672	ribosomal protein	920	6	1.2	232	2	D70537	hypothetical prote
848	6	1.2	216	2	S09509	outer membrane pro	921	6	1.2	232	2	T49391	hypothetical prote
849	6	1.2	216	2	S40720	hypothetical prote	922	6	1.2	232	2	I79358	hypothetical prote
850	6	1.2	216	2	T34527	hypothetical prote	923	6	1.2	233	2	I79357	IA-alpha polyprote
851	6	1.2	217	2	D82407	outer membrane pro	924	6	1.2	233	2	AF0110	probable hemolysin
852	6	1.2	217	2	F83502	hypothetical prote	925	6	1.2	233	2	B84237	hypothetical prote
853	6	1.2	218	2	T50070	superoxide dismuta	926	6	1.2	233	2	AF0419	probable ABC trans
854	6	1.2	218	2	S75100	ABC transport prot	927	6	1.2	234	1	QOBE43	membrane antigen g
855	6	1.2	218	2	S73675	hypothetical prote	928	6	1.2	234	2	AC0431	conserved hypothet
856	6	1.2	218	2	T23318	hypothetical prote	929	6	1.2	234	2	E64331	hypothetical prote
857	6	1.2	218	2	C72747	probable endonucle	930	6	1.2	234	2	AF1863	cobalamin biosynth
858	6	1.2	219	1	A35617	HDEL receptor ERD2	931	6	1.2	235	1	RWHUT8	T-cell surface gly
859	6	1.2	219	2	S75541	hypothetical prote	932	6	1.2	235	2	E86821	glucosamine-6-phos
860	6	1.2	219	2	B71511	probable sugar nuc	933	6	1.2	235	2	C98204	probable permease
861	6	1.2	219	2	T20732	hypothetical prote	934	6	1.2	235	2	AE3082	hypothetical prote
862	6	1.2	219	2	C70855	hypothetical prote	935	6	1.2	235	2	B70530	hypothetical prote
863	6	1.2	219	2	A99194	iron (III) ABC tra	936	6	1.2	235	2	F97391	probable transcrip
864	6	1.2	219	2	G87708	hypothetical prote	937	6	1.2	235	2	AG2609	transcription regu
865	6	1.2	219	2	H81824	hypothetical perip	938	6	1.2	236	2	T07260	sulfate transport
866	6	1.2	220	2	T43857	hypothetical prote	939	6	1.2	236	2	D72729	hypothetical prote
867	6	1.2	220	2	A75362	hypothetical prote	940	6	1.2	236	2	T50908	3'-phosphoadenosin
868	6	1.2	221	1	HLMSA1	H-2 class II histo	941	6	1.2	237	2	E82674	spiralin - Spiropl
869	6	1.2	222	2	H98178	ABC transporter, p	942	6	1.2	237	2	A36149	hypothetical prote
870	6	1.2	222	2	AD3108	ABC transporter, m	943	6	1.2	237	2	D70463	hypothetical prote
871	6	1.2	223	2	AG3263	propanediol dehydr	944	6	1.2	237	2	G87286	conserved hypothet
872	6	1.2	223	2	A86057	hypothetical prote	945	6	1.2	237	2	AG3573	6-phosphogluconola
873	6	1.2	223	2	F91210	hypothetical prote	946	6	1.2	237	2	S45463	probable membrane
874	6	1.2	224	2	AB1377	ABC transporter, p	947	6	1.2	238	1	LNRTMA	mannose-binding le
875	6	1.2	224	2	AD1746	ABC transporter, p	948	6	1.2	238	2	T10771	NADPH-ferrihemopro
876	6	1.2	224	2	B96586	hypothetical prote	949	6	1.2	238	2	C72576	probable glutamine
877	6	1.2	224	2	T35058	hypothetical prote	950	6	1.2	238	2	S67594	RAD59 protein - ye
878	6	1.2	224	2	S69635	hypothetical prote	951	6	1.2	238	2	T51072	hypothetical prote
879	6	1.2	224	2	T32655	hypothetical prote	952	6	1.2	238	2	H87578	transcription regu
880	6	1.2	225	1	WZVZG2	G2R protein - Amsa	953	6	1.2	238	2	B97634	probable transcrip
881	6	1.2	225	2	AC0587	KDP operon transcr	954	6	1.2	238	2	AD2857	transcription regu
882	6	1.2	225	2	T29632	hypothetical prote	955	6	1.2	238	2	AG2909	hypothetical prote
883	6	1.2	225	2	B72587	hypothetical prote	956	6	1.2	239	1	S34193	phosphoadenylyl-su
884	6	1.2	225	2	F72642	probable shikimate	957	6	1.2	239	1	LNMSMA	mannose-binding le
885	6	1.2	226	1	TVMVSS	PDGF-related trans	958	6	1.2	239	2	AF0261	fatty acid metabol
886	6	1.2	226	2	AG0388	probable short-cha	959	6	1.2	239	2	G97425	flagellar L-ring p
887	6	1.2	226	2	S75665	ABC-type transport	960	6	1.2	239	2	AG2643	flagellar L-ring p
888	6	1.2	226	2	G75342	hypothetical prote	961	6	1.2	240	1	QOBEG3	antigen BCM1 precu
889	6	1.2	226	2	H84213	hypothetical prote	962	6	1.2	240	2	JL0143	sulfate ABC transp
890	6	1.2	227	2	A75304	ABC transporter, A	963	6	1.2	240	2	D69261	branched-chain ami
891	6	1.2	227	2	T34990	hypothetical prote	964	6	1.2	240	2	A97531	hypothetical prote
892	6	1.2	227	2	B84696	probable glutathio	965	6	1.2	240	2	AB2750	hypothetical prote
893	6	1.2	227	2	AG1314	hypothetical prote	966	6	1.2	240	2	A36791	hypothetical prote
894	6	1.2	227	2	AG1686	hypothetical prote	967	6	1.2	240	2	D72415	zinc ABC transport
895	6	1.2	227	2	T45388	ribulose-phosphate	968	6	1.2	240	2	A39016	T-cell surface gly
896	6	1.2	228	2	T10507	dethiobiotin synth	969	6	1.2	241	1	D71233	probable 3-isoprop
897	6	1.2	228	2	B83583	hypothetical prote	970	6	1.2	241	2	A75200	hypothetical prote
898	6	1.2	228	2	H83639	hypothetical prote	971	6	1.2	242	2	F82620	superoxide dismuta
899	6	1.2	228	2	AG3330	hypothetical prote	972	6	1.2	242	2	S30888	PRP38 protein - ye
900	6	1.2	228	2	C87467	ABC transporter, A	973	6	1.2	243	1	WMVZP2	F2 protein - fowlp
901	6	1.2	229	2	S33182	probable transport	974	6	1.2	243	2	G72482	probable 3-oxoacyl
902	6	1.2	229	2	T34277	hypothetical prote	975	6	1.2	243	2	E72405	ABC transporter, p
903	6	1.2	229	2	F75482	transcription regu	976	6	1.2	243	2	T39002	26S proteasome reg
904	6	1.2	230	2	H83001	probable permease	977	6	1.2	243	2	T18851	hypothetical prote
905	6	1.2	230	2	F71122	hypothetical prote	978	6	1.2	244	2	G98320	fixR protein homol

979	6	1.2	244	2	AG2962	short-chain alcohol
980	6	1.2	244	2	C83953	ribosomal protein
981	6	1.2	244	2	A98330	sporulation transcr
982	6	1.2	244	2	AD2953	transcription regu
983	6	1.2	244	2	A39365	cyanamide hydratase
984	6	1.2	244	2	B83630	hypothetical prote
985	6	1.2	244	2	T39507	probable ATP synth
986	6	1.2	245	2	S43293	FLT3/Flk2 ligand (
987	6	1.2	245	2	T47501	dof6 zinc finger p
988	6	1.2	245	2	A70777	hypothetical prote
989	6	1.2	245	2	G90282	hypothetical prote
990	6	1.2	245	2	A97381	hypothetical trans
991	6	1.2	245	2	G98182	hypothetical prote
992	6	1.2	245	2	AH2598	transcription regu
993	6	1.2	245	2	AD3104	conserved hypotet
994	6	1.2	245	2	AG2203	glucose inhibited
995	6	1.2	246	2	T37021	probable methyltra
996	6	1.2	246	2	E75481	RNA methyltransfer
997	6	1.2	246	2	B87482	conserved hypotet
998	6	1.2	247	2	C98340	2-deoxy-D-gluconat
999	6	1.2	247	2	AG2942	2-deoxy-D-gluconat
1000	6	1.2	247	2	H70432	ABC transporter -

ALIGNMENTS

RESULT 1

aspartic proteinase (EC 3.4.23.-) BACE precursor - human
 N;Alternate names: beta-secretase; beta-site APP cleaving enzyme
 C;Species: Homo sapiens (man)
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000
 C;Accession: A59090
 R;Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Teplow,
 M.A.; Blere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Rozen
 Science 286, 735-741, 1999
 A;Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transmem
 A;Reference number: A59090; MUID:20002972; PMID:10531052
 A;Note: submitted to GenBank, September 1999
 A;Accession: A59090
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-501 <VAS>
 A;Cross-references: GB:AF190725; NID:G6118538; PIDN:AAF04142.1; PID:G6118539
 C;Genetics:
 A;Gene: BACE
 C;Superfamily: beta-secretase
 C;Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; pu
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-45/Domain: propeptide #status predicted <PRO>
 F;46-501/Product: acid proteinase BACE #status predicted <MAT>
 F;461-477/Domain: transmembrane #status predicted <TRN>
 F;93,289/Active site: Asp #status predicted
 F;153,172,223,354/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;330-380/Disulfide bonds: #status predicted

Query Match	2.3%;	Score 12;	DB 2;	Length 501;
Best Local Similarity	100.0%;	Pred. No. 0.0026;		
Matches 12; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 107 ILVDTGSSNFAY 118				
Db 90 ILVDTGSSNFAY 101				

RESULT 2

hypothetical protein ML1426 [imported] - *Mycobacterium leprae*
C/Species: *Mycobacterium leprae*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C/Accession: D87087
R/Cole, S.T.; Eijlmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hd

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;/Title: Massive gene decay in the leprosy bacillus.
A;/Reference number: A86909; MUID:21128732; PMID:11234002
A;/Accession: D87087
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-319 <STO>
A;/Cross-references: GB:AL450380; NID:g13093303; PIDN:CAC30377.1; GSPDB:GN00147
C;/Genetics:
A;/Gene: ML1426
C;/superfamily: inner membrane protein ugpA

Query Match	1.7%;	Score 9;	DB 2;	Length 319;
Best Local Similarity	100.0%;	Pred. No. 1.7;		
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 481 ALLVLLV 489
|||||||
Db 294 ALLVLLV 302

RESULT 3

3202634
 conserved hypothetical protein XF1641 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C;Species: *Xylella fastidiosa*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: E82654
 R;Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A;Reference number: A82515, MUID:20365717, PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: E82654
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-863 <SIM>
 A;Cross-references: GB:AE003991; GB:AE003849; NID:g9106696; PIDN:AAF84450.1; GSPDB:GN00
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins,
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
 ; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve
 M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF1641

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Query Match          1.7%;   Score 9;   DB 2;   Length 863;
Best Local Similarity 100.0%;   Pred. NO. 4;
Matches      9;   Conservative      0;   Mismatches      0;   Indels      0;   Gaps      0;

QY      59 GLALALEPA 67
      ||| ||| ||| ||| ||| |||
Db      153 GLALALEPA 161

```

RESULT 4

transcription regulator H1596, leucine-responsive - Haemophilus influenzae (strain Rd
H64131
N/Alternate names: leucine-responsive regulatory protein
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 26-Aug-1999

C;Accession: H64131
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64131
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-166 <TIGR>
A;Cross-references: GB:U32833; GB:L42023; NID:g1574432; PIDN:AAC23241.1; PID:g1574439; TIGR:U32833
C;Function:
A;Description: activates a number of operons in response to the presence of exogenous leucine
C;Superfamily: regulatory protein asnC
C;Keywords: DNA binding; transcription regulation
F;34-60/Region: helix-turn-helix motif

Query Match 1.5%; Score 8; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 305 GTTLRLP 312
Db 136 GTTLRLP 143

RESULT 5
T09585
high mobility group protein HMG1/Y-2 - sword bean
C;Species: Canavalia gladiata (sword bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T09585
R;Yamamoto, S.; Minamikawa, T. Plant Mol. Biol. 33, 537-544, 1997
A;Title: Two genes for the high mobility group protein HMG-Y are present in the genome of Canavalia gladiata
A;Reference number: Z16751; MUID:97201487; PMID:9049273
A;Accession: T09585
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-178 <YAM>
C;Cross-references: EMBL:D86595
C;Genetics:
A;Introns: 17/3
C;Superfamily: histone H1

Query Match 1.5%; Score 8; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VVAPTPGP 49
Db 149 VVAPTPGP 156

RESULT 6
A71935
hypothetical protein jhp0408 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: A71935
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Metberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: A71935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <ARN>
A;Cross-references: GB:AE001475; GB:AE001439; NID:g4154939; PIDN:AAD05989.1; PID:g415494

A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0408

Query Match 1.5%; Score 8; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 479 CGAILLVL 486
Db 29 CGAILLVL 36

RESULT 7
G64646
hypothetical protein HP1015 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Aug-1997
C;Accession: G64646
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64646
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-205 <TOM>
A;Cross-references: GB:AE000511; TIGR:HP1015

Query Match 1.5%; Score 8; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 479 CGAILLVL 486
Db 32 CGAILLVL 39

RESULT 8
JQ0729
60K inner-membrane protein - Proteus mirabilis (fragment)
C;Species: Proteus mirabilis
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
C;Accession: JQ0729
R;Skovgaard, O. Gene 93, 27-34, 1990
A;Title: Nucleotide sequence of a Proteus mirabilis DNA fragment homologous to the 60K-outer-membrane protein of Proteus mirabilis
A;Reference number: JQ0729; MUID:91033012; PMID:2172087
A;Accession: JQ0729
A;Molecule type: DNA
A;Residues: 1-237 <SKO>
A;Cross-references: GB:M58352; GB:M31295; NID:g150873; PIDN:AAA83954.1; PID:g150874
A;Experimental source: strain LM1509
C;Keywords: DNA replication; membrane protein

Query Match 1.5%; Score 8; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 DTGSSNFA 117
Db 206 DTGSSNFA 213

RESULT 9
JQ2332
ARI protein - cassava latent virus
C;Species: cassava latent virus
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: JQ2332

R,Hong, Y.G.; Robinson, D.J.; Harrison, B.D.

J. Gen. Virol. 74, 2437-2443, 1993

A/Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tran

A/Reference number: JQ2326; MUID:94065670; PMID:8245859

A/Accession: JQ2332

A/Molecule type: DNA

A/Residues: 1-257 <HON>

C/Superfamily: cassava latent virus coat protein

C/Keywords: coat protein

Query Match 1.5%; Score 8; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TNRVVAPT 46

Db 28 TNRVVAPT 35

RESULT 10

G96659

protein F2K11.24 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C/Accession: G96659

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: G96659

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-287 <STO>

A/Cross-references: GB:AE005173; NID:g6633844; PIDN:AAF19703.1; GSPDB:GN00141

C/Genetics:

A/Gene: F2K11.24

A/Map position: 1

C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 1.5%; Score 8; DB 2; Length 287;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 IVDGCTL 308

Db 269 IVDGCTL 276

RESULT 11

H75528

conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C/Accession: H75528

R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: H75528

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-303 <WHI>

A/Cross-references: GB:AE001896; GB:AE000513; NID:g6458032; PIDN:AAF09938.1; PID:g645803

A/Experimental source: strain R1

C/Genetics:

A/Gene: DR0358

A/Map position: 1

Query Match 1.5%; Score 8; DB 2; Length 303;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GGSVLVGG 253

Db 137 GGSVLVGG 144

RESULT 12

B95844

probable sugar ABC transporter permease protein ABC transporter SMB20015 [imported] - S

C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C/Accession: B95844

R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna

proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing end

A/Reference number: A95842; MUID:21396508; PMID:11481431

A/Accession: B95844

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-318 <KUR>

A/Cross-references: GB:AL51985; PIDN:CAC48418.1; PID:g15139890; GSPDB:GN00167

A/Experimental source: strain 1021, megaplasmid pSymb

R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure

heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

C/Genetics:

A/Gene: SMB20015

A/Genome: plasmid

C/Superfamily: l-arabinose transport system permease araH

Query Match 1.5%; Score 8; DB 2; Length 318;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 LVLIIVLL 491

Db 16 LVLIIVLL 23

RESULT 13

AG0742

high-affinity zinc uptake system periplasmic binding protein [imported] - Salmonella en

C/Species: Salmonella enterica subsp. enterica serovar Typhi

A/Note: this species has also been called Salmonella typhi

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C/Accession: AG0742

R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A/Reference number: AB0502; PMID:11677608

A/Accession: AG0742

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-319 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD05642.1; PID:g16503138; GSPDB:GN00176

C/Genetics:

A/Gene: STY2099

C;Superfamily: hypothetical protein HI0119

Query Match 1.5%; Score 8; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 AVEAVAR 325
|||
Db 271 AVEAVAR 278

RESULT 14

PRLJHD

Proteinase (EC 3.4.23.-) - squirrel monkey retrovirus SMRV-H

C;Species: squirrel monkey retrovirus SMRV-H

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Feb-1997

C;Accession: B31827

R;Oda, T.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Akiyama, K.; Mitsuobu, F.

Virology 167, 468-476, 1988

A;Title: Molecular cloning, complete nucleotide sequence, and gene structure of the prov

A;Reference number: A31827; MUID:89073750; PMID:3201749

A;Accession: B31827

A;Molecule type: DNA

A;Residues: 1-323 <ODA>

C;Genetics:

A;Gene: prt

C;Complex: homodimer

C;Superfamily: retroviral proteinase

C;Keywords: aspartic proteinase; homodimer; hydrolase

F;193/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 1.5%; Score 8; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 DLVTIPKG 168
|||
Db 126 DLVTIPKG 133

RESULT 15

T42999

ethanolamine-phosphate cytidyltransferase homolog - fission yeast (Schizosaccharomyces

C;Species: Schizosaccharomyces pombe

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C;Accession: T42999

R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.

DNA Res. 4, 363-369, 1997

A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.

A;Reference number: Z17323; MUID:98162722; PMID:9501991

A;Accession: T42999

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-327 <YOS>

A;Cross-references: EMBL:D89199; NID:g1749605; PIDN:BAAL3860.1; PID:g1749606

A;Experimental source: strain PR745

Query Match 1.5%; Score 8; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 SGTLLRL 311
|||
Db 153 SGTLLRL 160

Search completed: April 1, 2003, 11:46:40
Job time : 75 secs

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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:35:19 ; Search time 27 Seconds
(without alignments)
795.731 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 518
Sequence: 1 MGALARALLPLLAQWLLRA.....RRRDPEVNDSSLVRRHWK 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	100.0	518	1 BAE2_HUMAN	Q9y5z0 homo sapien
2	12	2.3	501	1 BACE_HUMAN	P56817 homo sapien
3	12	2.3	501	1 BACE_MOUSE	P56818 mus musculu
4	12	2.3	501	1 BACE_RAT	P56819 rattus norv
5	8	1.5	166	1 LRP_HAIEIN	P45265 haemophilus
6	8	1.5	237	1 60IM_PROMI	P22833 proteus mir
7	8	1.5	323	1 VPRT_SMRVH	P21407 squirrel mo
8	8	1.5	340	1 CARP_POLTU	P17576 polyporus t
9	8	1.5	362	1 YHDX_ECOLI	P45767 escherichia
10	8	1.5	365	1 ECT1_SCHPO	Q9ut16 schizosacch
11	8	1.5	481	1 LBP_HUMAN	P18428 homo sapien
12	8	1.5	548	1 60IM_ECOLI	P25714 escherichia
13	8	1.5	692	1 GLND_CORGL	Q9x706 corynebacte
14	8	1.5	1247	1 NIDO_HUMAN	P14543 homo sapien
15	8	1.5	1620	1 DNMI_MOUSE	P13864 mus musculu
16	8	1.5	1622	1 DNMI_RAT	Q92330 rattus norv
17	8	1.4	126	1 DOCR_HUMAN	O75956 homo sapien
18	7	1.4	126	1 G8_HUMAN	Q9ub46 homo sapien
19	7	1.4	136	1 YAI3_ARCFU	O29249 archaeoglob
20	7	1.4	149	1 YDCZ_ECOLI	P76111 escherichia
21	7	1.4	160	1 BIK_HUMAN	O13323 homo sapien
22	7	1.4	198	1 TTK_ECOLI	P06969 escherichia
23	7	1.4	238	1 EFA3_HUMAN	P52797 homo sapien
24	7	1.4	249	1 YBG0_STRCO	P40179 streptomyce
25	7	1.4	267	1 EX3_HAEIN	P44318 haemophilus
26	7	1.4	268	1 EX3_ECOLI	P09030 escherichia
27	7	1.4	276	1 PSB8_HUMAN	P28062 homo sapien
28	7	1.4	296	1 KHSE_LACLC	P52991 lactococcus
29	7	1.4	297	1 COBD_METTH	O27460 methanobact
30	7	1.4	298	1 CHIA_PHAAN	P29024 phaseolus a
31	7	1.4	298	1 YAKI_YEAST	P39551 saccharomyc
32	7	1.4	302	1 PPT2_HUMAN	Q9umt5 homo sapien
33	7	1.4	302	1 Y091_METUA	Q57556 methanococc

34	7	1.4	305	1 DDLB_ECO57	Q8x9y6 escherichia
35	7	1.4	305	1 DDLB_ECOLI	P07862 escherichia
36	7	1.4	305	1 DDLB_SALTI	Q829g7 salmonella
37	7	1.4	305	1 DDLB_SALTY	Q8zrul salmonella
38	7	1.4	324	1 PEP1_GADMO	P56272 gadus morhu
39	7	1.4	325	1 DLP3_HUMAN	O95886 homo sapien
40	7	1.4	326	1 YR75_ECOLI	P21314 escherichia
41	7	1.4	327	1 CD1A_HUMAN	P06126 homo sapien
42	7	1.4	327	1 PPAS_RAT	P29288 rattus norv
43	7	1.4	333	1 ILVC_MYCTU	O53248 mycobacteri
44	7	1.4	337	1 YXAG_BACSU	P42106 bacillus su
45	7	1.4	354	1 MURB_TREPA	O83128 treponema p
46	7	1.4	354	1 YGP1_YEAST	P38616 saccharomyc
47	7	1.4	356	1 RFI_BACSU	P45872 bacillus su
48	7	1.4	367	1 PEP4_CHICK	P00793 gallus gall
49	7	1.4	379	1 MRAW_TREPA	O83399 treponema p
50	7	1.4	381	1 CHYM_CALJA	Q9n2d2 callithrix
51	7	1.4	385	1 Y464_MYCGE	P47702 mycoplasma
52	7	1.4	386	1 CYB_SARGL	O63848 sarcophyton
53	7	1.4	386	1 PEP4_PIG	P00791 sus scrofa
54	7	1.4	387	1 PEP1_RABIT	P28712 oryctolagus
55	7	1.4	387	1 PEP2_RABIT	P27821 oryctolagus
56	7	1.4	387	1 PEP3_RABIT	P27822 oryctolagus
57	7	1.4	387	1 PEP4_RABIT	P28713 oryctolagus
58	7	1.4	387	1 PEP4_CALJA	O9n2d4 callithrix
59	7	1.4	388	1 PEP1_MACFU	P03954 macaca fusc
60	7	1.4	388	1 PEP2_MACFU	P27677 macaca fusc
61	7	1.4	388	1 PEP4_MACFU	P27678 macaca fusc
62	7	1.4	388	1 PEP4_HUMAN	P00790 homo sapien
63	7	1.4	388	1 PEP4_MACMU	P11489 macaca mula
64	7	1.4	394	1 PNCB_XYLFA	O9ped1 xylella fas
65	7	1.4	398	1 CATD_CHICK	O05744 gallus gall
66	7	1.4	408	1 LMP1_BOVIN	O05204 bos taurus
67	7	1.4	416	1 DAD2_PSEAE	O9hu99 pseudomonas
68	7	1.4	419	1 CARV_CANAL	P10977 candida alb
69	7	1.4	420	1 PAG2_PIG	Q29079 sus scrofa
70	7	1.4	428	1 SURA_ECOLI	P21202 escherichia
71	7	1.4	452	1 MTN3_CHICK	O42401 gallus gall
72	7	1.4	452	1 PLM1_PLAFA	P39898 plasmodium
73	7	1.4	453	1 GASR_CANFA	P30552 canis fami1
74	7	1.4	454	1 GASR_BOVIN	P79266 bos taurus
75	7	1.4	460	1 VATB_THEVO	O97cp9 thermoplasm
76	7	1.4	462	1 GSA_MYCTU	O06390 mycobacteri
77	7	1.4	473	1 CYP1_CYNCA	P40782 cynara card
78	7	1.4	494	1 CPS1_HUMAN	P08686 homo sapien
79	7	1.4	496	1 ASPR_ORYSA	P42211 oryza sativ
80	7	1.4	513	1 ASPR_CUCPE	O04057 cucurbita p
81	7	1.4	517	1 SVRI_HUMAN	O15223 homo sapien
82	7	1.4	550	1 SVR1_CORGL	P35868 corynebacte
83	7	1.4	558	1 YJ83_MYCTU	O10873 mycobacteri
84	7	1.4	560	1 Y663_HAEIN	P71355 haemophilus
85	7	1.4	569	1 YAP3_YEAST	P32329 saccharomyc
86	7	1.4	589	1 PHBC_ALCEU	P23608 a poly-beta
87	7	1.4	596	1 MKC7_YEAST	P53379 saccharomyc
88	7	1.4	602	1 VE1_MNPV	Q84356 mastomys na
89	7	1.4	603	1 PGH2_SHEEP	P79208 ovis aries
90	7	1.4	604	1 PGH2_BOVIN	O62698 bos taurus
91	7	1.4	604	1 PGH2_CAVPO	P70682 cavia porce
92	7	1.4	604	1 PGH2_HORSE	O19183 equus cabal
93	7	1.4	604	1 PGH2_HUMAN	P35354 homo sapien
94	7	1.4	604	1 PGH2_RABIT	O02768 oryctolagus
95	7	1.4	646	1 KDBE_SCHPO	Q10364 schizosacch
96	7	1.4	660	1 VNCS_PAVPN	P18547 porcine par
97	7	1.4	662	1 BGAL_CANFA	O9try9 canis fami1
98	7	1.4	662	1 VNCS_PAVPK	O13773 porcine par
99	7	1.4	697	1 YE9C_SCHPO	O13773 schizosacch
100	7	1.4	703	1 EFG_ECOLI	P02996 escherichia
101	7	1.4	703	1 EFG_SALTY	P26229 salmonella
102	7	1.4	715	1 LCCL_LACIA	O9cjb8 lactococcus
103	7	1.4	715	1 LCNC_LACIA	O00564 lactococcus
104	7	1.4	716	1 E2BE_RAT	O64350 rattus norv
105	7	1.4	717	1 COMA_STRPN	O03727 streptococc
106	7	1.4	721	1 E2BE_HUMAN	Q13144 homo sapien

107	7	1.4	721	1	E2BE_RABIT	P47823	oryctolagus	180	6	1.2	115	1	NU3M_FELCA	P48912	felis silve
108	7	1.4	733	1	YACK_RHIME	Q9x447	rhizobium m	181	6	1.2	115	1	NU3M_HALGR	P38600	halichoerus
109	7	1.4	754	1	YAF6_SCHPO	Q09860	schizosacch	182	6	1.2	115	1	NU3M_HIPAM	Q92zy4	hippopotamus
110	7	1.4	775	1	PTNC_MOUSE	P35831	mus musculus	183	6	1.2	115	1	NU3M_HORSE	P48654	equus caball
111	7	1.4	797	1	SHK3_HUMAN	Q9yb0	homo sapien	184	6	1.2	115	1	NU3M_HUMAN	P03897	homo sapien
112	7	1.4	831	1	NAPA_ALCEU	P39185	alcaligenes	185	6	1.2	115	1	NU3M_HYLLA	Q95708	hylobates l
113	7	1.4	841	1	RELA_STRAT	O85709	streptomyces	186	6	1.2	115	1	NU3M_MICPE	Q21519	microtus pe
114	7	1.4	843	1	DEOL_HPBBR	P03157	hepatitis b	187	6	1.2	115	1	NU3M_MOUSE	P03899	mus musculus
115	7	1.4	863	1	AD17_DROME	Q9vac5	drosophila	188	6	1.2	115	1	NU3M_PERGO	Q95881	peromyscus
116	7	1.4	899	1	YA8D_SCHPO	Q09778	schizosacch	189	6	1.2	115	1	NU3M_PERMA	Q95891	peromyscus
117	7	1.4	949	1	RSCC_ECOLI	P14376	escherichia	190	6	1.2	115	1	NU3M_PERPL	Q95897	peromyscus
118	7	1.4	958	1	IF3A_TOBAC	Q40554	nicotiana t	191	6	1.2	115	1	NU3M_PHOSU	Q95921	peromyscus
119	7	1.4	993	1	EBB2_MOUSE	P54763	mus musculus	192	6	1.2	115	1	NU3M_PROVI	Q21513	phodopus su
120	7	1.4	1009	1	WS14_CAEBL	P41846	caenorhabdi	193	6	1.2	115	1	NU3M_PHOVI	Q00541	phoca vitul
121	7	1.4	1015	1	BGAL_ARTSP	Q59140	archrobacte	194	6	1.2	115	1	NU3M_PIG	O79880	sus scrofa
122	7	1.4	1054	1	TREA_EMENI	P78617	emericeilla	195	6	1.2	115	1	NU3M_PIG	Q95915	polypterus
123	7	1.4	1055	1	EBB2_HUMAN	P29323	homo sapien	196	6	1.2	115	1	NU3M_PONPA	P92697	pongo pygma
124	7	1.4	1073	1	YFPD_YEAST	P43564	saccharomyc	197	6	1.2	115	1	NU3M_RABIT	O79434	oryctolagus
125	7	1.4	1163	1	CARB_RHIME	Q92p24	rhizobium m	198	6	1.2	115	1	NU3M_RAT	P05506	rattus norv
126	7	1.4	1238	1	SBCC_RHOCA	O68032	rhodobacter	199	6	1.2	115	1	NU3M_RHITUN	Q96066	rhinoceros
127	7	1.4	1336	1	MAMI_SCHPO	P78966	schizosacch	200	6	1.2	115	1	NU3M_SHEEP	O78755	ovis aries
128	7	1.4	1343	1	VGR2_RAT	O08775	rattus norv	201	6	1.2	115	1	NU3M_SIGHI	O21566	sigmodon hi
129	7	1.4	1533	1	PUM_DROME	P25822	drosophila	202	6	1.2	115	1	YNFD_ECOLI	P76172	escherichia
130	7	1.4	1625	1	CTPI_MYCTU	Q10900	mycobacteri	203	6	1.2	116	1	NU3M_BRARE	Q9mly3	brachydanio
131	7	1.4	1822	1	ITB4_HUMAN	P16144	homo sapien	204	6	1.2	116	1	NU3M_CARAU	O78686	carassius a
132	7	1.4	6486	1	TYCC_BACBR	O30409	b tyrocidin	205	6	1.2	116	1	NU3M_CYPCA	P18938	gallus gall
133	6	1.2	27	1	ACH4_MOUSE	O70174	mus musculus	206	6	1.2	116	1	NU3M_CYPCA	P24974	cyprinus ca
134	6	1.2	52	1	V59_BPT3	P20405	bacterioph	207	6	1.2	116	1	NU3M_DIDMA	P41306	didelphis m
135	6	1.2	52	1	V59_BPT7	P20406	bacterioph	208	6	1.2	116	1	NU3M_GADMO	P15957	gadus morhu
136	6	1.2	56	1	SCP2_MESMA	Q9njp7	mesobuthus	209	6	1.2	116	1	NU3M_LATCH	O03171	latimeria c
137	6	1.2	56	1	SCP3_MESMA	Q9u8d1	mesobuthus	210	6	1.2	116	1	NU3M_MACRO	P92666	macropus ro
138	6	1.2	58	1	Y06H_BPT4	P13315	bacterioph	211	6	1.2	116	1	NU3M_ONCGO	P20686	oncorhynch
139	6	1.2	71	1	VLYS_BPP21	P27360	bacterioph	212	6	1.2	116	1	NU3M_ONCKE	Q35262	oncorhynch
140	6	1.2	72	1	PEP2_THUTO	P20140	thynnus thy	213	6	1.2	116	1	NU3M_ONCKI	P20687	oncorhynch
141	6	1.2	72	1	PSBH_TOBAC	P06415	nicotiana t	214	6	1.2	116	1	NU3M_ONCMA	Q37108	oncorhynch
142	6	1.2	73	1	PEPC_PIG	P30879	sus scrofa	215	6	1.2	116	1	NU3M_ONCMY	P11629	oncorhynch
143	6	1.2	80	1	Y6A9_YEREN	O85269	yersinia en	216	6	1.2	116	1	NU3M_ONCNE	P20688	oncorhynch
144	6	1.2	80	1	Y6A9_YERPE	Q9zgw3	yersinia pe	217	6	1.2	116	1	NU3M_ONCTS	P25707	oncorhynch
145	6	1.2	81	1	VES_HPV35	P27226	human papil	218	6	1.2	116	1	NU3M_PAROL	P92817	paralichthy
146	6	1.2	83	1	YF24_ARCFU	O28748	archaeoglob	219	6	1.2	116	1	NU3M_SALSA	Q35929	salmo salar
147	6	1.2	87	1	Y123_BURCE	P24538	burkholderi	220	6	1.2	116	1	NU3M_SALTR	O03252	salmo trutt
148	6	1.2	88	1	LEVI_XENIA	P13684	xenopus lae	221	6	1.2	116	1	NU3M_SCYCA	O79408	scyllorhinu
149	6	1.2	89	1	IAPP_FELCA	P12967	felis silve	222	6	1.2	116	1	NU3M_SQUAC	Q9z247	squalus aca
150	6	1.2	96	1	Y598_MYCLA	O33024	mycobacteri	223	6	1.2	117	1	NU3M_STRCA	O79102	struthio ca
151	6	1.2	100	1	APC2_CAVPO	P27916	cavia porce	224	6	1.2	117	1	NLTP_PRUDU	Q43017	prunus dulc
152	6	1.2	100	1	PINL_HUMAN	O15428	homo sapien	225	6	1.2	117	1	NLTP_PRUAV	Q9m5x8	prunus aviu
153	6	1.2	101	1	ATPL_SULTO	P23040	sulfolobus	226	6	1.2	117	1	CHCI_SPIOI	P10976	spinacia ol
154	6	1.2	101	1	PIPI_PIG	P83106	sus scrofa	227	6	1.2	119	1	CHCI_BOOMO	P13531	bombyx mori
155	6	1.2	102	1	COLL_HSVSC	P22576	herpesvirus	228	6	1.2	119	1	CHC2_BOOMO	Q17212	bombyx mori
156	6	1.2	105	1	ATPL_MYCPN	Q59550	mycoplasma	229	6	1.2	119	1	CHC5_BOOMO	Q17214	bombyx mori
157	6	1.2	105	1	YKKD_BACSU	P49857	bacillus su	230	6	1.2	121	1	CHC4_BOOMO	P08829	bombyx mori
158	6	1.2	106	1	YOB5_MYCLE	Q49723	mycobacteri	231	6	1.2	122	1	UPTI_PIG	Q29100	sus scrofa
159	6	1.2	107	1	PRK2_RAT	Q8r413	rattus norv	232	6	1.2	124	1	GLUI_LOPAM	P01278	lophius ame
160	6	1.2	108	1	INS_AOTTR	P10604	actus trivi	233	6	1.2	124	1	HIS3_ZYMO	Q9x3w1	zymomonas m
161	6	1.2	108	1	INS_PIG	P01315	sus scrofa	234	6	1.2	124	1	RNP_CHIBR	P00675	chinchilla
162	6	1.2	108	1	INS_RODSP	P21563	rodentia sp	235	6	1.2	124	1	UCN1_HUMAN	P55089	homo sapien
163	6	1.2	108	1	RSBV_BACLI	O50230	bacillus li	236	6	1.2	125	1	SECG_BORBU	O51083	borrelia bu
164	6	1.2	109	1	CD1B_RABIT	P23042	oryctolagus	237	6	1.2	125	1	SZ09_HUMAN	Q07325	homo sapien
165	6	1.2	110	1	CSAA_BACSU	P37584	bacillus su	238	6	1.2	128	1	CYB_CROVV	Q95776	crotalus vi
166	6	1.2	110	1	INS_CANFA	P01321	canis famil	239	6	1.2	128	1	PRK2_MOUSE	Q9qxu7	mus musculus
167	6	1.2	110	1	INS_CERAE	P30407	cercopithec	240	6	1.2	129	1	CART_MOUSE	P56388	mus musculus
168	6	1.2	110	1	INS_HUMAN	P01308	homo sapien	241	6	1.2	129	1	CART_RAT	P49192	rattus norv
169	6	1.2	110	1	INS_MACFA	P30406	macaca fasc	242	6	1.2	131	1	FABB_BOVIN	Q09139	bos taurus
170	6	1.2	110	1	INS_PSAOB	Q62587	psammomys o	243	6	1.2	131	1	RRPB_CVPR8	Q04158	porcine res
171	6	1.2	110	1	INS_RABIT	P01311	oryctolagus	244	6	1.2	132	1	CRBI_MYCTU	P95089	mycobacteri
172	6	1.2	110	1	PEPA_BOVIN	P00792	bos taurus	245	6	1.2	132	1	YL64_ARCFU	O28118	archaeoglob
173	6	1.2	113	1	TYBP_HUMAN	O43914	homo sapien	246	6	1.2	133	1	RS9_FUSNN	O8rg98	fusobacteri
174	6	1.2	115	1	NU3M_BALPH	P24973	balaenopter	247	6	1.2	134	1	CC42_ANOGA	Q17031	anopheles g
175	6	1.2	115	1	NU3M_BOVIN	P03898	bos taurus	248	6	1.2	134	1	RS9_CHLPN	Q9z8tc	chlamydia p
176	6	1.2	115	1	NU3M_CANFA	Q9zz60	canis famil	249	6	1.2	134	1	VG24_BPMD2	O64218	mycobacteri
177	6	1.2	115	1	NU3M_CERSI	O03202	ceratotheri	250	6	1.2	137	1	PSBW_SPIOI	Q41387	spinacia ol
178	6	1.2	115	1	NU3M_DASNO	O21332	dasypus nov	251	6	1.2	137	1	RS9_SULTO	P95992	sulfolobus
179	6	1.2	115	1	NU3M_EQUAS	P92482	equus asinu	252	6	1.2	137	1	RS9_SULTO	Q96yw3	sulfolobus

253	6	1.2	138	1	YGJM_ECOLI	P42594	escherichia	326	6	1.2	195	1	TRPG_SUISO	006129	sulfolobus
254	6	1.2	140	1	RS12_CAEEL	P49196	caenorhabdi	327	6	1.2	196	1	HIS7_CAUCR	Q9a232	caulobacter
255	6	1.2	140	1	YB19_ARCFU	O29146	archaeoglob	328	6	1.2	196	1	Y449_TREPA	O83463	treponema p
256	6	1.2	141	1	HBA2_NOTCO	P16308	notothenia	329	6	1.2	197	1	HIS7_STRCO	P16247	streptomyce
257	6	1.2	141	1	TNG1_HUMAN	P56846	homo sapien	330	6	1.2	197	1	PTCA_MOUSE	Q64697	mus musculu
258	6	1.2	142	1	RPB6_SCHPO	P36595	schizosacch	331	6	1.2	198	1	CD8A_PONPY	P30433	pongo pygma
259	6	1.2	144	1	Y100_AQUAE	O67669	aquifex aeo	332	6	1.2	198	1	RL19_CAEEL	O02639	caenorhabdi
260	6	1.2	146	1	RBFA_RHIL0	O98b17	rhizobium 1	333	6	1.2	199	1	YB7J_RHIL0	Q98dy4	haemophilus
261	6	1.2	147	1	LECE_ANTCR	P06027	anthocidari	334	6	1.2	199	1	YE7J_HAEIN	Q57213	haemophilus
262	6	1.2	147	1	TTHY_SHEEP	P12303	ovis aries	335	6	1.2	202	1	COAT_BMYVF	P09508	beet wester
263	6	1.2	148	1	EXBB_AQUAE	O67637	aquifex aeo	336	6	1.2	202	1	COAT_BMYVG	P09509	beet wester
264	6	1.2	148	1	RNP_GERNI	O9wus2	gerbillus n	337	6	1.2	202	1	CUTI_BOTCI	Q00298	botrytis ci
265	6	1.2	152	1	PYRI_PYRAB	P77919	pyrococcus	338	6	1.2	202	1	LSPA_MYCTU	O10764	mycobacteri
266	6	1.2	153	1	YEH3_PSEAE	O9hub0	pseudomonas	339	6	1.2	205	1	DDL_ANACE	P35660	anaplasma c
267	6	1.2	155	1	BCCP_HAEIN	P43874	haemophilus	340	6	1.2	205	1	EFAI_HUMAN	P20827	homo sapien
268	6	1.2	156	1	RIB2_PHOLE	O93e92	photobacter	341	6	1.2	205	1	EFAI_MOUSE	P52793	mus musculu
269	6	1.2	160	1	COAT_CGMVS	P19521	cucumber gr	342	6	1.2	205	1	EFAI_RAT	P97553	rattus norv
270	6	1.2	160	1	Y964_MYCTU	P71546	mycobacteri	343	6	1.2	205	1	KGUA_LACTA	O9cee3	lactococcus
271	6	1.2	161	1	TPM_SCHPO	Q02088	schizosacch	344	6	1.2	205	1	NEF_HV1ZH	P05859	human immun
272	6	1.2	161	1	YAN8_YEAST	P39564	saccharomyc	345	6	1.2	205	1	YJ11_MYCTU	O07722	mycobacteri
273	6	1.2	163	1	LRP_ECOLI	P19494	escherichia	346	6	1.2	205	1	YK07_YEAST	P36061	saccharomyc
274	6	1.2	163	1	LRP_KLEPN	P37424	klebsiella	347	6	1.2	206	1	FGF4_BOVIN	P48803	bos taurus
275	6	1.2	163	1	LRP_SALT	P37403	salmonella	348	6	1.2	207	1	CCMA_ECOLI	P33931	escherichia
276	6	1.2	163	1	LRP_SERMA	P37425	serratia ma	349	6	1.2	207	1	HIS7_AZOBR	P18787	azospirillu
277	6	1.2	164	1	PUR6_HAEIN	P43849	haemophilus	350	6	1.2	207	1	SODM_CHLPN	Q929c4	chlamydia p
278	6	1.2	164	1	YBP3_ACIAM	P32987	acidianus a	351	6	1.2	208	1	NEF_HV1RH	P05858	human immun
279	6	1.2	165	1	DEST_HUMAN	P18282	homo sapien	352	6	1.2	209	1	HUPM_AZCOH	Q43954	azotobacter
280	6	1.2	165	1	RL10_BACSU	P42923	bacillus su	353	6	1.2	209	1	PRL_ANGAN	P33096	anguilla an
281	6	1.2	165	1	YGZD_YEAST	P53057	saccharomyc	354	6	1.2	210	1	FGFL_MOUSE	O9jfn1	mus musculu
282	6	1.2	165	1	YREP_BUCTS	O31289	buchnera ap	355	6	1.2	210	1	FLPA_ARCFU	O28192	archaeoglob
283	6	1.2	167	1	YREP_BUCPP	O9zeza	buchnera ap	356	6	1.2	211	1	DEOC_BACSU	P39121	bacillus su
284	6	1.2	168	1	NEU2_MOUSE	P35455	mus musculu	357	6	1.2	211	1	RL1_HALCU	P05966	halobacteri
285	6	1.2	168	1	SULA_SERMA	P08845	serratia ma	358	6	1.2	211	1	RL1_HALNI	P13575	halobacteri
286	6	1.2	169	1	MSA1_STAAM	Q99qd5	staphylococ	359	6	1.2	213	1	PYRF_METUA	Q57700	methanococc
287	6	1.2	169	1	SULA_ECOLI	P08846	escherichia	360	6	1.2	214	1	ATP6_ALBCO	P48893	albinaria c
288	6	1.2	169	1	SULA_ENTAE	P08848	enterobacte	361	6	1.2	214	1	CYB_AGRKO	P92845	agkistrodon
289	6	1.2	169	1	SULA_SALT	P08847	salmonella	362	6	1.2	214	1	CYB_AGRKA	P92852	agkistrodon
290	6	1.2	170	1	HPAC_KLEPN	Q48441	klebsiella	363	6	1.2	214	1	CYB_BOTAT	P92846	bothrops at
291	6	1.2	173	1	PACA_ONCNE	P41585	oncorhynch	364	6	1.2	214	1	CYB_BOTBI	P92847	bothriopsis
292	6	1.2	173	1	RUVG_BRUME	O8yiv7	brucella me	365	6	1.2	214	1	CYB_BOTSC	P92849	bothriopsis
293	6	1.2	173	1	VENV_LELV	Q04565	lelystad vi	366	6	1.2	214	1	CYB_CERCE	P87419	cerastes ce
294	6	1.2	174	1	CUIA_TENMO	P80681	tenebrio mo	367	6	1.2	214	1	CYB_CROAT	P92850	crotalus at
295	6	1.2	174	1	YG3B_YEAST	P53279	saccharomyc	368	6	1.2	214	1	CYB_LACMU	P92853	iachesis mu
296	6	1.2	174	1	YGAP_ECOLI	P55734	escherichia	369	6	1.2	214	1	CYB_TRIST	P92857	trimeresuru
297	6	1.2	175	1	DIAC_BOVIN	Q01458	bos taurus	370	6	1.2	215	1	YFGS_LACCA	P35924	lactobacill
298	6	1.2	176	1	HSLV_AQUAE	O67587	aquifex aeo	371	6	1.2	216	1	RL3_RICPR	P48952	rickettsia
299	6	1.2	178	1	ESMS_DROME	P13096	drosophila	372	6	1.2	216	1	YLH3_CAEEL	P34357	caenorhabdi
300	6	1.2	179	1	AXI6_PEA	P49680	pisum sativ	373	6	1.2	217	1	OMPW_VIBCH	P17266	vibrio chol
301	6	1.2	180	1	CFTF_CAVPO	Q9h6k4	homo sapien	374	6	1.2	218	1	SGAH_MYCPN	P75293	mycoplasma
302	6	1.2	180	1	APT_STRCO	Q00552	cavia porce	375	6	1.2	218	1	SODM_SCHPO	Q9uqx0	schizosacch
303	6	1.2	182	1	HSLV_RICCN	P52561	streptomyce	376	6	1.2	219	1	ERD2_YEAST	P18414	saccharomyc
304	6	1.2	182	1	HSLV_RICCN	Q92117	rickettsia	377	6	1.2	219	1	ISPD_CHLTR	O84468	chlamydia t
305	6	1.2	184	1	MUP3_MOUSE	Q9zdk9	rickettsia	378	6	1.2	220	1	TRBF_RHISN	P55403	rhizobium s
306	6	1.2	184	1	DSBE_SALTI	P04939	mus musculu	379	6	1.2	221	1	HAZQ_MOUSE	P04227	mus musculu
307	6	1.2	185	1	DSBE_SALTI	O8xfk6	salmonella	380	6	1.2	223	1	TPIS_AERPE	Q9ybr1	aeropyrum p
308	6	1.2	185	1	YXAK_BACSU	P42110	bacillus su	381	6	1.2	225	1	GIDB_THETH	O91cy2	thermus the
309	6	1.2	185	1	GCH1_BACHD	Q9kcc7	bacillus ha	382	6	1.2	225	1	VG2R_AMEPV	P29818	amsacta moo
310	6	1.2	188	1	TRAF_RHISN	P55417	rhizobium s	383	6	1.2	225	1	Y574_AERPE	Q9yek4	aeropyrum p
311	6	1.2	188	1	Y460_PYRHO	O58215	pyrococcus	384	6	1.2	225	1	YB67_AERPE	Q9ycus	aeropyrum p
312	6	1.2	188	1	YY05_MYCTU	Q50720	mycobacteri	385	6	1.2	226	1	TSIS_SMSAV	P01128	simian sarc
313	6	1.2	189	1	PUR2_CHRVI	Q46482	chromatium	386	6	1.2	228	1	RPE_RHOCA	Q91614	pseudomonas
314	6	1.2	189	1	Y006_CHLTR	O84009	chlamydia t	387	6	1.2	229	1	YOEL_STRAT	O53683	streptomyce
315	6	1.2	190	1	CAH2_FLALI	P46513	flaveria li	388	6	1.2	230	1	Y128_AQUAE	O67688	aquifex aeo
316	6	1.2	191	1	CC42_DROME	P40793	drosophila	389	6	1.2	231	1	YHS2_YEAST	P38829	saccharomyc
317	6	1.2	191	1	MOBA_PYRAB	Q9v0d0	pyrococcus	390	6	1.2	231	1	6PGL_CAUCR	O9a6n1	caulobacter
318	6	1.2	191	1	PIC2_AGRTU	P29113	agrobacteri	391	6	1.2	232	1	C1B3_SHEEP	P80943	ovis aries
319	6	1.2	191	1	RUVA_THETH	Q9fiq3	thermus the	392	6	1.2	233	1	HA2F_MOUSE	P14435	mus musculu
320	6	1.2	192	1	MOBA_PYRHO	O58708	pyrococcus	393	6	1.2	233	1	HA2R_MOUSE	P14436	mus musculu
321	6	1.2	192	1	TRPG_SERMA	P00900	serratia ma	394	6	1.2	233	1	HA2S_MOUSE	P14437	mus musculu
322	6	1.2	193	1	HIS7_BACHD	P71381	haemophilus	395	6	1.2	234	1	VG8B_EBV	P03224	epstein-bar
323	6	1.2	194	1	CSF3_PIG	Q9k6z3	bacillus ha	396	6	1.2	235	1	CD8A_HUMAN	P01732	homo sapien
324	6	1.2	195	1		O02837	sus scrofa	397	6	1.2	236	1		P56344	chlorella v
325	6	1.2						398	6	1.2					

399	6	1.2	237	1	CYSH_XYLFA	Q9pdd82	xyliella fas
400	6	1.2	237	1	YBSO_YEAST	P38242	saccharomyc
401	6	1.2	237	1	YI94_AQUAE	O67734	aquifex aeo
402	6	1.2	238	1	MABA_RAT	P19999	rattus norv
403	6	1.2	239	1	CD8A_CANFA	P33706	canis fam1l
404	6	1.2	239	1	CYSH_THIRO	P52672	thiocapsa r
405	6	1.2	239	1	FLGH_AGRIS	Q44342	agrobacteri
406	6	1.2	239	1	MABA_MOUSE	P39039	mus musculu
407	6	1.2	240	1	CD48_MOUSE	P18181	mus musculu
408	6	1.2	240	1	CD7_HUMAN	P09564	homo sapien
409	6	1.2	240	1	TPMT_MOUSE	O55060	mus musculu
410	6	1.2	240	1	TPMT_MUSSP	Q9qxx22	mus spretus
411	6	1.2	240	1	US19_HCMVA	P09725	human cytom
412	6	1.2	240	1	VG45_HSVI1	Q00111	ictalurid h
413	6	1.2	240	1	Y124_THEMEA	Q9wxix8	thermotoga
414	6	1.2	241	1	LAT_RAT	O70601	rattus norv
415	6	1.2	241	1	SPIR_SPIME	P21625	spiroplasma
416	6	1.2	242	1	LAT_MOUSE	O54957	mus musculu
417	6	1.2	242	1	PR38_YEAST	Q00723	saccharomyc
418	6	1.2	243	1	RPNA_SCHPO	O94444	schizosacch
419	6	1.2	243	1	VI28_FOWPV	P15910	fowlpox vir
420	6	1.2	244	1	CYAH_MYRVE	P22143	myrothecium
421	6	1.2	244	1	NGN1_MOUSE	P70660	mus musculu
422	6	1.2	244	1	NGN1_RAT	P70595	rattus norv
423	6	1.2	244	1	RS2_BACHD	Q9ka63	bacillus ha
424	6	1.2	245	1	GIDB_ANASP	O8ysa7	anabaena sp
425	6	1.2	245	1	YM29_MYCTU	O10513	mycobacteri
426	6	1.2	246	1	YOR4_ANATH	Q44408	anaerocellu
427	6	1.2	247	1	LPXH_XANCP	P58976	xanthomonas
428	6	1.2	247	1	SLT1_CAEEL	Q9u3n5	caenorhabdi
429	6	1.2	247	1	YFBB_HAEIN	P44611	haemophilus
430	6	1.2	247	1	YG29_ARCFU	O28644	archaeoglob
431	6	1.2	249	1	HMX1_CHICK	P28361	gallus gall
432	6	1.2	249	1	PSM2_HALVO	Q9v2v5	halobacteri
433	6	1.2	249	1	PYR2_FREDI	P18543	fremyella d
434	6	1.2	249	1	YK73_MYCTU	O10681	mycobacteri
435	6	1.2	251	1	E1A_ADE41	P10542	human adeno
436	6	1.2	251	1	GLO2_BUCAI	P57336	buchnera ap
437	6	1.2	251	1	TRPC_HALVO	P18304	halobacteri
438	6	1.2	251	1	Y484_MYCTU	Q11150	mycobacteri
439	6	1.2	251	1	ZNUC_ECOLI	P52648	escherichia
440	6	1.2	252	1	KDSB_VIBCH	Q9kqx2	vibrio chol
441	6	1.2	253	1	RL2_YEAST	P05736	saccharomyc
442	6	1.2	254	1	HA2J_MOUSE	P23150	mus musculu
443	6	1.2	254	1	ST19_MOUSE	Q9jhn8	mus musculu
444	6	1.2	255	1	GLO2_RHOBL	P05446	rhodopsendo
445	6	1.2	255	1	SSUB_ECOLI	P38053	escherichia
446	6	1.2	256	1	HA2D_MOUSE	P04228	mus musculu
447	6	1.2	256	1	MYF5_NOTVI	Q91154	notophthalm
448	6	1.2	256	1	Y929_TREPA	O83899	treponema p
449	6	1.2	259	1	BAC2_HALS2	P29563	halobacteri
450	6	1.2	259	1	EXB4_ARATH	Q9shd1	arabidopsis
451	6	1.2	259	1	MURB_HELPJ	Q9zjj4	helicobacte
452	6	1.2	259	1	MURB_HELPJ	O25963	helicobacte
453	6	1.2	259	1	SSAT_SALTY	P96068	salmonella
454	6	1.2	259	1	T10C_HUMAN	O14798	h tumor nec
455	6	1.2	259	1	Y500_METUA	Q57923	methanococc
456	6	1.2	259	1	YG47_SYNY3	P74369	synechocyst
457	6	1.2	260	1	PSA1_CHICK	O42265	gallus gall
458	6	1.2	261	1	DER3_DERPT	P39675	dermatophag
459	6	1.2	261	1	YHEB_CHLVI	P56160	chlorobium
460	6	1.2	263	1	SUMT_SYNY3	Q55749	synechocyst
461	6	1.2	263	1	YD56_MYCTU	Q11026	mycobacteri
462	6	1.2	263	1	YHCK_ECOLI	P45427	escherichia
463	6	1.2	264	1	VAL1_MDV	P06847	wheat dwarf
464	6	1.2	265	1	MYO2_LYCES	P54927	lycopersico
465	6	1.2	266	1	ETFB_MYCLE	O33095	mycobacteri
466	6	1.2	266	1	ETFB_MYCTU	O53276	mycobacteri
467	6	1.2	266	1	TRP1_CYACA	Q9clw8	cyanidium c
468	6	1.2	267	1	PM27_STRPU	Q26616	strongyloce
469	6	1.2	267	1	Y123_THEMEA	Q9wxix7	thermotoga
470	6	1.2	267	1	Y441_METUA	Q57883	methanococc
471	6	1.2	267	1	YSR4_CAEEL	Q09952	caenorhabdi
472	6	1.2	268	1	CHI4_BRANA	Q06209	brassica na
473	6	1.2	268	1	EX3_SALTY	Q92612	salmonella
474	6	1.2	268	1	MIND_BACSU	Q01464	bacillus su
475	6	1.2	268	1	Y489_METUA	O57913	methanococc
476	6	1.2	269	1	LGT_BACSU	O34752	bacillus su
477	6	1.2	269	1	SAPF_HAEIN	P19867	haemophilus
478	6	1.2	269	1	TRPA_BACST	P45393	escherichia
479	6	1.2	269	1	YRBF_ECOLI	P42872	haemophilus
480	6	1.2	270	1	TONB_HAEIN	Q9xym0	drosofila
481	6	1.2	271	1	CRK_DROME	Q13162	homo sapien
482	6	1.2	271	1	PDX4_HUMAN	O05879	mycobacteri
483	6	1.2	271	1	YW34_MYCTU	O66414	aquifex aeo
484	6	1.2	271	1	YZ23_AQUAE	P26754	saccharomyc
485	6	1.2	273	1	RFA2_YEAST	O10477	schizosacch
486	6	1.2	273	1	YDF5_SCHPO	P34254	caenorhabdi
487	6	1.2	273	1	YKX2_CAEEL	P41217	homo sapien
488	6	1.2	274	1	OX2G_HUMAN	Q9bgi2	bos taurus
489	6	1.2	274	1	PDX4_BOVIN	Q9srh5	arabidopsis
490	6	1.2	275	1	POR1_ARATH	P42055	solanum tub
491	6	1.2	275	1	POR4_SOLTU	O17488	artemia san
492	6	1.2	275	1	TF2D_ARTSF	P29900	paracoccus
493	6	1.2	276	1	MOXJ_PARDE	Q08869	pasteurella
494	6	1.2	276	1	PLPB_PASHA	P25942	homo sapien
495	6	1.2	277	1	TNR5_HUMAN	Q9cm16	cyandidium c
496	6	1.2	278	1	CEMA_CYACA	P04218	rattus norv
497	6	1.2	278	1	OX2G_RAT	P12881	drosofila
498	6	1.2	279	1	PSA1_DROME	Q15744	homo sapien
499	6	1.2	281	1	CEBE_HUMAN	P35182	saccharomyc
500	6	1.2	281	1	P2C1_YEAST	P23106	pseudomonas
501	6	1.2	281	1	XYLF_PSEPU	Q9hw69	pseudomonas
502	6	1.2	283	1	PANC_PSEAE	P29036	zea mays (m
503	6	1.2	285	1	FR11_MAIZE	P18251	enterobacte
504	6	1.2	286	1	BLA1_ENTCL	P35196	saccharomyc
505	6	1.2	286	1	RER2_YEAST	O02771	bos taurus
506	6	1.2	287	1	SMN_BOVIN	P91409	caenorhabdi
507	6	1.2	287	1	STX4_CAEEL	Q9ydx4	aeropyrum p
508	6	1.2	287	1	AOX4_AERPE	Q05917	gallus gall
509	6	1.2	288	1	HME2_CHICK	P50223	gallus gall
510	6	1.2	288	1	HMX3_CHICK	P19117	schizosacch
511	6	1.2	288	1	IPYR_SCHPO	P50605	caenorhabdi
512	6	1.2	288	1	SDC_CAEEL	P37270	thermus the
513	6	1.2	288	1	CRTB_THETH	P70396	mus musculu
514	6	1.2	289	1	DLX5_MOUSE	P50575	rattus norv
515	6	1.2	289	1	DLX5_RAT	Q9ugx7	candida alb
516	6	1.2	290	1	RAS1_CANAL	P47482	mycoplasma
517	6	1.2	292	1	Y240_MYCGE	P14171	rhodobacter
518	6	1.2	293	1	BLAC_RHOCA	O14161	schizosacch
519	6	1.2	293	1	CMFL_SCHPO	P54856	ustilago ma
520	6	1.2	294	1	DPM1_USTMA	O07134	mycobacteri
521	6	1.2	294	1	MENA_MYCLE	Q9zed7	ricketsia
522	6	1.2	295	1	Y005_RICPR	Q60258	methanococc
523	6	1.2	295	1	YZ34_METUA	Q15006	homo sapien
524	6	1.2	297	1	Y103_HUMAN	Q58762	methanococc
525	6	1.2	297	1	YD67_METUA	O86841	streptomyce
526	6	1.2	297	1	DAPA_STRCO	Q9c004	homo sapien
527	6	1.2	299	1	SPY4_HUMAN	P19516	saccharomyc
528	6	1.2	300	1	COX2_YEAST	P52406	solanum tub
529	6	1.2	302	1	CHI4_SOLTU	O67798	aquifex aeo
530	6	1.2	302	1	HTPX_AQUAE	P12982	drosofila
531	6	1.2	302	1	PP12_DROME	Q05547	drosofila
532	6	1.2	302	1	PP13_DROME	O35448	mus musculu
533	6	1.2	302	1	PPT2_MOUSE	O70489	rattus norv
534	6	1.2	302	1	PPT2_RAT	Q53968	salmonella
535	6	1.2	303	1	SPAO_SALDU	P40602	salmonella
536	6	1.2	303	1	SPAO_SALTI	Q06099	salmonella
537	6	1.2	303	1	ISPE_SALTY	O05596	mycobacteri
538	6	1.2	306	1	YHBE_HAEIN	P71360	haemophilus
539	6	1.2	306	1	MTH3_HAEIN	P43871	haemophilus
540	6	1.2	309	1	GLS1_ECOLI	P77454	escherichia
541	6	1.2	310	1	TUS_KLEPO	O52715	klebsiella
542	6	1.2	310	1	HEM3_NEIMA	Q9jvs4	neisseria m
543	6	1.2	311	1			
544	6	1.2					

545	6	1.2	311	1	HEM3_NEIMB	Q9k0p6 neisseria m	618	6	1.2	351	1	COLF_ARATH	Q9fhb8 arabidopsis
546	6	1.2	312	1	FMF_MYCTU	P71674 mycobacteri	619	6	1.2	351	1	KLf2_RAT	Q9et58 rattus norv
547	6	1.2	312	1	VMEN_EBV	P03208 epstein-bar	620	6	1.2	351	1	ROM1_BOVIN	P52205 bos taurus
548	6	1.2	312	1	YC39_CYACA	O19883 cyanidium c	621	6	1.2	351	1	ROM1_HUMAN	O03395 homo sapien
549	6	1.2	313	1	LDH_CIOAB	Q97md1 clostetridium	622	6	1.2	351	1	ROM1_MOUSE	P32958 mus musculu
550	6	1.2	314	1	YC39_GUITH	O78472 guillardia	623	6	1.2	352	1	CLT1_MOUSE	Q99ja4 mus musculu
551	6	1.2	317	1	KDT2_SALTI	O8z8h3 salmonella	624	6	1.2	353	1	Y634_CHLMU	Q9pk39 chlamydia m
552	6	1.2	317	1	KDT2_SALTY	Q8zqz4 salmonella	625	6	1.2	353	1	YNCB_ECOLI	P76113 escherichia
553	6	1.2	317	1	MTX1_HUMAN	O13505 homo sapien	626	6	1.2	354	1	AC14_HUMAN	P35250 homo sapien
554	6	1.2	317	1	MTX1_MOUSE	P47802 mus musculu	627	6	1.2	354	1	KLf2_MOUSE	Q60843 mus musculu
555	6	1.2	317	1	YJ96_MYCTU	O10862 mycobacteri	628	6	1.2	355	1	CYSA_SYNY3	P74548 synchocyst
556	6	1.2	318	1	Y986_THEMA	Q9x081 thermotoga	629	6	1.2	355	1	DEGS_ECOLI	P31137 escherichia
557	6	1.2	319	1	YC39_PORPU	P51238 porphyra pu	630	6	1.2	355	1	KLf2_HUMAN	O9y5w3 treponema p
558	6	1.2	319	1	YF18_MYCTU	Q50590 mycobacteri	631	6	1.2	355	1	Y121_TREPA	O83158 treponema p
559	6	1.2	320	1	RLPA_RICPR	O9zde1 rickettsia	632	6	1.2	356	1	HITC_HAEIN	P44513 haemophilus
560	6	1.2	321	1	YC39_CYAPA	P48279 cyanophora	633	6	1.2	356	1	SPAS_SALTY	P40702 salmonella
561	6	1.2	322	1	ARGI_HUMAN	P05089 homo sapien	634	6	1.2	357	1	AMRP_RAT	Q99068 rattus norv
562	6	1.2	323	1	CMGB_BACHD	Q9k920 bacillus ha	635	6	1.2	358	1	VCOM_ADE40	P48753 human adeno
563	6	1.2	323	1	VANH_ENTFA	Q47748 enterococcu	636	6	1.2	358	1	Y4EE_RHISN	P55428 rhizobium s
564	6	1.2	325	1	LXB1_PHOLE	P09141 photobacter	637	6	1.2	359	1	AC14_CHICK	P53033 gallus gall
565	6	1.2	326	1	GGH_ARATH	O65355 arabidopsis	638	6	1.2	359	1	WECE_ECOLI	Q8xaq8 escherichia
566	6	1.2	326	1	PHP_MYCTU	P96413 mycobacteri	639	6	1.2	359	1	WECE_ECOLI	P56258 escherichia
567	6	1.2	327	1	XYNA_ASPAC	O59859 aspergillus	640	6	1.2	360	1	AMRP_MOUSE	P55302 mus musculu
568	6	1.2	327	1	YBC5_CHLVI	O50310 chlorobium	641	6	1.2	360	1	MANB_BACSU	P55278 bacillus su
569	6	1.2	328	1	AFUC_HAEIN	P44531 haemophilus	642	6	1.2	362	1	ILVE_STRCO	O86505 streptomyce
570	6	1.2	328	1	GRHR_BOVIN	P32236 bos taurus	643	6	1.2	363	1	BASS_ECOLI	P30844 escherichia
571	6	1.2	328	1	GRHR_SHEEP	P32237 ovis aries	644	6	1.2	364	1	CD33_HUMAN	P20138 homo sapien
572	6	1.2	329	1	COT4_HUMAN	Q9bxj3 homo sapien	645	6	1.2	364	1	RECF_AZOVI	P49997 azotobacter
573	6	1.2	329	1	CTAO_BACSU	O31652 bacillus su	646	6	1.2	365	1	CATD_SHEEP	Q9mzs8 ovis aries
574	6	1.2	329	1	IPNS_STRCL	P10621 streptomyce	647	6	1.2	365	1	CYSA_ECOLI	P16676 escherichia
575	6	1.2	330	1	GP43_HUMAN	O15552 homo sapien	648	6	1.2	365	1	CYSA_SALTY	P40860 salmonella
576	6	1.2	330	1	YH75_ARCFU	O28499 archaeoglob	649	6	1.2	365	1	Y1I3_YEAST	P40506 saccharomyc
577	6	1.2	332	1	TRPD_VIBPA	P22096 vibrio para	650	6	1.2	366	1	PMEA_ERMCH	P07863 erwinia chr
578	6	1.2	333	1	C1B1_SHEEP	Q28565 ovis aries	651	6	1.2	366	1	YGHO_ECOLI	Q46840 escherichia
579	6	1.2	333	1	C1B2_SHEEP	Q29422 ovis aries	652	6	1.2	367	1	DCUP_HUMAN	P06132 homo sapien
580	6	1.2	333	1	HK32_HUMAN	P78367 homo sapien	653	6	1.2	368	1	ILVE_MYCTU	Q10399 mycobacteri
581	6	1.2	334	1	MRPL_CAEEL	O93459 caenorhabdi	654	6	1.2	368	1	ST19_HUMAN	P49842 homo sapien
582	6	1.2	334	1	PIT_RHIME	O30499 rhizobium m	655	6	1.2	369	1	MURB_HUMAN	Q11148 mycobacteri
583	6	1.2	334	1	UNG_HSV11	P10186 herpes simp	656	6	1.2	370	1	CYB_COREN	O48039 coralus en
584	6	1.2	334	1	YCI1_METTH	O27279 methanobact	657	6	1.2	370	1	CYB_EPIAN	O48041 epicrates a
585	6	1.2	335	1	YD59_SCHPO	O10312 schizosacch	658	6	1.2	370	1	CYB_EPIE	O48043 epicrates c
586	6	1.2	335	1	YE81_MYCTU	P71762 mycobacteri	659	6	1.2	370	1	CYB_EPIX	O48047 epicrates e
587	6	1.2	337	1	CLT1_HUMAN	O9y271 homo sapien	660	6	1.2	370	1	CYB_EPIF	O48049 epicrates f
588	6	1.2	337	1	PXA2_PSEAE	O911q5 pseudomonas	661	6	1.2	370	1	CYB_EPIF	O48060 epicrates s
589	6	1.2	337	1	SYW_TREPA	O83640 treponema p	662	6	1.2	370	1	CYB_EPIF	O48060 epicrates s
590	6	1.2	338	1	KHSE_SCHPO	O43056 schizosacch	663	6	1.2	370	1	CYB_EPISM	O48055 epicrates s
591	6	1.2	338	1	YFJV_ECOLI	P52137 escherichia	664	6	1.2	370	1	CYB_EPIS	O48057 epicrates s
592	6	1.2	339	1	CLT1_RAT	Q924t8 rattus norv	665	6	1.2	370	1	CYB_EPIST	O48053 epicrates s
593	6	1.2	339	1	ILVC_CAUCR	O9a6h4 caulobacter	666	6	1.2	370	1	CYB_EPIST	O48062 eunectes s
594	6	1.2	339	1	RLA0_ARCFU	O28781 archaeoglob	667	6	1.2	370	1	CYB_EPISU	O48065 eunectes no
595	6	1.2	339	1	SG12_CAEEL	P46564 caenorhabdi	668	6	1.2	370	1	GP10_RAT	O64121 rattus norv
596	6	1.2	340	1	CLT1_PIG	O95n02 sus scrofa	669	6	1.2	370	1	H2AY_RAT	O02874 rattus norv
597	6	1.2	340	1	YMAJ_CAEEL	P34486 caenorhabdi	670	6	1.2	370	1	ODPA_BACSU	P21881 bacillus su
598	6	1.2	341	1	ACBB_ACTS5	O9zae8 actinoplan	671	6	1.2	371	1	AMIB_PSEAE	O51416 pseudomonas
599	6	1.2	341	1	CATL_DROME	O95029 drosophila	672	6	1.2	371	1	CYB_BOACO	P92848 boa constri
600	6	1.2	341	1	CREM_MOUSE	P27699 mus musculu	673	6	1.2	371	1	CYB_CAIKE	Q9mld7 calliophis
601	6	1.2	341	1	CREM_RAT	Q03061 rattus norv	674	6	1.2	371	1	CYB_CALMC	O9mld6 calliophis
602	6	1.2	342	1	TRPD_IACCA	P17170 lactobacill	675	6	1.2	371	1	CYB_CANAS	O48023 candoia asp
603	6	1.2	342	1	YN9A_YEAST	P53757 saccharomyc	676	6	1.2	371	1	CYB_CANCA	O48025 candoia car
604	6	1.2	344	1	CREM_CANFA	P79145 canis famil	677	6	1.2	371	1	CYB_CASDU	O48027 casarea dus
605	6	1.2	344	1	CYSA_SYNP7	P14788 synchococc	678	6	1.2	371	1	CYB_COLCO	O9m110 coluber con
606	6	1.2	345	1	CATD_PIG	P00795 sus scrofa	679	6	1.2	371	1	CYB_EPIMO	O48052 epicrates m
607	6	1.2	345	1	SFUC_SERMA	P21410 serratia ma	680	6	1.2	371	1	CYB_ERYCO	O48056 eryx colubr
608	6	1.2	345	1	YAT2_SCHPO	O10149 schizosacch	681	6	1.2	371	1	CYB_ERYCL	O48067 eryx colubr
609	6	1.2	346	1	MRAW_BRUME	O8yi74 brucella me	682	6	1.2	371	1	CYB_ERYEL	O48073 eryx elegan
610	6	1.2	347	1	MREB_ECOLI	P13519 escherichia	683	6	1.2	371	1	CYB_ERYJA	O48076 eryx jaculi
611	6	1.2	348	1	ADH1_PICST	O00097 pichia stip	684	6	1.2	371	1	CYB_ERYMI	O48079 eryx miliar
612	6	1.2	348	1	AFUC_ACTPL	O57293 actinobacil	685	6	1.2	371	1	CYB_ERYTN	O48080 eryx miliar
613	6	1.2	348	1	AFUC_ECOLI	P37009 escherichia	686	6	1.2	371	1	CYB_ERYTA	O48085 eryx tatari
614	6	1.2	348	1	CYSA_MESVI	O9mun1 mesostigma	687	6	1.2	371	1	CYB_MICEU	O9m1k5 micruroides
615	6	1.2	348	1	NR13_HUMAN	Q14994 homo sapien	688	6	1.2	371	1	CYB_TOXPR	O9m1k3 toxicocalan
616	6	1.2	350	1	ADH1_CANAL	P43067 candida alb	689	6	1.2	371	1	DUT_HSV11	P10234 herpes simp
617	6	1.2	350	1	Y170_METJA	Q57634 methanococc	690	6	1.2	371	1	H2AY_HUMAN	O75367 homo sapien

691	6	1.2	371	1	TGT CAUCR	Q9a7y1 caulobacter	764	6	1.2	390	1	TGFI_HUMAN	P01137 homo sapien
692	6	1.2	371	1	y816_SYN3	P74041 synechocyst	765	6	1.2	390	1	TGFI_PIG	P07200 sus scrofa
693	6	1.2	372	1	CD14_RABIT	Q28680 oryctolagus	766	6	1.2	390	1	TGFI_SHEEP	P50414 ovis aries
694	6	1.2	372	1	CYB_ACRDU	O48010 acrantophis	767	6	1.2	391	1	CAR1_CANAL	P28872 candida alb
695	6	1.2	372	1	CYB_ACRMA	O48012 acrantophis	768	6	1.2	391	1	CATE_CAVPO	P25796 cavia porce
696	6	1.2	372	1	CYB_ASPSC	Q9mlk0 aspidelaps	769	6	1.2	392	1	PEPC_RAT	P04073 rattus norv
697	6	1.2	372	1	CYB_ELABA	O9g250 elaphe baïr	770	6	1.2	393	1	IL1S_CERAE	Q29612 cercopithec
698	6	1.2	372	1	CYB_ELAVU	O9g210 elaphe obso	771	6	1.2	393	1	IRK9_MOUSE	Q92806 homo sapien
699	6	1.2	372	1	CYB_HETSI	O9g964 elaphe vulp	772	6	1.2	393	1	IRK9_MOUSE	P48543 mus musculu
700	6	1.2	372	1	CYB_PARMU	Q9ml18 heterodon s	773	6	1.2	393	1	IRK9_RAT	O63511 rattus norv
701	6	1.2	372	1	CYB_SANME	Q9mlj1 paranaia mu	774	6	1.2	394	1	PEPC_CAVPO	O64411 cavia porce
702	6	1.2	372	1	CYB_WALAE	O48114 sanzania ma	775	6	1.2	394	1	SUC1_STRCO	Q9ky56 streptomyc
703	6	1.2	372	1	UL16_HSV11	Q9mlj0 walterinnes	776	6	1.2	395	1	IF5_SCHPO	O09689 schizosacch
704	6	1.2	373	1	DNB1_HSV11	P10200 herpes simp	777	6	1.2	395	1	LIPG_RAT	P04634 rattus norv
705	6	1.2	375	1	EFVU_SPIAU	Q03444 equine herp	778	6	1.2	396	1	ARRS_RANCA	P51478 rana catesb
706	6	1.2	375	1	HIS7_XANAC	P42478 spirochaeta	779	6	1.2	396	1	ARRS_RANPI	P51479 rana pipien
707	6	1.2	375	1	HIS7_XANCP	P58881 xanthomonas	780	6	1.2	396	1	CARP_XENLA	P51477 xenopus lae
708	6	1.2	375	1	HIS7_XYLFA	P58882 xanthomonas	781	6	1.2	396	1	CATE_HUMAN	P14091 homo sapien
709	6	1.2	375	1	ACT1_PLAFA	O9pbc7 xylella fas	782	6	1.2	396	1	DCAM_YEAST	P21182 saccharomyc
710	6	1.2	376	1	PAG2_BOVIN	P10988 plasmodium	783	6	1.2	396	1	SOTB_PSEAE	Q9hwr7 pseudomonas
711	6	1.2	376	1	PEPC_MACFU	Q28057 bos taurus	784	6	1.2	397	1	CATE_MOUSE	P70269 mus musculu
712	6	1.2	377	1	TTL_BOVIN	P03955 macaca fusc	785	6	1.2	397	1	APLI_HUMAN	O14791 homo sapien
713	6	1.2	377	1	CKD6_MOUSE	P38584 bos taurus	786	6	1.2	398	1	ASP3_CAEEL	P55956 caenorhabdi
714	6	1.2	378	1	CYB_PHOGR	O08707 mus musculu	787	6	1.2	398	1	CATE_CANAL	P28871 candida alb
715	6	1.2	379	1	TTL_PIG	Q35457 phoca groen	788	6	1.2	398	1	IL1S_HUMAN	P16228 rattus norv
716	6	1.2	379	1	VPP_BPMU	P38160 sus scrofa	789	6	1.2	398	1	TRFR_BOVIN	P27930 homo sapien
717	6	1.2	380	1	AROC_AERPE	P08558 bacterioph	790	6	1.2	398	1	TRFR_BOVIN	O46639 bos taurus
718	6	1.2	380	1	CYB_HALCA	Q9ye14 aeropyrum p	791	6	1.2	398	1	TRFR_HUMAN	P24981 homo sapien
719	6	1.2	380	1	PAGI_BOVIN	O79204 halobaena c	792	6	1.2	398	1	TRFR_HUMAN	Q28596 ovis aries
720	6	1.2	380	1	SEL_P_MOUSE	Q29432 bos taurus	793	6	1.2	398	1	PRTZ_SHEEP	P22891 homo sapien
721	6	1.2	381	1	CYB_THYCY	P70274 mus musculu	794	6	1.2	400	1	RENI_SHEEP	P52115 ovis aries
722	6	1.2	381	1	RM13_CHICK	Q36012 thylacinus	795	6	1.2	400	1	YV6L_CAEEL	Q19978 caenorhabdi
723	6	1.2	381	1	SEL_P_MOUSE	Q90972 gallus gall	796	6	1.2	400	1	RENI_MOUSE	P95013 mycobacteri
724	6	1.2	381	1	YG12_YEAST	P49908 homo sapien	797	6	1.2	401	1	C123_MYCTU	P00796 mus musculu
725	6	1.2	381	1	CARA_ECOLI	P53155 saccharomyc	798	6	1.2	401	1	CAR1_CANPA	P77902 mycobacteri
726	6	1.2	382	1	CARA_ECOLI	P00907 escherichia	799	6	1.2	402	1	CN7B_SCHPO	P32951 candida par
727	6	1.2	382	1	CARA_SALTI	Q8z918 salmoneilla	800	6	1.2	402	1	DGT1_BRUME	Q09722 schizosacch
728	6	1.2	382	1	EDG1_SALTY	P14845 salmoneilla	801	6	1.2	402	1	PA11_MOUSE	P22777 mus musculu
729	6	1.2	382	1	EDG1_MOUSE	O08530 mus musculu	802	6	1.2	402	1	RENI_MOUSE	P06281 mus musculu
730	6	1.2	382	1	LXPB_ECO57	Q8x8x7 escherichia	803	6	1.2	402	1	SEL_P_BOVIN	P17560 sus scrofa
731	6	1.2	382	1	LXPB_ECOLI	P10441 escherichia	804	6	1.2	402	1	CINA_DEIRA	P4907 bos taurus
732	6	1.2	382	1	LXPB_SALTI	Q8z9a1 salmoneilla	805	6	1.2	402	1	PRSB_XENLA	O32508 deinococcus
733	6	1.2	382	1	LXPB_SALTY	Q8zrn9 salmoneilla	806	6	1.2	402	1	RRAL_SALTY	O42586 xenopus lae
734	6	1.2	382	1	PAGI_SHEEP	Q28755 ovis aries	807	6	1.2	404	1	ARRS_HUMAN	P10523 homo sapien
735	6	1.2	382	1	VE2_HEV61	Q06000 bacillus ce	808	6	1.2	404	1	BMP4_CHICK	Q90752 gallus gall
736	6	1.2	382	1	YC44_ODOSI	Q80951 human papil	809	6	1.2	404	1	PRSA_XENLA	O42778 candida alb
737	6	1.2	382	1	AMCI_ORYSA	P49539 odontella s	810	6	1.2	405	1	CARP_YEAST	P07267 saccharomyc
738	6	1.2	383	1	EDG1_RAT	P27940 oryza sativ	811	6	1.2	405	1	DGT1_AGR5	Q8uep3 agrobacteri
739	6	1.2	383	1	PEPE_CHICK	P48303 rattus norv	812	6	1.2	405	1	DGT1_RHIME	Q92q32 rhizobium m
740	6	1.2	383	1	CKD6_HUMAN	O00590 homo sapien	813	6	1.2	405	1	PRSA_XENLA	O42587 xenopus lae
741	6	1.2	384	1	Y243_METJA	P16476 gallus gall	814	6	1.2	405	1	DXR_MYCLE	Q9cbu3 mycobacteri
742	6	1.2	384	1	NR21_CHICK	Q91379 gallus gall	815	6	1.2	406	1	LMP1_MOUSE	P11438 mus musculu
743	6	1.2	385	1	SEL_P_RAT	P25236 rattus norv	816	6	1.2	406	1	RENI_HUMAN	P00797 homo sapien
744	6	1.2	385	1	BCSY_ACEXY	P58335 homo sapien	817	6	1.2	406	1	LMP1_RAT	P24268 rattus norv
745	6	1.2	386	1	CMG2_HUMAN	Q03168 aedes aegypt	818	6	1.2	407	1	LMP1_RAT	P14562 rattus norv
746	6	1.2	386	1	ASPP_AEDAE	P05501 schizosacch	819	6	1.2	407	1	BMP4_DAMDA	P12644 homo sapien
747	6	1.2	387	1	GLGC_BACST	O08326 bacillus st	820	6	1.2	408	1	BMP4_HUMAN	P21275 mus musculu
748	6	1.2	387	1	MSOX_BACSN	P23342 bacillus sp	821	6	1.2	408	1	BMP4_MOUSE	Q06826 rattus norv
749	6	1.2	387	1	SAT_DEIRA	P56864 deinococcus	822	6	1.2	408	1	BMP4_RAT	O46576 corynebacte
750	6	1.2	387	1	YHFX_ECOLI	P45550 escherichia	823	6	1.2	408	1	BMP4_RABIT	P18242 mus musculu
751	6	1.2	387	1	PEPC_CALJA	Q9n2d3 callithrix	824	6	1.2	409	1	ARRS_RANCA	P51479 rana pipien
752	6	1.2	388	1	PEPC_HUMAN	P20142 homo sapien	825	6	1.2	410	1	ARRS_RANPI	P51477 xenopus lae
753	6	1.2	388	1	PEPF_RABIT	P27823 oryctolagus	826	6	1.2	410	1	CARP_XENLA	P14091 homo sapien
754	6	1.2	388	1	PAGI_PIG	Q29078 sus scrofa	827	6	1.2	410	1	SOTB_PSEAE	Q9hwr7 pseudomonas
755	6	1.2	389	1	CARP_SACFI	P22929 saccharomyc	828	6	1.2	410	1	CATE_MOUSE	P70269 mus musculu
756	6	1.2	390	1	CATD_BOVIN	P80209 bos taurus	829	6	1.2	410	1	APLI_HUMAN	O14791 homo sapien
757	6	1.2	390	1	TGFI_CANPA	P54831 canis famli	830	6	1.2	411	1	ASP3_CAEEL	P28871 candida alb
758	6	1.2	390	1	TGFI_CAVPO	Q9z1y6 cavia porce	831	6	1.2	411	1	IL1S_CERAE	Q29612 cercopithec
759	6	1.2	390	1	TGFI_HORSE	P09533 cercopithec	832	6	1.2	412	1	IRK9_MOUSE	O63511 rattus norv
760	6	1.2	390	1			833	6	1.2	412	1	IRK9_MOUSE	P48543 mus musculu
761	6	1.2	390	1			834	6	1.2	412	1	IRK9_MOUSE	O63511 rattus norv
762	6	1.2	390	1			835	6	1.2	412	1	IRK9_MOUSE	O64411 cavia porce
763	6	1.2	390	1			836	6	1.2	412	1	IRK9_MOUSE	Q9ky56 streptomyc

837	6	1.2	413	1	DXR_MYCTU	Q10798 mycobacteri	910	6	1.2	440	1	BIK1_YEAST	P11709 saccharomyc
838	6	1.2	413	1	NODC_RHISN	P50357 rhizobium s	911	6	1.2	440	1	HIPa_ECOLI	P23874 escherichia
839	6	1.2	414	1	GLTP_BACSU	P39817 bacillus su	912	6	1.2	441	1	HLID_AQUAE	O67805 aquifex aeo
840	6	1.2	414	1	LMP1_CHICK	P05300 gallus gall	913	6	1.2	441	1	HISX_STRCO	P16245 streptomyce
841	6	1.2	414	1	MTR_ECOLI	P22306 escherichia	914	6	1.2	441	1	SYS_THEAC	Q9hxx5 thermoplasm
842	6	1.2	414	1	P2C3_SCHPO	O09173 schizosacch	915	6	1.2	442	1	PRSA_MOUSE	O88685 mus musculu
843	6	1.2	415	1	Y232_RICPR	Q9zdu2 rickettsia	916	6	1.2	443	1	UHPC_SALTY	P27669 salmonella
844	6	1.2	416	1	LMP1_HUMAN	P11279 homo sapien	917	6	1.2	443	1	FTSA_AGR75	O30991 agrobacteri
845	6	1.2	416	1	PGK2_RAT	P16617 rattus norv	918	6	1.2	444	1	C120_SYNY3	Q59990 synechocyst
846	6	1.2	416	1	PGK_CRIGR	P50310 cricetulus	919	6	1.2	444	1	CDT1_SCHPO	P40382 schizosacch
847	6	1.2	416	1	PGK_HORSE	P00559 equus cabal	920	6	1.2	444	1	XK_HUMAN	P51811 homo sapien
848	6	1.2	417	1	CAR4_CANAL	P43093 candida alb	921	6	1.2	445	1	OST4_CANFA	Q05052 canis famil
849	6	1.2	418	1	CAR5_CANAL	P43094 candida alb	922	6	1.2	445	1	YGCS_ECOLI	Q46909 escherichia
850	6	1.2	418	1	CAR6_CANAL	P43095 candida alb	923	6	1.2	447	1	VANS_ENTFA	Q47745 enterococcu
851	6	1.2	418	1	LEU2_THETN	O8rdk2 thermoaner	924	6	1.2	449	1	G64F_DROME	P83297 drosophila
852	6	1.2	418	1	RHAA_BACHD	Q9kcl9 bacillus ha	925	6	1.2	449	1	GAD_MOUSE	P22933 mus musculu
853	6	1.2	419	1	GSC_DROME	P54366 drosophila	926	6	1.2	449	1	GAD_RAT	P18506 rattus norv
854	6	1.2	419	1	KAS2_STRCN	Q02579 streptomyce	927	6	1.2	449	1	XYLA_LACBR	P29443 lactobacill
855	6	1.2	419	1	KDAP_MOUSE	O09043 mus musculu	928	6	1.2	450	1	ACHX_HUMAN	Q9gzz6 homo sapien
856	6	1.2	419	1	NOEE_RHISN	P55472 rhizobium s	929	6	1.2	450	1	GASR_PRANA	P30796 praomys nat
857	6	1.2	419	1	RHO_BUCAL	P57652 buchnera ap	930	6	1.2	450	1	MOO_HELPJ	Q9zmy5 helicobacte
858	6	1.2	420	1	NAP1_HUMAN	O96009 homo sapien	931	6	1.2	450	1	MOO_HELPJ	O24913 helicobacte
859	6	1.2	420	1	PGK_TETTH	P50313 tetrahymena	932	6	1.2	451	1	SYS_ARATH	Q39230 arabidopsis
860	6	1.2	420	1	PUR2_STRPN	Q97ct98 streptococc	933	6	1.2	453	1	HRAJ_HUMAN	P83110 homo sapien
861	6	1.2	420	1	RHO_HAEIN	P44619 haemophilus	934	6	1.2	453	1	OP2_MAIZE	P12959 zea mays (m
862	6	1.2	420	1	VIT3_DROME	P06607 drosophila	935	6	1.2	453	1	PLM2_PLAFA	P46925 plasmodium
863	6	1.2	421	1	ACRO_HUMAN	P10323 homo sapien	936	6	1.2	453	1	VG_DROME	Q26366 drosophila
864	6	1.2	421	1	PPAL_MOUSE	P24638 mus musculu	937	6	1.2	454	1	MNTH_RHIL0	Q98199 rhizobium 1
865	6	1.2	421	1	PUR2_STRPY	O9aly7 streptococc	938	6	1.2	454	1	YGBN_ECOLI	Q46892 escherichia
866	6	1.2	421	1	TRAB_AGR75	Q44351 agrobacteri	939	6	1.2	456	1	MNTH_BRUME	O8yi76 bruceella me
867	6	1.2	423	1	PPAL_HUMAN	P11117 homo sapien	940	6	1.2	456	1	OST4_HUMAN	P39656 homo sapien
868	6	1.2	423	1	PPAL_RAT	P20611 rattus norv	941	6	1.2	458	1	ACHO_HUMAN	Q05901 homo sapien
869	6	1.2	424	1	KAS2_STRCO	P23156 streptomyce	942	6	1.2	458	1	YGEH_ECOLI	P76639 escherichia
870	6	1.2	426	1	MNTH_MYCLE	Q50103 mycobacteri	943	6	1.2	459	1	EX7L_PSEAE	Q9hx18 pseudomonas
871	6	1.2	426	1	S6AA_HUMAN	P53796 homo sapien	944	6	1.2	461	1	NCB1_HUMAN	O9yic0 oryzias lat
872	6	1.2	426	1	VA20_VACCC	P20995 vaccinia vi	945	6	1.2	461	1	NIFN_SYN8	O02818 homo sapien
873	6	1.2	426	1	VA20_VARV	P33843 variola vir	946	6	1.2	461	1	NIFN_SYN8	O07356 synechococc
874	6	1.2	427	1	DSL1_CHICK	P34822 gallus gall	947	6	1.2	462	1	EF10_XENLA	P13549 xenopus lae
875	6	1.2	427	1	RHO_BACSU	Q03222 bacillus su	948	6	1.2	462	1	EF11_CRIGR	P20001 cricetulus
876	6	1.2	428	1	AMY1_ORYSA	P17654 oryza sativ	949	6	1.2	462	1	EF11_HUMAN	P04720 homo sapien
877	6	1.2	428	1	DCTA_ECO57	O8x5m2 escherichia	950	6	1.2	462	1	EF11_MOUSE	P10126 mus musculu
878	6	1.2	428	1	DCTA_ECOLI	P37312 escherichia	951	6	1.2	462	1	EF1A_BRARE	Q92005 brachydanio
879	6	1.2	428	1	GLYA_AQUAE	O66776 aquifex aeo	952	6	1.2	462	1	EF1A_CHICK	Q90835 gallus gall
880	6	1.2	428	1	ZF26_MOUSE	P10076 mus musculu	953	6	1.2	462	1	OCT2_MOUSE	Q00196 mus musculu
881	6	1.2	429	1	PUR2_ECOLI	P15640 escherichia	954	6	1.2	463	1	COAT_FRG3V	O67473 frog virus
882	6	1.2	429	1	PUR2_SALT1	Q8z334 salmonella	955	6	1.2	463	1	COAT_RTRV	Q91qz8 rana tigrin
883	6	1.2	429	1	PUR2_SALT2	P26977 salmonella	956	6	1.2	463	1	MURD_RHIME	Q52953 rhizobium m
884	6	1.2	429	1	URAA_ECOLI	P33780 escherichia	957	6	1.2	463	1	Y096_MYCTU	Q10892 mycobacteri
885	6	1.2	430	1	GLGC_ECOLI	P00584 escherichia	958	6	1.2	464	1	CASB_KLEOX	Q48409 klebsiella
886	6	1.2	431	1	NQOE_THETH	Q56229 thermus the	959	6	1.2	466	1	DLDH_ZYMMO	P50970 zymomonas m
887	6	1.2	432	1	ENV2_MOUSE	P11370 mus musculu	960	6	1.2	467	1	CYSP_TRYCR	P25779 trypanosoma
888	6	1.2	432	1	Y41L_RHISN	P55495 rhizobium s	961	6	1.2	467	1	EUTA_SALTY	Q9zfv2 salmonella
889	6	1.2	433	1	ENO_CAEEL	Q27527 caenorhabdi	962	6	1.2	468	1	SYPA_SULSO	P95961 sulfolobus
890	6	1.2	433	1	RHO_CHRVI	P52152 chromatium	963	6	1.2	471	1	LMRB_LISIN	Q2zeel listeria in
891	6	1.2	434	1	HPD_HORVU	O48604 hordeum vul	964	6	1.2	471	1	LMRB_LISMO	Q8y9k8 listeria mo
892	6	1.2	434	1	PRSA_YEAST	P33297 saccharomyc	965	6	1.2	471	1	YEGB_ECOLI	P36554 escherichia
893	6	1.2	435	1	FIXC_BRAJA	P10331 bradyrhizob	966	6	1.2	473	1	YHU6_YEAST	P38770 saccharomyc
894	6	1.2	435	1	NHG2_PSEPU	Q53552 pseudomonas	967	6	1.2	473	1	RUMA_RHOGE	Q9jp88 rhodocyclus
895	6	1.2	435	1	OADB_HAEDU	Q9rf98 haemophilus	968	6	1.2	474	1	CREC_ECOLI	P08401 escherichia
896	6	1.2	435	1	YQD7_CAEEL	Q09267 caenorhabdi	969	6	1.2	474	1	DLDH_ALCEU	P52992 alcaligenes
897	6	1.2	436	1	COAT_CHVP1	P30328 paramecium	970	6	1.2	475	1	MOTD_RHIME	O52964 rhizobium m
898	6	1.2	436	1	EPE2_RALSO	Q45411 talstonia s	971	6	1.2	475	1	S611_CANFA	P38377 canis famil
899	6	1.2	436	1	MNTH_DEIRA	O9rt98 deinococcus	972	6	1.2	475	1	S612_HUMAN	P38378 homo sapien
900	6	1.2	437	1	GLA2_RHIL0	Q98a81 rhizobium 1	973	6	1.2	475	1	S612_HUMAN	Q9y2r3 homo sapien
901	6	1.2	437	1	NEOR_STRCY	P14501 streptomyce	974	6	1.2	475	1	S612_MOUSE	Q9jlr1 mus musculu
902	6	1.2	437	1	YQEZ_BACSU	P54465 bacillus su	975	6	1.2	475	1	S61A_HALRO	Q25147 halocynthia
903	6	1.2	438	1	PRSA_SCHPO	O14126 schizosacch	976	6	1.2	477	1	BAIG_EUBSP	P32369 eubacterium
904	6	1.2	438	1	SYS_HELAN	O81983 helianthus	977	6	1.2	477	1	FIBB_PETMA	P02678 petromyzon
905	6	1.2	438	1	Y16R_MYCIO	Q49573 mycoplasma	978	6	1.2	477	1	NOM1_PSEAE	Q913y3 pseudomonas
906	6	1.2	439	1	IDNT_ECOLI	P39344 escherichia	979	6	1.2	478	1	ALDA_ECOLI	P25553 escherichia
907	6	1.2	439	1	PRSA_HUMAN	P17980 homo sapien	980	6	1.2	478	1	CARL_HUMAN	Q9uhj6 homo sapien
908	6	1.2	439	1	PRSA_RAT	Q63569 rattus norv	981	6	1.2	478	1	EGR4_RAT	Q00911 rattus norv
909	6	1.2	439	1	UHPC_ECOLI	P09836 escherichia	982	6	1.2	478	1	OCT2_HUMAN	P09086 homo sapien

983	6	1.2	478	1	PUO_MICRU	P40974	micrococcus
984	6	1.2	478	1	YOHG_ECOLI	P33369	escherichia
985	6	1.2	479	1	6PGD_TRYBB	P31072	trypanosoma
986	6	1.2	479	1	HYED_ECOLI	P77416	escherichia
987	6	1.2	479	1	S6IA_SCHPO	P79088	schizosacch
988	6	1.2	481	1	YEAV_ECOLI	P76252	escherichia
989	6	1.2	482	1	HOXA_ALCEU	P29267	alcaligenes
990	6	1.2	482	1	MANC_ECO57	O85342	escherichia
991	6	1.2	482	1	TYPH_HUMAN	P19971	homo sapien
992	6	1.2	483	1	MURE_LACLA	O9cent1	lactococcus
993	6	1.2	484	1	HEMZ_HORVU	P42045	hordium vul
994	6	1.2	485	1	YGFRO_ECOLI	O46815	escherichia
995	6	1.2	487	1	SYE2_THEMA	O9x218	thermotoga
996	6	1.2	489	1	FLIF_AQUAB	O67241	aquifex aeo
997	6	1.2	489	1	YHIP_ECOLI	P36837	escherichia
998	6	1.2	490	1	MODF_ECOLI	P31060	escherichia
999	6	1.2	490	1	MURE_THEMA	O9wy79	thermotoga
1000	6	1.2	492	1	TIG_RHIL0	O981e8	rhizobium 1

ALIGNMENTS

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RESULT 1
BAE2_HUMAN
ID BAE2_HUMAN STANDARD; PRT; 518 AA.
AC Q9Y5Z0; Q9JUT6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta secretase 2 precursor (EC 3.4.23.-) (Beta-site APP-cleaving
DE enzyme 2) (Aspartyl protease 1) (Asp 1) (ASPI) (Membrane-associated
DE aspartic protease 1) (Memapsin-1).
GN BACE2 OR ASP21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashler J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Xin H., Stephens J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,
RA Giese K.;
RT "Identification of a novel aspartic-like protease differentially
RT expressed in human breast cancer cell lines.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;
RT "Cloning of a gene from chromosome 21 Down region encoding a potential
RT transmembrane aspartyl protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Solans A., Estivill X., de la Luna S.;
RT "Cloning of a novel mammalian aspartyl protease.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20120043; PubMed=10656250;
RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA Smith T.S., Simons D.L., Walsh F.S., Dingwall C., Christie G.;
RT "Identification of a novel aspartic proteinase (Asp 2) as
```

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RT beta-secretase.";
RL Mol. Cell. Neurosci. 14:419-427(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=20144060; PubMed=10677483;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
RT beta-amyloid precursor protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; AF200342; AAF17078.1; -.
DR EMBL; AF117892; AAD45240.1; -.
DR EMBL; AF050171; AAD45963.1; -.
DR EMBL; AF178532; AAF29494.1; -.
DR EMBL; AF204944; AAF26368.1; -.
DR EMBL; AF200192; AAF13714.1; -.
DR EMBL; AL163284; CAB90458.1; -.
DR EMBL; AL163285; CAB90554.1; -.
DR EMBL; BC014453; AAH14453.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR Genew; HGNC:934; BACE2.
DR MIM; 605668; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 ? POTENTIAL.
FT CHAIN ? 518 BETA SECRETASE 2.
FT DOMAIN 21 473 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 474 494 POTENTIAL.
FT DOMAIN 495 518 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 110 110 BY SIMILARITY.
FT ACT_SITE 303 303 BY SIMILARITY.
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 36 36 A -> T (IN REF. 6).
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SQ SEQUENCE 518 AA; 56180 MW; 2E903150823760D3 CRC64;
Query Match 100.0%; Score 518; DB 1; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALAPALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVAVPTPGPTPAERHADGL 60
DB 1 MGALAPALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVAVPTPGPTPAERHADGL 60
QY 61 ALALEPALLASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAG 120
DB 61 ALALEPALLASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTOGSWTGFVGEDLVTPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTOGSWTGFVGEDLVTPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFFDSLVTQANTPNVFSMQMGAGLPVA 240
DB 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFFDSLVTQANTPNVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMYTPIKEWYQIEILKEIGQSINLDCREYNADKA 300
DB 241 GSGTNGGSLVLGGIEPSLYKGDIMYTPIKEWYQIEILKEIGQSINLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVPDAVVEAARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLRLPQKVPDAVVEAARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENGSSRSFRITILPOLYIQPMNGAGLNYECYRFGISPTNALVIGATWMEGFYVIFD 420
DB 361 YLRDENGSSRSFRITILPOLYIQPMNGAGLNYECYRFGISPTNALVIGATWMEGFYVIFD 420
QY 421 RAQKRVGFASPACAEIAGAASEISGPFSTEDVASNCVPAQSLSEPIILWISYALMSVCG 480
DB 421 RAQKRVGFASPACAEIAGAASEISGPFSTEDVASNCVPAQSLSEPIILWISYALMSVCG 480
QY 481 AILLVILVLLLPFCQRRPRDEPVNDESSLVRHRWK 518
DB 481 AILLVILVLLLPFCQRRPRDEPVNDESSLVRHRWK 518
RESULT 2
BACE_HUMAN
ID BACE_HUMAN STANDARD; PRT; 501 AA.
AC P56817; Q9JUT5; Q9BYC1; Q9BYC0; Q9BYB9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
DE protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
DE (Memapsin-2).
GN BACE OR BACE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Roses S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Ederson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND

RP CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20057171; PubMed=10591214;
RA Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
RA Tatsuno G., Tung J., Schenk D., Seubert P., Suomensaari S.M., Wang S.,
RA Walker D., Zhao J., McConlogue L., Varghese J.;
RT "Purification and cloning of amyloid precursor protein beta-secretase
RT from human brain.";
RL Nature 402:537-540(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashler J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
RT secretase activity.";
RL Nature 402:533-537(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20120043; PubMed=10656250;
RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
RT secretase.";
RL Mol. Cell. Neurosci. 14:419-427(1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Brain, and Pancreas;
RA Michel B., De Pietri Tonelli D., Zaccchetti D., Keller P.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
RT human brain and pancreas.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC TISSUE=Pancreas;
RA Zaccchetti D., De Pietri Tonelli D., Schnurbus R.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
RT human pancreas.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC TISSUE=Brain;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site
RT amyloid precursor protein cleaving enzyme (BACE) and their effect on
RT amyloid beta-peptide production.";
RL Neurosci. Lett. 307:9-12(2001).
RN [8]
RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
RX MEDLINE=20144060; PubMed=10677483;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
RT beta-amyloid precursor protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=21950860; PubMed=11953458;
RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
RT "The disulphide bonds in the catalytic domain of BACE are critical but
RT not essential for amyloid precursor protein processing activity.";
RL J. Neurochem. 80:1079-1088(2002).
RN [10]
RP FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
RX THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
RX LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
RX SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
RX FRAGMENT WHICH IS LATER RELEASE BY GAMMA-SECRETASE.
RN [11]
RP SUBCELLULAR LOCATION: Type I membrane protein.


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CC -!- ALTERNATIVE PRODUCTS: 4 isoforms; A/BACE-1A/BAC-501 (shown here),
CC B/BACE-1B/BACE-I-476; C/BACE-1C/BACE-I-457 and D/BACE-1D/BACE-I-
CC 432; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; AF190725; AAF04142.1; -
DR EMBL; AF201468; AAF18982.1; -
DR EMBL; AF200343; AAF17079.1; -
DR EMBL; AF204943; AAF26367.1; -
DR EMBL; AF338816; AAK38374.1; -
DR EMBL; AF338817; AAK38375.1; -
DR EMBL; AB050436; BAB40931.1; -
DR EMBL; AB050437; BAB40932.1; -
DR EMBL; AB050438; BAB40933.1; -
DR EMBL; AF200193; AAF13715.1; -
DR HSSP; P32329; 1YPS.
DR MEROPS; A01.004; -
DR Genew; HGNC:933; BACE.
DR MIM; 604252; -
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR KW Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420 BY SIMILARITY.
FT DISULFID 278 443
FT DISULFID 330 380
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 146 189 MISSING (IN ISOFORM C AND ISOFORM D).
FT VARSPPLIC 190 214 MISSING (IN ISOFORM B AND ISOFORM D).
SQ SEQUENCE 501 AA; 55763 MW; 377CE4C824ACEF05 CRC64;

Query Match 2.3%; Score 12; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 ILVDTGSSNFAV 118
| | | | | | | | | |
Db 90 ILVDTGSSNFAV 101

RESULT 3
BACE_MOUSE STANDARD; PRT; 501 AA.
AC P56818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
DE protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)

```

```

DE (Memapsin-2).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amaranter P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
RN [2]
RP REVISIONS TO 6 AND 81-87.
RA Bennett B.D., Vassar R., Citron M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Torry M.C., Pauley A.M.,
RA Bashier J.R., Strachan N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).
CC -!- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; AF190726; AAF04143.2; -
DR EMBL; AF200346; AAF17082.1; -
DR HSSP; P56272; 1AM5.
DR MEROPS; A01.004; -
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45 POTENTIAL.
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420 BY SIMILARITY.
FT DISULFID 278 443 BY SIMILARITY.
FT DISULFID 330 380 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55747 MW; C085A013145E474E CRC64;

Query Match 2.3%; Score 12; DB 1; length 501;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
 |||||
 Db 90 ILVDTGSSNFAV 101

RESULT 4
 BACE_RAT
 ID BACE RAT STANDARD; PRT; 501 AA.

AC P56819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
 DE protease 2) (ASP 2) (ASP2) (Membrane-associated aspartic protease 2)
 DE (Memapsin-2).
 GN BACE.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Ederson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.;
 RA "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).

CC -!- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
 CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
 CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
 CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASE BY GAMMA-SECRETASE (BY
 CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

CC -----
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CC -----
 CC EMBL; AF190727; AAF04144.1; -.

DR HSSP; P32329; 1YPS.
 DR MEROPS; A01.004; -.
 DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW signal.

FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 45 POTENTIAL.
 FT CHAIN 46 501 BETA-SECRETASE.
 FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 458 478 POTENTIAL.
 FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 93 93 BY SIMILARITY.
 FT ACT_SITE 289 289 BY SIMILARITY.
 FT DISULFID 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT DISULFID 330 380 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55806 MW; 24B445BC8BE87DE3 CRC64;

Query Match 2.3%; Score 12; DB 1; length 501;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
 |||||
 Db 90 ILVDTGSSNFAV 101

RESULT 5

LRP_HAEIN
 ID LRP HAEIN STANDARD; PRT; 166 AA.

AC P45265;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Leucine-responsive regulatory protein.
 DE LRP OR H11596.

GN Haemophilus influenzae.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OK NCBI_TaxID=727;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischohn R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;

RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).

CC -!- FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE
 CC AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS; LRP
 CC MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS
 CC (BY SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.

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CC -----
 CC EMBL; U32833; AAC23241.1; -.
 DR TIGR; H11596; -.
 DR InterPro; IPR000485; ASNC_trans_reg.
 DR Pfam; PF01037; ASNC_trans_reg; 1.
 DR PRINTS; PR00033; HTHASNC.
 DR SMART; SM00344; HTH_ASNC; 1.

DR PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
KW DNA-binding; Transcription regulation; Activator; Complete proteome.
FT DNA_BIND 35 54 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 166 AA; 18910 MW; 22C0F1B78B110CEB CRC64;
Query Match 1.5%; Score 8; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 305 GTTLRLP 312
| | | | |
Db 136 GTTLRLP 143
RESULT 6
60IM PROMI STANDARD; PRT; 237 AA.
AC P22833;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa inner-membrane protein homolog (Fragment).
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM1509;
RX MEDLINE=91033012; PubMed=2172087;
RA Skovgaard O.;
RT "Nucleotide sequence of a Proteus mirabilis DNA fragment homologous
to the 60K-rnpA-rpmH-dnaA-dnaN-recF-gyrB region of Escherichia
coli.";
RL Gene 93:27-34(1990).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(Probable).
CC -!- SIMILARITY: BELONGS TO THE OXA1 / 60 KDA IMP FAMILY.
CC -----
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CC -----
DR EMBL; M58352; AAA83954.1; -.
DR PIR; JQ0729; JQ0729.
KW Transmembrane; Inner membrane.
FT TRANSMEM 7 23 POTENTIAL.
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 26664 MW; 07FCC405B9DB3F36 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 DTGSSNFA 117
| | | | |
Db 206 DTGSSNFA 213
RESULT 7
VPRT SMRVH
ID VPRT SMRVH STANDARD; PRT; 323 AA.
AC P21407;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protease (EC 3.4.23.-).
GN PRT.
OS Squirrel monkey retrovirus (SMRV-H) (SMRV-HLB).

OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073750; PubMed=3201749;
RA Oda T., Ikeda S., Watanabe S., Hatsushika M., Akiyama K.,
RA Mitsunobu F.;
RT "Molecular cloning, complete nucleotide sequence, and gene structure
of the provirus genome of a retrovirus produced in a human
lymphoblastoid cell line.";
RL Virology 167:468-476(1988).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A2.
CC -!- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
CC -----
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CC -----
DR EMBL; M23385; AAA66452.1; ALT_INIT.
DR PIR; B31827; PRLJHD.
DR HSSP; P06968; 1EUW.
DR MEROPS; A02.UPW; -.
DR InterPro; IPR001995; Aspprotease_rtrv.
DR InterPro; IPR001969; Aspprotease_site.
DR InterPro; IPR001428; DeoxyUTPase.
DR InterPro; IPR000467; G_patch.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00692; dUTPase; 1.
DR Pfam; PF01585; G_patch; 1.
DR ProDom; PD000946; DeoxyUTPase; 1.
DR SMART; SM00443; G_patch; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
DR PROSITE; PS50174; G_PATCH; 1.
KW Hydroxylase; Aspartyl protease.
FT DOMAIN 275 321 G-PATCH.
FT ACT_SITE 193 193 BY SIMILARITY.
SQ SEQUENCE 323 AA; 35126 MW; 5D6CEA38BA932786 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 161 DVTIPKG 168
| | | | |
Db 126 DVTIPKG 133
RESULT 8
CARP POLTV
ID CARP POLTV STANDARD; PRT; 340 AA.
AC P17576;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Polyporopepsin (EC 3.4.23.29) (Aspartic proteinase).
OS Polyporus tulipiferae (Irpex lacteus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Polyporaceae; Polyporus.
OX NCBI_TaxID=29885;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
RA Kobayashi H., Sekibata S., Shibuya H., Yoshida S., Kusakabe I.,
RA Murakami K.;
RT "Cloning and sequence analysis of cDNA for Irpex lacteus aspartic
proteinase.";
RL Agric. Biol. Chem. 53:1927-1933(1989).
CC -!- CATALYTIC ACTIVITY: Milk clotting activity, broad specificity, but
fails to cleave 15-Leu-|-Tyr-16 or 16-Tyr-|-Leu-17 of insulin B

```
CC chain.
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
CC EMBL; D00589; BAA00467.1; -.
CC PIR; J00057; PEIKL.
CC HSSP; P32329; 1YPS.
CC MEROPS; A01.019; -.
CC InterPro; IPR001461; AsproteaseA1.
CC InterPro; IPR001969; Asprotease_site.
CC Pfam; PF00026; asp; 1.
CC PRINTS; PR00792; PEPsin.
CC PROSITE; PS00141; ASP_PROTEASE; 2.
CC Hydrolase; Aspartyl protease; Glycoprotein.
CC FT ACT_SITE 32 32
CC FT ACT_SITE 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 238 238
CC SQ SEQUENCE 340 AA; 35050 MW; 9BAF837264D42FEF CRC64;

Query Match 1.5%; Score 8; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 LVDTGSSN 115
Db 30 LVDTGSSN 37

RESULT 9
YHDX_ECOLI STANDARD; PRT; 362 AA.
AC P45767;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical amino-acid ABC transporter_permease protein yhdx.
GN YHDX OR B3269.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -! FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM YDHXYZ FOR AN AMINO ACID; PROBABLY RESPONSIBLE FOR THE
CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC -! SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -! SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. HISWQ SUBFAMILY. SEEMS TO BE THE ORTHOLOG
CC OF R.LEGUMINOSARUM AAPQ.
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CC -----
CC EMBL; U18997; AAA58073.1; ALT_INIT.
CC EMBL; AE000405; AAC76301.1; ALT_INIT.
CC EcoGene; EG12835; yhdx.
CC InterPro; IPR000515; BPD_transp.
CC Pfam; PF00528; BPD_transp; 1.
CC PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; 1.
CC Hypothetical protein;Transport; Amino-acid transport; Transmembrane;
CC Inner membrane; Complete proteome.
CC FT TRANSMEM 21 41 POTENTIAL.
CC FT TRANSMEM 92 112 POTENTIAL.
CC FT TRANSMEM 128 148 POTENTIAL.
CC FT TRANSMEM 180 200 POTENTIAL.
CC FT TRANSMEM 219 239 POTENTIAL.
CC FT TRANSMEM 256 276 POTENTIAL.
CC FT TRANSMEM 333 353 POTENTIAL.
CC SQ SEQUENCE 362 AA; 39749 MW; 946105FBA0761BD6 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LPLAQWL 17
Db 227 LPLAQWL 234

RESULT 10
ECT1_SCHPO STANDARD; PRT; 365 AA.
AC Q9UT16;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable ethanolamine-phosphate cytidyltransferase (EC 2.7.7.14)
DE (phosphorylethanolamine transferase) (Cfr:phosphoethanolamine
DE cytidyltransferase).
GN SPAC15E1.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymompres B.,
RA Weltyjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Fuchs W., Filtz C., Holzer E., Moesti D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado I., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cernutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Usseery D., Barrell B.G., Nurse P.;
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RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- CATALYTIC ACTIVITY: CTP + ethanolamine phosphate = diphosphate +
CC CDP-ethanolamine.
CC -1- PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CDP-ETHANOLAMINE SYNTHESIS;
CC SECOND STEP.
CC -1- SIMILARITY: BELONGS TO THE CYTIDYLYLTRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL; AL109770; CAB52424.1; -
DR InterPro; IPR004821; Cyt tran rel.
DR InterPro; IPR004820; Cytidylyltransf.
DR Pfam; PF01467; Cytidylyltransf; 1.
DR TIGRPFAMs; TIGR00125; cyt_tran_rel; 2.
DR Transferrase; Nucleotidyltransferase; Phospholipid biosynthesis.
FT DOMAIN 1 182 CATALYTIC (POTENTIAL).
SQ SEQUENCE 365 AA; 41556 MW; ACDB6A974ABB4734 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 SGTLLRL 311
Db 191 SGTLLRL 198

RESULT 11
LBP_HUMAN
ID_LBP_HUMAN STANDARD; PRT; 481 AA.
AC P18428; Q92672; Q43438; Q9UD66; Q9H403;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lipopolysaccharide-binding protein precursor (LBP).
GN LBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90385281; PubMed=2402637;
RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,
RA Mathison J.C., Tobias P.S., Ulevitch R.J.;
RT "Structure and function of lipopolysaccharide binding protein.";
RL Science 249:1429-1431(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292492; PubMed=7517398;
RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,
RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
RT "Bactericidal/permeability-increasing protein and lipopolysaccharide
RT (LPS)-binding protein. LPS binding properties and effects on LPS-
RT mediated cell activation.";
RL J. Biol. Chem. 269:17411-17416(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Hubacek J.A., Aslanidis C., Schmitz G.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98110577; PubMed=9441745;
RA Kirschning C.J., Au-Young J., Lamping N., Reuter D., Pfeil D.,
RA Seilhamer J.J., Schumann R.R.;
RT "Similar organization of the lipopolysaccharide-binding protein (LBP)

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RT and phospholipid transfer protein (PLTP) genes suggests a common gene
RT family of lipid-binding proteins.";
RL Genomics 46:416-425(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Long J.Y., Liu J.Q., Xue Y.N., Wang H.X.;
RT "Cloning and sequencing of human lipopolysaccharide-binding protein
RT gene.";
RL Sheng Wu Huaxue Yu Shengwu Wuli Jinzhan 25:469-471(1998).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehtsaalaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [7]
RP SEQUENCE OF 1-41 FROM N.A.
RA Sutton C.L., Smith R.I.F., Centola M.B., Theofan G.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [8]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=98227852; PubMed=9568897;
RA Beamer L.J., Carroll S.F., Eisenberg D.;
RT "The BPI/LBP family of proteins: a structural analysis of conserved
RT regions.";
RL Protein Sci. 7:906-914(1998).
CC -1- FUNCTION: BINDS TO THE LIPID A MOIETY OF BACTERIAL
CC LIPOPOLYSACCHARIDES (LPS), A GLYCOLIPID PRESENT IN THE OUTER
CC MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS COMPLEX SEEMS
CC TO INTERACT WITH THE CD14 RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
DR EMBL; M35533; AAA59493.1; -
DR EMBL; X98657; CAA67226.1; -
DR EMBL; X98658; CAA67226.1; JOINED.
DR EMBL; X98659; CAA67226.1; JOINED.
DR EMBL; X98660; CAA67226.1; JOINED.
DR EMBL; X98661; CAA67226.1; JOINED.
DR EMBL; X98662; CAA67226.1; JOINED.
DR EMBL; X98663; CAA67226.1; JOINED.

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DR EMBL; X98664; CAA67226.1; JOINED.
DR EMBL; X98665; CAA67226.1; JOINED.
DR EMBL; X98666; CAA67226.1; JOINED.
DR EMBL; X98667; CAA67226.1; JOINED.
DR EMBL; X98668; CAA67226.1; JOINED.
DR EMBL; AF013512; AAC39547.1; -.
DR EMBL; AF013500; AAC39547.1; JOINED.
DR EMBL; AF013501; AAC39547.1; JOINED.
DR EMBL; AF013502; AAC39547.1; JOINED.
DR EMBL; AF013503; AAC39547.1; JOINED.
DR EMBL; AF013504; AAC39547.1; JOINED.
DR EMBL; AF013505; AAC39547.1; JOINED.
DR EMBL; AF013506; AAC39547.1; JOINED.
DR EMBL; AF013507; AAC39547.1; JOINED.
DR EMBL; AF013508; AAC39547.1; JOINED.
DR EMBL; AF013510; AAC39547.1; JOINED.
DR EMBL; AF013511; AAC39547.1; JOINED.
DR EMBL; AF105067; AAD21962.1; -.
DR EMBL; AL080249; CAC10462.1; -.
DR EMBL; L42172; AAA66446.1; -.
DR PIR; A35843; A35843.
DR HSSP; P17213; 1BP1.
DR Genew; HGNC:6517; LBP.
DR MIM; 151990; -.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP_1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
KW Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 481 LIPOLYSACCHARIDE-BINDING PROTEIN.
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 6 6 R -> H (IN REF. 2).
FT CONFLICT 22 22 E -> C (IN REF. 2).
FT CONFLICT 82 82 N -> K (IN REF. 4).
FT CONFLICT 128 128 S -> F (IN REF. 4).
FT CONFLICT 154 157 VTAS -> GYCL (IN REF. 1).
FT CONFLICT 174 174 L -> S (IN REF. 1).
FT CONFLICT 257 257 R -> S (IN REF. 4).
FT CONFLICT 266 270 VMSLP -> A (IN REF. 1).
FT CONFLICT 369 369 L -> H (IN REF. 4).
FT CONFLICT 436 436 L -> F (IN REF. 2, 4 AND 6).
SQ SEQUENCE 481 AA; 53349 MW; 816E4B9E5E6864D0 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARAL 8
Db 1 MGALARAL 8

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RESULT 12
60IM_ECOLI STANDARD; PRT; 548 AA.
ID 60IM_ECOLI
AC P25714;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa inner-membrane protein.
GN YIDC OR B3705.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=93315143; PubMed=7686882;
RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
RL genome: organizational symmetry around the origin of replication.";
RN Genomics 16:551-561(1993).
RP [2]
RP SEQUENCE OF 1-2 FROM N.A.
RX MEDLINE=86056995; PubMed=2415431;
RA Hansen F.G., Hansen E.B., Atlung T.;
RT "Physical mapping and nucleotide sequence of the rnpA gene that
RT encodes the protein component of ribonuclease P in Escherichia
RT coli.";
RL Gene 38:85-93(1985).
RN [3]
RP TOPOLOGY.
RX MEDLINE=99023968; PubMed=9804807;
RA Saeaeef A., Monne M., de Gier J.W., von Heijne G.;
RT "Membrane topology of the 60-kDa Oxa1p homologue from Escherichia
RT coli.";
RL J. Biol. Chem. 273:30415-30418(1998).
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC CC (Probable).
CC CC -1- SIMILARITY: BELONGS TO THE OXA1 / 60 KDA IMP FAMILY.
CC CC -----
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CC CC -----
DR EMBL; L10328; AAA62056.1; -.
DR EMBL; AE000447; AAC76728.1; -.
DR EMBL; M11056; -; NOT ANNOTATED_CDS.
DR Ecogen; EG1197; y1dC.
DR InterPro; IPR001708; 60kDa_innermeb.
DR Pfam; PF02096; 60KD_IMP; 1.
DR PRINTS; PR00701; 60KDINNERMP.
KW Transmembrane; Inner membrane; Complete proteome.
FT DOMAIN 1 5 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 6 23 PROBABLE.
FT DOMAIN 24 342 PERIPLASMIC (PROBABLE).
FT TRANSMEM 343 370 PROBABLE.
FT DOMAIN 371 416 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 417 446 PROBABLE.
FT DOMAIN 447 463 PERIPLASMIC (PROBABLE).
FT TRANSMEM 464 481 PROBABLE.
FT DOMAIN 482 493 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 494 509 PROBABLE.
FT DOMAIN 510 512 PERIPLASMIC (PROBABLE).
FT TRANSMEM 513 535 PROBABLE.
FT DOMAIN 536 548 CYTOPLASMIC (PROBABLE).
SQ SEQUENCE 548 AA; 61526 MW; 95EBC5DAB4F2FCFB CRC64;

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Query Match 1.5%; Score 8; DB 1; Length 548;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 DTGSSNFA 117
Db 207 DTGSSNFA 214

RESULT 13
GLND_CORGL STANDARD; PRT; 692 AA.
ID GLND_CORGL
AC Q9X706;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE [Protein-PII] uridylyltransferase (EC 2.7.7.59) (PII uridylyl-
DE transferase) (Uridylyl removing enzyme) (UTase).
GN GLND OR CGL2059.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX MEDLINE=99243747; PubMed=10227160;
RA Jakoby M.J., Kraemer R., Burkowski A.;
RT "Nitrogen regulation in Corynebacterium glutamicum: isolation of genes
RT involved and biochemical characterization of corresponding proteins.";
RL FEWS Microbiol. Lett. 173:303-310(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX Nakagawa S.;
RA "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MODIFIES, BY URIDYLYLATION OR DEURIDYLYLATION THE PII
CC (GLNB) REGULATORY PROTEIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: UTP + [protein-PII] = diphosphate + uridylyl-
CC [protein-PII].
CC -!- SIMILARITY: BELONGS TO THE GLND FAMILY.
CC -----
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CC -----
CC EMBL; AJ010319; CAB39374.1; -.
DR EMBL; AP005280; BAB99452.1; -.
DR InterPro; IPR002819; HD.
DR InterPro; IPR003607; ME_PpIase_HDC.
DR InterPro; IPR002934; NTP_transf.
DR Pfam; PF01909; NTP_transf_2; 1.
DR Pfam; PF01966; HD; 1.
DR SMART; SM00471; HDC; 1.
DR Transference; Nucleotidylyltransferase.
KM SEQUENCE 692 AA; 75969 MW; A7AC19614C133676 CRC64;
SQ
Query Match 1.5%; Score 8; DB 1; Length 692;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 31 LPLRVAAA 38
Db 295 LPLRVAAA 302
RESULT 14
NIDO_HUMAN
ID NIDO_HUMAN STANDARD; PRT; 1247 AA.
AC P14543; Q14942;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nidogen precursor (Entactin).
GN NID.
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90091745; PubMed=2574658;
RA Nagayoshi T., Sanborn D., Hickok N.J., Olsen D.R., Fazio M.J.,

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RA Chu M.-L., Knowlton R., Mann K., Deutzmann R., Timpl R., Uitto J.;
RT "Human nidogen: complete amino acid sequence and structural domains
RT deduced from cDNAs, and evidence for polymorphism of the gene.";
RL DNA 8:581-594 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96044428; PubMed=7557988;
RA Zimmermann K., Hoischen S., Hafner M., Nischt R.;
RT "Genomic sequences and structural organization of the human nidogen
RT gene (NID).";
RL Genomics 27:245-250 (1995).
RN [3]
RP SEQUENCE OF 667-1247 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89270475; PubMed=24711408;
RA Olsen D.R., Nagayoshi T., Fazio M., Mattei M.-G., Passage E., Weil D.,
RA Timpl R., Chu M.L., Uitto J.;
RT "Human nidogen: cDNA cloning, cellular expression, and mapping of the
RT gene to chromosome 1q43.";
RL Am. J. Hum. Genet. 44:876-885 (1989).
CC -1- FUNCTION: SULFATED GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN
CC BASEMENT MEMBRANES AND THAT IS TIGHTLY ASSOCIATED WITH LAMININ.
CC ALSO BINDS TO COLLAGEN IV. IT PROBABLY HAS A ROLE IN CELL-
CC EXTRACELLULAR MATRIX INTERACTIONS.
CC -1- SUBCELLULAR LOCATION: BASEMENT MEMBRANES.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 LDL-RECEPTOR YWTD DOMAINS.
CC -----
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CC -----
DR EMBL; M30269; AAA59932.1; -.
DR EMBL; X82245; CAA57709.1; -.
DR EMBL; X84819; CAA57709.1; JOINED.
DR EMBL; X84820; CAA57709.1; JOINED.
DR EMBL; X84821; CAA57709.1; JOINED.
DR EMBL; X84822; CAA57709.1; JOINED.
DR EMBL; X84823; CAA57709.1; JOINED.
DR EMBL; X84824; CAA57709.1; JOINED.
DR EMBL; X84825; CAA57709.1; JOINED.
DR EMBL; X84826; CAA57709.1; JOINED.
DR EMBL; X84827; CAA57709.1; JOINED.
DR EMBL; X84828; CAA57709.1; JOINED.
DR EMBL; X84829; CAA57709.1; JOINED.
DR EMBL; X84830; CAA57709.1; JOINED.
DR EMBL; X84831; CAA57709.1; JOINED.
DR EMBL; X84832; CAA57709.1; JOINED.
DR EMBL; X84833; CAA57709.1; JOINED.
DR EMBL; X84834; CAA57709.1; JOINED.
DR EMBL; X84835; CAA57709.1; JOINED.
DR EMBL; X84836; CAA57709.1; JOINED.
DR EMBL; X84837; CAA57709.1; JOINED.
DR EMBL; M27445; AAA57261.1; -.
DR PIR; A33322; MMHUND.
DR HSSP; P35555; 1EMN.
DR Genew; HGNC:7821; NID.
DR MIM; 131390; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR000716; Thyroglobulin_1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF00058; Ldl_recept_b; 3.
DR Pfam; PF00086; thyroglobulin_1; 1.

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DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_like; 4.
DR SMART; SM00135; LY; 5.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00211; TY; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01187; EGF_CA; 2.
KW Basement membrane; Extracellular matrix; Glycoprotein; Sulfation;
Signal; Calcium-binding; Repeat; EGF-like domain; Cell adhesion.
FT SIGNAL 1 28
FT CHAIN 29 1247 NIDOGEN.
FT DOMAIN 29 669 I (LARGER GLOBULAR DOMAIN).
FT DOMAIN 670 917 II (CYSTEINE-RICH).
FT DOMAIN 918 1247 III (SMALLER GLOBULAR DOMAIN).
FT DOMAIN 386 426 EGF-LIKE 1.
FT DOMAIN 668 709 EGF-LIKE 2.
FT DOMAIN 710 751 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 758 801 EGF-LIKE 4.
FT DOMAIN 802 840 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 872 919 THYROGLOBULIN TYPE I.
FT DOMAIN 989 1030 LDL-RECEPTOR YWTD MOTIF 1.
FT DOMAIN 1032 1073 LDL-RECEPTOR YWTD MOTIF 2.
FT DOMAIN 1075 1118 LDL-RECEPTOR YWTD MOTIF 3.
FT DOMAIN 1124 1163 LDL-RECEPTOR YWTD MOTIF 4.
FT DOMAIN 1208 1244 EGF-LIKE 6.
FT MOD_RES 289 289 SULFATION (POTENTIAL).
FT MOD_RES 296 296 SULFATION (POTENTIAL).
FT DISULFID 672 685 BY SIMILARITY.
FT DISULFID 679 695 BY SIMILARITY.
FT DISULFID 697 708 BY SIMILARITY.
FT DISULFID 714 727 BY SIMILARITY.
FT DISULFID 721 736 BY SIMILARITY.
FT DISULFID 738 750 BY SIMILARITY.
FT DISULFID 762 777 BY SIMILARITY.
FT DISULFID 769 787 BY SIMILARITY.
FT DISULFID 789 800 BY SIMILARITY.
FT DISULFID 806 817 BY SIMILARITY.
FT DISULFID 811 826 BY SIMILARITY.
FT DISULFID 828 839 BY SIMILARITY.
FT DISULFID 1212 1223 BY SIMILARITY.
FT DISULFID 1219 1232 BY SIMILARITY.
FT DISULFID 1234 1243 BY SIMILARITY.
FT SITE 702 704 CELL ATTACHMENT SITE.
FT CARBOHYD 1137 1137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 33 34 EL -> SS (IN REF. 2).
FT CONFLICT 37 42 FGPGQG -> SAPDR (IN REF. 2).
FT CONFLICT 1115 1115 H -> T (IN REF. 3).
SQ SEQUENCE 1247 AA; 136488 MW; 4681B5B3CEC1575B CRC64;

Query Match 1.5%; Score 8; DB 1; Length 1247;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RALLPL 13
Db 14 RALLPL 21

RESULT 15
DNM1_MOUSE STANDARD; PRT; 1620 AA.
ID DNM1_MOUSE
AC P13864; P97413; Q9OXX6; Q9CSC6;
DT 01-JAN-1990 (Rel. 13, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA
methyltransferase Mmu1) (DNA Mase Mmu1) (MCMT) (M.Mmu1) (Met-1).
GN DNM1 OR DNMT OR UIM OR MET1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89094873; PubMed=3210246;
RA Bestor T.H., Laudano A., Mattaliano R., Ingram V.;
RT "Cloning and sequencing of a cDNA encoding DNA methyltransferase of
RT mouse cells. The carboxyl-terminal domain of the mammalian enzymes is
RT related to bacterial restriction methyltransferases.";
RL J. Mol. Biol. 203:971-983(1988).
RN [2]
RP REVISIONS TO N-TERMINUS.
RC TISSUE=Embryo;
RX MEDLINE=97094871; PubMed=8940105;
RA Yoder J.A., Yen R.-W.C., Vertino P.M., Bestor T.H., Baylín S.B.;
RT "New 5' regions of the murine and human genes for DNA (cytosine-5)-
RT methyltransferase.";
RL J. Biol. Chem. 271:31092-31097(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Skeletal muscle;
RX MEDLINE=20515133; PubMed=11063128;
RA Aguirre-Arteaga A.M., Grunewald I., Cardoso M.C., Leonhardt H.;
RT "Expression of an alternative Dnmt1 isoform during muscle
RT differentiation.";
RL Cell Growth Differ. 11:551-559(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=C57BL/6;
RX MEDLINE=20181859; PubMed=10715201;
RA Margot J.B., Aguirre-Arteaga A.M., Di Giacco B.V., Pradhan S.,
RA Roberts R.J., Cardoso M.C., Leonhardt H.;
RT "Structure and function of the mouse DNA methyltransferase gene: Dnmt1
RT shows a tripartite structure.";
RL J. Mol. Biol. 297:293-300(2000).
RN [5]
RP SEQUENCE OF 1-27 AND 119-1619 FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=98119799; PubMed=9449671;
RA Merlino C., Yoder J.A., Taketo T., Laird D.W., Trasler J.M.,
RA Bestor T.H.;
RT "Sex-specific exons control DNA methyltransferase in mammalian germ
RT cells.";
RL Development 125:889-897(1998).
RN [6]
RP SEQUENCE OF 1-144 FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 3-6.
RC STRAIN=129/Sv, and BALB/c; TISSUE=Embryonic stem cells;
RX MEDLINE=99047652; PubMed=9830015;
RA Gaudet F., Talbot D., Leonhardt H., Jaenisch R.;
RT "A short DNA methyltransferase isoform restores methylation in vivo.";
RL J. Biol. Chem. 273:32725-32729(1998).
RN [7]
RP SEQUENCE OF 1-119 FROM N.A. (ISOFORM 1).
RC STRAIN=129/Sv; TISSUE=Embryonic stem cells, and Kidney;
RX MEDLINE=97075093; PubMed=8917520;
RA Tucker K.L., Talbot D., Lee M.A., Leonhardt H., Jaenisch R.;
RT "Complementation of methylation deficiency in embryonic stem cells by
RT a DNA methyltransferase minigene.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12920-12925(1996).
RN [8]
RP SEQUENCE OF 1-272 FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:40:49 ; Search time 38 Seconds
(without alignments)
2808.748 Million cell updates/sec

Title: US-09-668-314C-2

Perfect score: 518

Sequence: 1 MGALARALLPLLAQWLRA.....RPRDPEVVNDESSLVRHRWK 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	439	84.7	439	4 Q9H2V8	Q9h2v8 homo sapien
2	378	73.0	396	4 Q9NZL1	Q9nzl1 homo sapien
3	328	63.3	468	4 Q9NZL2	Q9nzl2 homo sapien
4	59	11.4	514	11 Q9JL18	Q9jll8 mus musculu
5	38	7.3	255	11 Q9R1P7	Q9rip7 mus musculu
6	12	2.3	432	4 Q9BYB9	Q9byb9 homo sapien
7	12	2.3	457	4 Q9BYC0	Q9byc0 homo sapien
8	12	2.3	476	4 Q9BYC1	Q9byc1 homo sapien
9	12	2.3	532	4 Q9ULS1	Q9uls1 homo sapien
10	9	1.7	213	4 Q9P0D2	Q9pod2 homo sapien
11	9	1.7	266	11 Q9CUU5	Q9cuu5 mus musculu
12	9	1.7	319	16 Q32940	Q32940 mycobacteri
13	9	1.7	863	16 Q9PCW3	Q9pcw3 xylella fas
14	9	1.7	1121	11 Q99MX8	Q99mx8 mus musculu
15	8	1.5	94	2 O07312	O07312 rhodobacter
16	8	1.5	96	10 Q9M8Y6	Q9m8y6 arabidopsis

17	8	1.5	159	16 Q9CP14	Q9cp14 pasteurella
18	8	1.5	178	10 Q42492	Q42492 canavalia g
19	8	1.5	202	16 Q9ZM15	Q9zml5 helicobacte
20	8	1.5	241	16 Q9L0R0	Q9l0r0 streptomyce
21	8	1.5	244	5 Q8WQY9	Q8wqy9 aphrocallis
22	8	1.5	250	12 Q72887	Q72887 african cas
23	8	1.5	254	16 Q983Z3	Q983z3 rhizobium 1
24	8	1.5	257	12 Q09347	Q09347 cassava gem
25	8	1.5	257	12 Q09348	Q09348 cassava gem
26	8	1.5	257	12 Q9WR12	Q9wr12 west africa
27	8	1.5	257	12 Q09351	Q09351 east africa
28	8	1.5	257	12 Q8V383	Q8v383 east africa
29	8	1.5	257	12 Q09350	Q09350 african cas
30	8	1.5	257	12 Q09349	Q09349 cassava gem
31	8	1.5	287	10 Q9SH24	Q9sh24 arabidopsis
32	8	1.5	303	16 Q9RXF5	Q9rxf5 deinococcus
33	8	1.5	318	16 Q92XE4	Q92xe4 rhizobium m
34	8	1.5	319	16 Q8Z5W7	Q8z5w7 salmonella
35	8	1.5	327	3 P78849	P78849 schizosacch
36	8	1.5	333	16 Q8ZNV8	Q8znv8 salmonella
37	8	1.5	341	6 Q46495	Q46495 bos taurus
38	8	1.5	342	2 Q68868	Q68868 synecococc
39	8	1.5	352	17 Q9YER7	Q9yer7 aeropyrum p
40	8	1.5	364	16 Q97LG4	Q97lg4 clostridium
41	8	1.5	386	10 Q8S1T9	Q8slt9 oryza sativ
42	8	1.5	393	16 Q8X5G4	Q8x5g4 escherichia
43	8	1.5	443	16 Q9RKZ4	Q9rkz4 streptomyce
44	8	1.5	449	10 Q9S9K4	Q9s9k4 arabidopsis
45	8	1.5	451	10 Q9LGF1	Q9lgl1 oryza sativ
46	8	1.5	471	11 Q91XR7	Q91xr7 rattus norv
47	8	1.5	472	4 Q96PQ4	Q96pq4 homo sapien
48	8	1.5	472	4 Q8WUX1	Q8wux1 homo sapien
49	8	1.5	473	5 Q9VEE0	Q9vee0 drosophila
50	8	1.5	474	5 Q8SQZ9	Q8sqz9 encephalito
51	8	1.5	476	4 Q9UTU8	Q9utu8 homo sapien
52	8	1.5	477	4 Q8TCF0	Q8tcf0 homo sapien
53	8	1.5	482	2 Q8RMG9	Q8rmg9 acetobacter
54	8	1.5	504	4 Q99624	Q99624 homo sapien
55	8	1.5	504	11 Q9JHZ9	Q9jhz9 rattus norv
56	8	1.5	505	11 Q9DCP2	Q9dcp2 mus musculu
57	8	1.5	505	11 Q9JL18	Q9jll8 mus musculu
58	8	1.5	548	16 Q8Z2N7	Q8z2n7 salmonella
59	8	1.5	548	16 Q8XB42	Q8xb42 escherichia
60	8	1.5	548	16 Q8ZKY4	Q8zky4 salmonella
61	8	1.5	580	17 Q59381	Q59381 pyrococcus
62	8	1.5	581	17 Q8U0D8	Q8u0d8 pyrococcus
63	8	1.5	592	5 Q9VTS5	Q9vts5 drosophila
64	8	1.5	612	5 Q8T0E6	Q8t0e6 drosophila
65	8	1.5	637	10 Q82612	Q82612 arabidopsis
66	8	1.5	671	17 Q8TJA8	Q8tja8 methanosarc
67	8	1.5	682	16 Q8XVM2	Q8xvm2 ralstonia s
68	8	1.5	904	16 Q9HUM7	Q9hum7 pseudomonas
69	8	1.5	985	3 Q8X027	Q8x027 neurospora
70	8	1.5	1104	10 Q9FU60	Q9fu60 oryza sativ
71	8	1.5	1477	3 Q9C250	Q9c250 neurospora
72	7	1.4	22	4 Q9NNY7	Q9nny7 homo sapien
73	7	1.4	32	16 Q98AB6	Q98ab6 rhizobium 1
74	7	1.4	45	12 Q68620	Q68620 hepatitis c
75	7	1.4	45	12 Q68613	Q68613 hepatitis c
76	7	1.4	45	12 Q68614	Q68614 hepatitis c
77	7	1.4	45	12 Q68617	Q68617 hepatitis c
78	7	1.4	45	12 Q68618	Q68618 hepatitis c
79	7	1.4	45	12 Q68619	Q68619 hepatitis c
80	7	1.4	45	12 Q68625	Q68625 hepatitis c
81	7	1.4	62	8 Q8WGC3	Q8wgq3 sphacelaria
82	7	1.4	62	8 Q8WGQ2	Q8wgq2 sphacelaria
83	7	1.4	68	5 Q9GTY0	Q9gty0 tribolium c
84	7	1.4	76	12 Q68499	Q68499 hepatitis c
85	7	1.4	76	12 Q68496	Q68496 hepatitis c
86	7	1.4	76	12 Q68497	Q68497 hepatitis c
87	7	1.4	76	12 Q68498	Q68498 hepatitis c
88	7	1.4	77	4 Q8TE42	Q8te42 homo sapien
89	7	1.4	80	12 Q9W8C0	Q9w8c0 hepatitis c

90	7	1.4	80	12	Q9WA47	Q9wa47 hepatitis c
91	7	1.4	80	12	Q9WA15	Q9wa15 hepatitis c
92	7	1.4	80	12	Q9W9W8	Q9w9w8 hepatitis c
93	7	1.4	80	12	Q9W9B4	Q9w9b4 hepatitis c
94	7	1.4	80	12	Q9W903	Q9w903 hepatitis c
95	7	1.4	80	12	Q9W852	Q9w852 hepatitis c
96	7	1.4	80	12	Q9W9M3	Q9w9m3 hepatitis c
97	7	1.4	80	12	Q9W9K3	Q9w9k3 hepatitis c
98	7	1.4	80	12	Q9WN77	Q9wn77 hepatitis c
99	7	1.4	80	12	Q9WN76	Q9wn76 hepatitis c
100	7	1.4	80	12	Q9WN75	Q9wn75 hepatitis c
101	7	1.4	80	12	Q9WN74	Q9wn74 hepatitis c
102	7	1.4	80	12	Q9WN73	Q9wn73 hepatitis c
103	7	1.4	80	12	Q9WN72	Q9wn72 hepatitis c
104	7	1.4	80	12	Q9WN70	Q9wn70 hepatitis c
105	7	1.4	80	12	Q9WN69	Q9wn69 hepatitis c
106	7	1.4	80	12	Q9WN68	Q9wn68 hepatitis c
107	7	1.4	80	12	Q9WN67	Q9wn67 hepatitis c
108	7	1.4	80	12	Q9WN64	Q9wn64 hepatitis c
109	7	1.4	80	12	Q9WN63	Q9wn63 hepatitis c
110	7	1.4	80	12	Q9WN62	Q9wn62 hepatitis c
111	7	1.4	80	12	Q9WN61	Q9wn61 hepatitis c
112	7	1.4	80	12	Q9WN60	Q9wn60 hepatitis c
113	7	1.4	80	12	Q9WN59	Q9wn59 hepatitis c
114	7	1.4	80	12	Q9WN58	Q9wn58 hepatitis c
115	7	1.4	80	12	Q9WN57	Q9wn57 hepatitis c
116	7	1.4	80	12	Q9WN56	Q9wn56 hepatitis c
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119	7	1.4	80	12	Q9WN53	Q9wn53 hepatitis c
120	7	1.4	80	12	Q9WN52	Q9wn52 hepatitis c
121	7	1.4	80	12	Q9WN50	Q9wn50 hepatitis c
122	7	1.4	80	12	Q9WN48	Q9wn48 hepatitis c
123	7	1.4	82	12	Q9Q3U3	Q9q3u3 hepatitis c
124	7	1.4	84	17	Q8TWE3	Q8twe3 methanopyru
125	7	1.4	85	2	Q9AF00	Q9ap00 burkholderi
126	7	1.4	86	2	Q9WXF8	Q9wxf8 rhodococcus
127	7	1.4	86	8	Q95786	Q95786 diabtrotica
128	7	1.4	86	8	Q95778	Q95778 diabtrotica
129	7	1.4	86	8	Q95787	Q95787 diabtrotica
130	7	1.4	92	16	Q98JG3	Q98jg3 rhizobium 1
131	7	1.4	96	16	Q9HYQ7	Q9hyq7 pseudomonas
132	7	1.4	97	4	Q16755	Q16755 homo sapien
133	7	1.4	103	2	Q9ZEH7	Q9zeh7 enterococcu
134	7	1.4	104	16	Q92D67	Q92d67 listeria in
135	7	1.4	106	17	Q9HN89	Q9hn89 halobacteri
136	7	1.4	107	3	Q8XLT7	Q8xlt7 pholiota na
137	7	1.4	109	12	Q8VAT4	Q8vat4 white spot
138	7	1.4	112	5	Q9VLE8	Q9vle8 drosophila
139	7	1.4	114	12	Q9IPM8	Q9ipm8 hepatitis c
140	7	1.4	114	12	Q9IPM7	Q9ipm7 hepatitis c
141	7	1.4	114	12	Q9IPM6	Q9ipm6 hepatitis c
142	7	1.4	114	12	Q9IPM5	Q9ipm5 hepatitis c
143	7	1.4	114	12	Q9IPM4	Q9ipm4 hepatitis c
144	7	1.4	114	12	Q9IPM3	Q9ipm3 hepatitis c
145	7	1.4	114	12	Q9IPM1	Q9ipm1 hepatitis c
146	7	1.4	114	12	Q9IPL9	Q9ipl9 hepatitis c
147	7	1.4	114	12	Q9IPL8	Q9ipl8 hepatitis c
148	7	1.4	114	12	Q9IPL7	Q9ipl7 hepatitis c
149	7	1.4	114	12	Q9IPL4	Q9ipl4 hepatitis c
150	7	1.4	114	12	Q9IPL3	Q9ipl3 hepatitis c
151	7	1.4	114	12	Q9IPL2	Q9ipl2 hepatitis c
152	7	1.4	114	12	Q9IPL1	Q9ipl1 hepatitis c
153	7	1.4	114	12	Q9IPL0	Q9ipl0 hepatitis c
154	7	1.4	114	12	Q9IPK9	Q9ipk9 hepatitis c
155	7	1.4	114	12	Q9IPK8	Q9ipk8 hepatitis c
156	7	1.4	114	12	Q9IPK7	Q9ipk7 hepatitis c
157	7	1.4	114	12	Q9IPK6	Q9ipk6 hepatitis c
158	7	1.4	114	12	Q9IPK5	Q9ipk5 hepatitis c
159	7	1.4	114	12	Q9IPK4	Q9ipk4 hepatitis c
160	7	1.4	114	12	Q9IPK3	Q9ipk3 hepatitis c
161	7	1.4	114	12	Q9IPK2	Q9ipk2 hepatitis c
162	7	1.4	114	12	Q9IPK1	Q9ipk1 hepatitis c
163	7	1.4	114	12	Q9IPK0	Q9ipk0 hepatitis c
164	7	1.4	114	12	Q9IPJ9	Q9ipj9 hepatitis c
165	7	1.4	115	2	P72321	P72321 rhodospiril
166	7	1.4	119	9	Q9AZT7	Q9azt7 bacterioph
167	7	1.4	119	11	Q9QXI4	Q9qxi4 rattus norv
168	7	1.4	119	16	Q9CFR1	Q9cfr1 lactococcus
169	7	1.4	121	12	Q72213	Q72213 hepatitis c
170	7	1.4	123	15	Q9YU02	Q9yv02 human immun
171	7	1.4	123	15	Q9YU25	Q9yu25 human immun
172	7	1.4	127	11	Q9CPY4	Q9cpy4 mus musculu
173	7	1.4	131	16	Q98QNI	Q98qni mycoplasma
174	7	1.4	132	16	Q8YFH5	Q8yfh5 brucella me
175	7	1.4	135	12	Q68188	Q68188 hepatitis c
176	7	1.4	137	12	Q911H1	Q911h1 hepatitis c
177	7	1.4	137	12	Q911I0	Q911i0 hepatitis c
178	7	1.4	137	12	Q911H9	Q911h9 hepatitis c
179	7	1.4	137	12	Q911H8	Q911h8 hepatitis c
180	7	1.4	137	12	Q911H7	Q911h7 hepatitis c
181	7	1.4	137	12	Q911H6	Q911h6 hepatitis c
182	7	1.4	137	12	Q911H5	Q911h5 hepatitis c
183	7	1.4	137	12	Q911H4	Q911h4 hepatitis c
184	7	1.4	137	12	Q911H3	Q911h3 hepatitis c
185	7	1.4	137	12	Q911H2	Q911h2 hepatitis c
186	7	1.4	137	12	Q911H1	Q911h1 hepatitis c
187	7	1.4	137	12	Q911H0	Q911h0 hepatitis c
188	7	1.4	137	12	Q911G9	Q911g9 hepatitis c
189	7	1.4	137	12	Q911G8	Q911g8 hepatitis c
190	7	1.4	137	12	Q911G7	Q911g7 hepatitis c
191	7	1.4	137	12	Q911G6	Q911g6 hepatitis c
192	7	1.4	137	12	Q911G5	Q911g5 hepatitis c
193	7	1.4	137	12	Q911G4	Q911g4 hepatitis c
194	7	1.4	137	12	Q911G3	Q911g3 hepatitis c
195	7	1.4	137	12	Q911G2	Q911g2 hepatitis c
196	7	1.4	137	12	Q911G1	Q911g1 hepatitis c
197	7	1.4	137	12	Q911G0	Q911g0 hepatitis c
198	7	1.4	137	12	Q911F9	Q911f9 hepatitis c
199	7	1.4	137	12	Q911F8	Q911f8 hepatitis c
200	7	1.4	137	12	Q911F6	Q911f6 hepatitis c
201	7	1.4	137	12	Q911F5	Q911f5 hepatitis c
202	7	1.4	137	12	Q911F4	Q911f4 hepatitis c
203	7	1.4	137	12	Q911F3	Q911f3 hepatitis c
204	7	1.4	137	12	Q911F2	Q911f2 hepatitis c
205	7	1.4	137	12	Q911F1	Q911f1 hepatitis c
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207	7	1.4	137	12	Q911E9	Q911e9 hepatitis c
208	7	1.4	137	12	Q911E8	Q911e8 hepatitis c
209	7	1.4	137	12	Q911E7	Q911e7 hepatitis c
210	7	1.4	137	12	Q911E6	Q911e6 hepatitis c
211	7	1.4	137	12	Q911E5	Q911e5 hepatitis c
212	7	1.4	137	12	Q911E4	Q911e4 hepatitis c
213	7	1.4	141	16	Q9KCU3	Q9kcuc3 bacillus ha
214	7	1.4	149	5	Q9VAI6	Q9vaie6 drosophila
215	7	1.4	149	16	Q8X9W7	Q8x9w7 escherichia
216	7	1.4	150	16	Q8XKV6	Q8xkv6 clostridium
217	7	1.4	153	12	Q9DVZ4	Q9dvz4 pluteila xy
218	7	1.4	154	12	Q916J8	Q916j8 hepatitis c
219	7	1.4	154	12	Q916J7	Q916j7 hepatitis c
220	7	1.4	154	12	Q916J6	Q916j6 hepatitis c
221	7	1.4	154	12	Q916J5	Q916j5 hepatitis c
222	7	1.4	154	12	Q916J4	Q916j4 hepatitis c
223	7	1.4	154	12	Q916J3	Q916j3 hepatitis c
224	7	1.4	154	12	Q916J2	Q916j2 hepatitis c
225	7	1.4	154	12	Q916J1	Q916j1 hepatitis c
226	7	1.4	154	12	Q916J0	Q916j0 hepatitis c
227	7	1.4	154	12	Q916I9	Q916i9 hepatitis c
228	7	1.4	154	12	Q916I8	Q916i8 hepatitis c
229	7	1.4	154	12	Q916I7	Q916i7 hepatitis c
230	7	1.4	154	12	Q916I6	Q916i6 hepatitis c
231	7	1.4	154	12	Q916I5	Q916i5 hepatitis c
232	7	1.4	154	12	Q916I4	Q916i4 hepatitis c
233	7	1.4	154	12	Q916I3	Q916i3 hepatitis c
234	7	1.4	154	12	Q8QOF0	Q8qof0 hepatitis c
235	7	1.4	154	12	Q8QOE9	Q8qoe9 hepatitis c



236	7	1.4	154	12	Q8Q0E8	Q8qge8 hepatitis c	309	7	1.4	205	8	Q9G8Z9	Q9g8z9 ochromonas
237	7	1.4	154	12	Q8Q0E7	Q8qge7 hepatitis c	310	7	1.4	206	10	Q9LSK3	Q9lsk3 arabidopsis
238	7	1.4	160	16	Q98K01	Q98k01 rhizobium l	311	7	1.4	206	10	Q9LSK2	Q9lsk2 arabidopsis
239	7	1.4	161	16	Q9K088	Q9k088 neisseria m	312	7	1.4	206	16	Q8UE19	Q8ue19 agrobacteri
240	7	1.4	161	16	Q9JY98	Q9jv98 neisseria m	313	7	1.4	210	2	Q9XCJ9	Q9xcj9 streptococc
241	7	1.4	167	3	Q9C1S0	Q9cis0 candida gla	314	7	1.4	211	2	Q93V18	Q93vl8 salmonella
242	7	1.4	168	16	Q25912	Q25912 helicobacte	315	7	1.4	212	16	Q8X580	Q8x580 escherichia
243	7	1.4	168	16	Q9ZJM9	Q9zjm9 helicobacte	316	7	1.4	218	2	Q9XCK5	Q9xck5 streptococc
244	7	1.4	169	12	Q917P8	Q917p8 hepatitis c	317	7	1.4	219	10	Q9SUH9	Q9suh9 arabidopsis
245	7	1.4	170	16	Q927W0	Q927w0 listeria in	318	7	1.4	219	16	Q981K1	Q981k1 rhizobium l
246	7	1.4	170	16	Q8Y4B8	Q8y4b8 listeria mo	319	7	1.4	222	12	P89443	P89443 herpes simp
247	7	1.4	174	6	Q951E0	Q951e0 canis faml	320	7	1.4	222	12	Q65570	Q65570 bovine herp
248	7	1.4	175	13	Q98TU3	Q98tut3 brachydanio	321	7	1.4	223	16	Q9L218	Q9l218 streptomyce
249	7	1.4	180	16	P71704	P71704 mycobacteri	322	7	1.4	227	8	Q9XPE9	Q9xpe9 eumeces egr
250	7	1.4	182	16	Q9KZR9	Q9kzr9 streptomyce	323	7	1.4	227	16	Q9RRM2	Q9rrm2 deinococcus
251	7	1.4	185	16	Q25457	Q25457 helicobacte	324	7	1.4	227	16	Q981Y2	Q981y2 rhizobium l
252	7	1.4	186	12	Q91YZ2	Q9iyz2 hepatitis c	325	7	1.4	230	10	Q8SSJ3	Q8ssj3 oryza sativ
253	7	1.4	186	12	Q91YZ1	Q9iyz1 hepatitis c	326	7	1.4	235	2	Q9XCK9	Q9xcck9 streptococc
254	7	1.4	186	12	Q91YZ0	Q9iyz0 hepatitis c	327	7	1.4	235	16	Q9JRU0	Q9jru0 chlamydia p
255	7	1.4	186	12	Q91YY9	Q9iy9 hepatitis c	328	7	1.4	235	16	Q9Z742	Q9z742 chlamydia p
256	7	1.4	186	12	Q91YY8	Q9iy8 hepatitis c	329	7	1.4	240	11	Q9D1A3	Q9dl13 mus musculu
257	7	1.4	186	12	Q91YY7	Q9iy7 hepatitis c	330	7	1.4	241	16	Q9PLK3	Q9plk3 chlamydia m
258	7	1.4	186	12	Q91YY6	Q9iy6 hepatitis c	331	7	1.4	241	16	Q84728	Q84728 chlamydia t
259	7	1.4	186	12	Q91YY5	Q9iy5 hepatitis c	332	7	1.4	244	2	Q93KR0	Q93kr0 yersinia en
260	7	1.4	186	12	Q91YY4	Q9iy4 hepatitis c	333	7	1.4	244	16	Q8YJH0	Q8ymj4 pseudomonas
261	7	1.4	186	12	Q91YY3	Q9iy3 hepatitis c	334	7	1.4	249	2	Q8VMJ4	Q8vmj4 pseudomonas
262	7	1.4	186	12	Q91YY2	Q9iy2 hepatitis c	335	7	1.4	249	10	Q9AX28	Q9ax28 oryza sativ
263	7	1.4	186	12	Q91YY1	Q9iy1 hepatitis c	336	7	1.4	251	16	Q9KGI0	Q9kgi0 bacillus ha
264	7	1.4	186	12	Q91YY0	Q9iy0 hepatitis c	337	7	1.4	253	2	Q9L4V7	Q9l4v7 streptomyce
265	7	1.4	186	12	Q91YX9	Q9iyx9 hepatitis c	338	7	1.4	253	5	Q61709	Q61709 caenorhabdi
266	7	1.4	186	12	Q91YX8	Q9iyx8 hepatitis c	339	7	1.4	254	16	Q9A3X5	Q9a3x5 caulobacter
267	7	1.4	186	12	Q91YX7	Q9iyx7 hepatitis c	340	7	1.4	255	10	Q43406	Q43406 brassica ol
268	7	1.4	186	12	Q91YX6	Q9iyx6 hepatitis c	341	7	1.4	257	2	Q69217	Q69217 azotobacter
269	7	1.4	186	12	Q91YX5	Q9iyx5 hepatitis c	342	7	1.4	258	2	Q9X414	Q9x414 chlamydophi
270	7	1.4	186	12	Q91YL2	Q9iy12 hepatitis c	343	7	1.4	260	10	Q94AV8	Q94av8 arabidopsis
271	7	1.4	186	12	Q91YL1	Q9iy11 hepatitis c	344	7	1.4	264	2	Q9JRS5	Q9jrs5 actinobacil
272	7	1.4	186	12	Q91YL0	Q9iy10 hepatitis c	345	7	1.4	266	2	Q9ZFB0	Q9zfb0 rhodobacter
273	7	1.4	186	12	Q91YK9	Q9iyk9 hepatitis c	346	7	1.4	267	2	Q05382	Q05382 actinobacil
274	7	1.4	186	12	Q91YK8	Q9iyk8 hepatitis c	347	7	1.4	267	2	Q66261	Q66261 actinobacil
275	7	1.4	186	12	Q91YK6	Q9iyk6 hepatitis c	348	7	1.4	267	5	Q9VHH4	Q9vhh4 drosophila
276	7	1.4	186	12	Q91YK5	Q9iyk5 hepatitis c	349	7	1.4	267	16	Q9HWB2	Q9hwb2 pseudomonas
277	7	1.4	186	12	Q91YK4	Q9iyk4 hepatitis c	350	7	1.4	267	16	Q9CMM2	Q9cmw2 pasteurella
278	7	1.4	186	12	Q91YK3	Q9iyk3 hepatitis c	351	7	1.4	268	16	Q8XDY5	Q8xdy5 escherichia
279	7	1.4	186	12	Q91YK2	Q9iyk2 hepatitis c	352	7	1.4	269	2	Q9RFW5	Q9rfw5 mycoplasma
280	7	1.4	186	12	Q91YK1	Q9iyk1 hepatitis c	353	7	1.4	269	4	Q9UKP1	Q9ukp1 homo sapien
281	7	1.4	186	12	Q91YK0	Q9iyk0 hepatitis c	354	7	1.4	270	16	P71638	P71638 mycobacteri
282	7	1.4	186	12	Q91YJ9	Q9iyj9 hepatitis c	355	7	1.4	276	16	Q9ZBN3	Q9zbn3 streptomyce
283	7	1.4	186	12	Q91YJ8	Q9iyj8 hepatitis c	356	7	1.4	277	2	Q9F5Q9	Q9f5q9 vibrio chol
284	7	1.4	186	12	Q91YJ7	Q9iyj7 hepatitis c	357	7	1.4	278	2	Q9RHL8	Q9rhl8 actinobacil
285	7	1.4	186	12	Q91YJ6	Q9iyj6 hepatitis c	358	7	1.4	281	2	Q93Q45	Q93q45 clostridium
286	7	1.4	186	12	Q91YJ5	Q9iyj5 hepatitis c	359	7	1.4	289	11	Q8R296	Q8r296 mus musculu
287	7	1.4	186	12	Q91YJ4	Q9iyj4 hepatitis c	360	7	1.4	289	12	Q9QAI8	Q9qa18 murid herpe
288	7	1.4	186	12	Q91YJ3	Q9iyj3 hepatitis c	361	7	1.4	289	16	Q8Z8W9	Q8z8w9 salmonella
289	7	1.4	186	12	Q91YJ1	Q9iyj1 hepatitis c	362	7	1.4	289	16	Q9X6R1	Q9x6r1 pseudomonas
290	7	1.4	186	12	Q91YJ0	Q9iyj0 hepatitis c	363	7	1.4	289	17	Q8U2B8	Q8u2b8 pyrococcus
291	7	1.4	186	12	Q91YI9	Q9iyi9 hepatitis c	364	7	1.4	290	16	Q8YFE8	Q8yfe8 brucella me
292	7	1.4	186	12	Q91YI8	Q9iyi8 hepatitis c	365	7	1.4	291	16	Q9KMY5	Q9kmy5 vibrio chol
293	7	1.4	186	12	Q91YI7	Q9iyi7 hepatitis c	366	7	1.4	294	5	Q9VB61	Q9vb61 drosophila
294	7	1.4	186	12	Q91YI6	Q9iyi6 hepatitis c	367	7	1.4	295	16	Q9K3X0	Q9k3x0 streptomyce
295	7	1.4	186	12	Q91YI5	Q9iyi5 hepatitis c	368	7	1.4	298	5	Q9VOA8	Q9vga8 drosophila
296	7	1.4	186	16	Q92FG6	Q92fg6 listeria in	369	7	1.4	299	16	Q8UKB5	Q8ukb5 agrobacteri
297	7	1.4	187	8	Q03012	Q03012 molitugo ver	370	7	1.4	302	17	Q52882	Q52882 rhizobium m
298	7	1.4	189	2	Q9EW69	Q9ew69 streptococc	371	7	1.4	305	16	Q8Z2Z9	Q8z2z9 pyrobaculum
299	7	1.4	192	12	Q81414	Q81414 hepatitis c	372	7	1.4	306	16	Q8ZRU1	Q8zru1 salmonella
300	7	1.4	192	12	Q81432	Q81432 hepatitis c	373	7	1.4	306	16	Q8Z9G7	Q8z9g7 salmonella
301	7	1.4	192	12	Q81435	Q81435 hepatitis c	374	7	1.4	308	16	Q8X9Y6	Q8x9y6 escherichia
302	7	1.4	192	12	Q81397	Q81397 hepatitis c	375	7	1.4	308	2	Q9JPL4	Q9jpl4 neisseria m
303	7	1.4	192	16	Q8ZEG6	Q8zeg6 yersinia pe	376	7	1.4	312	11	Q9D7V4	Q9d7v4 mus musculu
304	7	1.4	195	4	Q96LW6	Q96lw6 homo sapien	377	7	1.4	313	5	Q9VMY0	Q9vmy0 drosophila
305	7	1.4	197	2	Q9WM61	Q9wm61 streptococc	378	7	1.4	314	2	Q9JPD2	Q9jpd2 rhodocyclu
306	7	1.4	200	16	Q9Z4W8	Q9z4w8 streptomyce	379	7	1.4	315	12	Q98UL4	Q98ul4 hepatitis c
307	7	1.4	203	16	Q8YQJ0	Q8yqj0 anabaena sp	380	7	1.4	315	12	Q98UL3	Q98ul3 hepatitis c
308	7	1.4	204	17	Q8TUA6	Q8tua6 methanosarc	381	7	1.4	316	16	Q9KMU0	Q9kmu0 vibrio chol

382	7	1.4	319	2	Q32485	032485 enterobacte	455	7	1.4	381	6	Q9GK11	Q9gk11 camelus dro
383	7	1.4	319	5	Q9N3J6	Q9n3j6 caenorhabdi	456	7	1.4	381	8	Q9ARJ0	Q9arj0 chimaera mo
384	7	1.4	319	5	Q8T0E8	Q8t0e8 drosophila	457	7	1.4	382	13	Q9PRG9	Q9prg9 gallus gall
385	7	1.4	319	16	Q9CMU4	Q9cmu4 pasteurella	458	7	1.4	383	5	Q9S503	Q9s503 drosophila
386	7	1.4	319	16	Q8YDM9	Q8ydm9 brucella me	459	7	1.4	383	13	Q9DEC3	Q9dec3 xenopus lae
387	7	1.4	320	2	Q9KHS4	Q9khs4 leptospira	460	7	1.4	384	13	Q91322	Q91322 rana catesb
388	7	1.4	320	2	Q9L586	Q9l586 leptospira	461	7	1.4	385	5	Q9BKP3	Q9bcp3 caenorhabdi
389	7	1.4	320	2	Q48546	Q48546 leptospira	462	7	1.4	386	6	Q9GMV6	Q9gmv6 canis faml
390	7	1.4	320	16	Q9JXR6	Q9jxr6 neisseria m	463	7	1.4	386	6	Q9GMV7	Q9gmv7 rhinolphus
391	7	1.4	320	16	Q9JW56	Q9jw56 neisseria m	464	7	1.4	386	6	Q9GMV6	Q9gmv6 canis faml
392	7	1.4	322	5	Q9N3J7	Q9n3j7 caenorhabdi	465	7	1.4	387	6	Q9TWT8	Q9tlw8 capra hircu
393	7	1.4	322	5	Q01945	Q01945 meloidogyne	466	7	1.4	387	6	Q9GMV9	Q9gmv9 suncus muri
394	7	1.4	323	16	Q989C6	Q989c6 rhizobium l	467	7	1.4	387	6	Q9GMV8	Q9gmv8 sores ungui
395	7	1.4	325	16	Q92TI8	Q92ti8 rhizobium m	468	7	1.4	387	6	Q46496	Q46496 bos taurus
396	7	1.4	326	16	Q54118	Q54118 streptomyc	469	7	1.4	388	6	Q46524	Q46524 felis silve
397	7	1.4	326	16	Q8Y0J4	Q8y0j4 ralstonia s	470	7	1.4	389	3	Q9Y775	Q9y775 candida tro
398	7	1.4	327	16	Q92WF7	Q92wf7 rhizobium m	471	7	1.4	389	6	Q9MYK3	Q9myk3 sus scrofa
399	7	1.4	328	16	Q9K1E3	Q9k1e3 neisseria m	472	7	1.4	389	6	Q9MYK2	Q9myk2 sus scrofa
400	7	1.4	328	16	Q9JX56	Q9jx56 neisseria m	473	7	1.4	390	6	Q9GK10	Q9gk10 camelus dro
401	7	1.4	330	11	Q8VCK6	Q8vck6 mus musculu	474	7	1.4	392	17	Q9UZ28	Q9uz28 pyrococcus
402	7	1.4	331	16	Q9RLI2	Q9rl12 deinococcus	475	7	1.4	394	16	Q9PED1	Q9ped1 xylella fas
403	7	1.4	331	16	Q9I561	Q9i561 pseudomonas	476	7	1.4	394	16	P72780	P72780 synechocyst
404	7	1.4	333	2	Q9XAT5	Q9xat5 rhizobium l	477	7	1.4	395	16	Q05773	Q05773 mycobacteri
405	7	1.4	333	16	Q8ZEG7	Q8zeg7 yersinia pe	478	7	1.4	396	13	Q93428	Q93428 chionodraco
406	7	1.4	335	5	Q965L5	Q965l5 caenorhabdi	479	7	1.4	398	13	Q93458	Q93458 deinococcus
407	7	1.4	335	16	Q9PIG0	Q9pi90 campylobact	480	7	1.4	407	17	Q9HJF2	Q9hjf2 thermoplas
408	7	1.4	336	10	Q74472	Q74472 schizosacch	481	7	1.4	411	2	P71136	P71136 chlamydomph
409	7	1.4	336	10	Q65453	Q65453 arabidopsis	482	7	1.4	411	2	Q06380	Q06380 chlamydia p
410	7	1.4	337	16	Q92VV7	Q92vv7 rhizobium m	483	7	1.4	413	3	Q14413	Q14413 pichia angu
411	7	1.4	338	12	Q65547	Q65547 bovine herp	484	7	1.4	413	16	Q8RG42	Q8rg42 fusobacteri
412	7	1.4	339	16	Q91IH2	Q91lh2 pseudomonas	485	7	1.4	416	16	Q987L1	Q987l1 rhizobium l
413	7	1.4	339	16	Q8XXA2	Q8xxa2 ralstonia s	486	7	1.4	416	16	Q8ZH85	Q8zh85 yersinia pe
414	7	1.4	340	16	Q98C73	Q98c73 rhizobium l	487	7	1.4	417	8	Q8WQ4	Q8wgq4 sphacelaria
415	7	1.4	341	2	Q9X4N4	Q9x4n4 bacteroides	488	7	1.4	419	10	Q94HMB	Q94hm8 oryza sativ
416	7	1.4	341	6	Q02728	Q02728 ovis aries	489	7	1.4	423	2	Q9EZF6	Q9ezf6 streptococc
417	7	1.4	341	6	Q19478	Q19478 mus musculu	490	7	1.4	423	2	Q9EZF6	Q9ezf6 streptococc
418	7	1.4	345	5	Q96439	Q96439 leishmania	491	7	1.4	430	16	Q8X147	Q8xi47 clostridium
419	7	1.4	345	16	Q9RRR0	Q9rrr0 deinococcus	492	7	1.4	434	16	Q9RT22	Q9rtl2 deinococcus
420	7	1.4	345	16	Q8Z359	Q8z359 salmonella	493	7	1.4	434	16	Q8ZIK4	Q8zik4 yersinia pe
421	7	1.4	345	16	Q8UKA3	Q8uka3 agrobacteri	494	7	1.4	436	16	Q9ALM0	Q9alm0 streptococc
422	7	1.4	346	6	Q02729	Q02729 ovis aries	495	7	1.4	436	16	Q97NK7	Q97nk7 streptococc
423	7	1.4	346	12	Q68543	Q68543 horseradish	496	7	1.4	437	2	Q9EZF7	Q9ezf7 streptococc
424	7	1.4	346	16	Q9KG26	Q9kg26 bacillus ha	497	7	1.4	438	10	Q8W347	Q8w347 oryza sativ
425	7	1.4	346	16	Q9CHK6	Q9chk6 lactococcus	498	7	1.4	441	17	Q8TW66	Q8tw66 methanopyru
426	7	1.4	347	16	Q8ZOK4	Q8zok4 anabaena sp	499	7	1.4	444	5	Q45891	Q45891 caenorhabdi
427	7	1.4	350	16	Q9PFI2	Q9pf12 xylella fas	500	7	1.4	446	2	Q05375	Q05375 actinobacil
428	7	1.4	353	2	P70901	P70901 borrelia he	501	7	1.4	448	8	Q9B8G5	Q9b8g5 heterodocus
429	7	1.4	353	8	Q80037	Q80037 citonia abd	502	7	1.4	449	17	Q8TWG3	Q8twg3 methanopyru
430	7	1.4	354	5	Q9GXY7	Q9gyx7 boophilus m	503	7	1.4	450	5	Q60989	Q60989 plasmodium
431	7	1.4	358	2	P70899	P70899 borrelia he	504	7	1.4	450	5	Q76965	Q76965 plasmodium
432	7	1.4	358	10	Q9FRW5	Q9frw5 nepenthes a	505	7	1.4	451	16	Q8RHG6	Q8rhg6 fusobacteri
433	7	1.4	360	2	P70905	P70905 borrelia he	506	7	1.4	452	10	Q9L173	Q9ll173 arabidopsis
434	7	1.4	361	16	Q92S90	Q92s90 rhizobium m	507	7	1.4	457	8	Q9SAL3	Q9sal3 cladostephu
435	7	1.4	366	2	P70900	P70900 borrelia he	508	7	1.4	457	8	Q8WQ00	Q8wgq0 sphacelaria
436	7	1.4	366	2	Q8SNU3	Q8snj3 raticus norv	509	7	1.4	457	8	Q8WGP7	Q8wgp7 sphacelaria
437	7	1.4	367	16	Q98JF1	Q98jfl rhizobium l	510	7	1.4	460	4	Q9H8M0	Q9h8m0 homo sapien
438	7	1.4	368	16	Q8UDD2	Q8udd2 agrobacteri	511	7	1.4	461	10	Q9FUL9	Q9ful9 zea mays (m
439	7	1.4	371	2	Q9EZH2	Q9ezh2 streptococc	512	7	1.4	465	4	Q96NU8	Q96nu8 homo sapien
440	7	1.4	371	4	Q16748	Q16748 homo sapien	513	7	1.4	465	5	Q9VEK5	Q9vek5 drosophila
441	7	1.4	371	4	Q16746	Q16746 homo sapien	514	7	1.4	468	17	Q28528	Q28528 archaeglob
442	7	1.4	372	16	Q8U748	Q8u748 agrobacteri	515	7	1.4	470	11	Q99LK8	Q99lk8 mus musculu
443	7	1.4	373	10	Q9SDJ0	Q9sd30 arabidopsis	516	7	1.4	473	4	Q96A99	Q96a99 homo sapien
444	7	1.4	373	10	P93031	P93031 arabidopsis	517	7	1.4	474	2	Q50185	Q50185 mycobacteri
445	7	1.4	374	6	Q9TTW0	Q9ttw0 bos taurus	518	7	1.4	475	10	Q9SD14	Q9sd14 arabidopsis
446	7	1.4	374	16	Q927X3	Q927x3 listeria in	519	7	1.4	477	5	Q9V395	Q9v395 drosophila
447	7	1.4	375	11	Q8R5C3	Q8r5c3 mus musculu	520	7	1.4	482	4	Q8TEC2	Q8tec2 homo sapien
448	7	1.4	378	13	Q9PUR9	Q9pur9 pseudopleur	521	7	1.4	484	2	Q9Z911	Q9z911 magnetospir
449	7	1.4	379	4	Q96MC1	Q96mcl homo sapien	522	7	1.4	484	17	Q26245	Q26245 methanobact
450	7	1.4	379	11	Q9UJX1	Q9ujxl raticus norv	523	7	1.4	486	10	Q9SL30	Q9sl30 arabidopsis
451	7	1.4	380	6	Q46492	Q46492 bos taurus	524	7	1.4	486	10	Q38934	Q38934 arabidopsis
452	7	1.4	380	6	Q9TTW5	Q9ttw5 capra hircu	525	7	1.4	486	13	Q8QGX2	Q8qgx2 brachydanio
453	7	1.4	380	6	Q9TTV4	Q9ttv4 bos taurus	526	7	1.4	488	2	Q9ZFS7	Q9zf57 neisseria m
454	7	1.4	380	6	Q02723	Q02723 ovis aries	527	7	1.4				

528	7	1.4	488	16	Q9K165	Q9K165 neisseria m
529	7	1.4	490	16	Q9J5R3	Q9J5R3 neisseria m
530	7	1.4	491	16	P71586	P71586 mycobacteri
531	7	1.4	491	16	Q8U9P9	Q8U9P9 agrobacteri
532	7	1.4	491	17	Q9HN17	Q9hn17 halobacteri
533	7	1.4	492	16	Q9CDE6	Q9cde6 mycobacteri
534	7	1.4	495	4	Q16741	Q16741 homo sapien
535	7	1.4	495	4	Q16742	Q16742 homo sapien
536	7	1.4	495	4	Q16749	Q16749 homo sapien
537	7	1.4	495	4	Q16874	Q16874 h cytochrom
538	7	1.4	496	16	Q9HXB9	Q9hxb9 pseudomonas
539	7	1.4	497	5	Q9GY92	Q9gy92 leishmania
540	7	1.4	501	16	Q8XX19	Q8xx19 ralstonia s
541	7	1.4	501	17	Q8THN4	Q8thn4 methanosarc
542	7	1.4	504	10	Q9XFX3	Q9xfx3 cynara card
543	7	1.4	504	16	Q53858	Q53858 mycobacteri
544	7	1.4	505	10	Q9FRW6	Q9frw6 nepenthes a
545	7	1.4	506	10	Q39311	Q39311 brassica na
546	7	1.4	506	10	Q40140	Q40140 lycopersico
547	7	1.4	506	10	Q65390	Q65390 arabidopsis
548	7	1.4	507	10	Q9FRW7	Q9frw7 nepenthes a
549	7	1.4	508	10	Q948P0	Q948p0 glycine max
550	7	1.4	508	10	Q9XEC4	Q9xec4 arabidopsis
551	7	1.4	509	10	Q9SSZ1	Q9ssz1 helianthus
552	7	1.4	510	16	Q99WR2	Q99wr2 staphylococ
553	7	1.4	512	10	Q04593	Q04593 arabidopsis
554	7	1.4	513	10	Q8VYL3	Q8vy13 arabidopsis
555	7	1.4	514	10	Q9FRW9	Q9frw9 nepenthes a
556	7	1.4	517	11	Q91XS7	Q91xs7 rattus norv
557	7	1.4	519	10	Q9SD16	Q9sdl6 arabidopsis
558	7	1.4	525	16	Q99ZJ0	Q99zj0 streptococc
559	7	1.4	526	2	Q93N65	Q93n65 coxiella bu
560	7	1.4	526	10	Q82783	Q82783 oryza sativ
561	7	1.4	527	10	Q9SU21	Q9su21 arabidopsis
562	7	1.4	527	16	Q9ZAH8	Q9zah8 staphylococ
563	7	1.4	528	16	Q8XRK4	Q8xrk4 ralstonia s
564	7	1.4	529	10	Q9FG87	Q9fg87 arabidopsis
565	7	1.4	529	10	Q94CA1	Q94cal arabidopsis
566	7	1.4	529	17	Q8U2T6	Q8u2t6 pyrococcus
567	7	1.4	532	2	P95760	P95760 streptococc
568	7	1.4	537	5	Q9V8K8	Q9v8k8 drosophila
569	7	1.4	537	6	Q9MZU5	Q9mzu5 sus scrofa
570	7	1.4	540	5	Q962J4	Q962j4 plasmodium.
571	7	1.4	541	4	Q8TBY2	Q8tby2 homo sapien
572	7	1.4	544	12	Q41936	Q41936 murid herpe
573	7	1.4	547	16	Q9A2T2	Q9a2t2 caulobacter
574	7	1.4	548	10	Q8RU81	Q8ru81 oryza sativ
575	7	1.4	551	2	Q68258	Q68258 escherichia
576	7	1.4	551	5	Q20673	Q20673 caenorhabdi
577	7	1.4	554	16	Q9PAC4	Q9pac4 xylella fas
578	7	1.4	555	5	O76789	O76789 caenorhabdi
579	7	1.4	555	10	Q9C7N0	Q9c7n0 arabidopsis
580	7	1.4	556	16	Q9KV74	Q9kv74 vibrio chol
581	7	1.4	559	10	Q9FKP2	Q9fkp2 arabidopsis
582	7	1.4	561	16	Q9CKX7	Q9ckx7 pasteurella
583	7	1.4	562	10	Q81837	Q81837 arabidopsis
584	7	1.4	565	10	Q8VYY5	Q8vyy5 arabidopsis
585	7	1.4	570	16	Q9HWG6	Q9hwg6 pseudomonas
586	7	1.4	581	16	Q8RI17	Q8ri17 fusobacteri
587	7	1.4	582	11	Q8VHU6	Q8vhu6 rattus norv
588	7	1.4	583	5	Q9BHA5	Q9bha5 plasmodium
589	7	1.4	583	5	Q9BHB3	Q9bhb3 plasmodium
590	7	1.4	583	16	Q8RCR3	Q8rcr3 thermoanaer
591	7	1.4	588	5	Q8WPJ7	Q8wpj7 leishmania
592	7	1.4	589	15	Q90LX2	Q90lx2 porcine end
593	7	1.4	600	2	Q9R613	Q9r613 rhodobacter
594	7	1.4	600	5	Q9U2N6	Q9u2n6 caenorhabdi
595	7	1.4	601	2	Q9R879	Q9r879 rhodobacter
596	7	1.4	601	2	Q53189	Q53189 rhodobacter
597	7	1.4	601	10	Q80960	Q80960 arabidopsis
598	7	1.4	604	6	Q8SFR3	Q8spr3 sus scrofa
599	7	1.4	609	2	O05334	O05334 rhodobacter
600	7	1.4	609	10	Q9AU9Y	Q9auy9 arabidopsis
601	7	1.4	601	8	Q951J2	Q951j2 phoxinus er
602	7	1.4	613	16	Q98C87	Q98c87 rhizobium l
603	7	1.4	615	13	Q42565	Q42565 xenopus lae
604	7	1.4	622	5	Q9VZE3	Q9vze3 drosophila
605	7	1.4	625	16	Q9HWN4	Q9hwn4 pseudomonas
606	7	1.4	626	16	Q9KQX9	Q9kqx9 vibrio chol
607	7	1.4	633	16	Q98LR9	Q98lr9 rhizobium l
608	7	1.4	638	6	O62705	O62705 sus scrofa
609	7	1.4	638	6	O62707	O62707 sus scrofa
610	7	1.4	638	15	Q90LX5	Q90lx5 porcine end
611	7	1.4	638	15	Q90LX4	Q90lx4 porcine end
612	7	1.4	638	17	Q59112	Q591x3 porcine end
613	7	1.4	639	16	Q9K4H5	Q9k4h5 streptomyce
614	7	1.4	641	15	Q8Q6Y9	Q8q6y9 porcine end
615	7	1.4	644	16	O69917	O69917 streptomyce
616	7	1.4	646	5	Q21689	Q21689 caenorhabdi
617	7	1.4	649	4	Q9HOT2	Q9hot2 homo sapien
618	7	1.4	649	15	Q8Q6Z1	Q8q6z1 porcine end
619	7	1.4	653	15	Q8Q6Z0	Q8q6z0 porcine end
620	7	1.4	659	12	Q66383	Q66383 dengue viru
621	7	1.4	659	15	Q9Q9X3	Q9q9x3 porcine end
622	7	1.4	659	15	Q8Q6Y8	Q8q6y8 porcine end
623	7	1.4	659	15	Q8Q6Y7	Q8q6y7 porcine end
624	7	1.4	659	15	Q8Q6Y6	Q8q6y6 porcine end
625	7	1.4	666	10	Q94GB7	Q94gb7 oryza sativ
626	7	1.4	674	4	Q9H917	Q9h917 homo sapien
627	7	1.4	677	5	Q9VBK7	Q9vbk7 drosophila
628	7	1.4	682	16	Q8ZJ57	Q8zj57 yersinia pe
629	7	1.4	689	8	Q37618	Q37618 prototheca
630	7	1.4	690	16	Q9KL86	Q9kl86 vibrio chol
631	7	1.4	690	16	Q8UAQ1	Q8uag1 agrobacteri
632	7	1.4	699	10	Q9ZU69	Q9zu69 arabidopsis
633	7	1.4	702	17	Q8ZU82	Q8zu82 pyrobaculum
634	7	1.4	707	16	Q9CD82	Q9cd82 mycobacteri
635	7	1.4	709	5	Q22548	Q22548 caenorhabdi
636	7	1.4	711	5	Q24205	Q24205 drosophila
637	7	1.4	712	16	Q92LS9	Q92ls9 rhizobium m
638	7	1.4	713	1	Q8X268	Q8x268 pyrococcus
639	7	1.4	717	2	Q9X478	Q9x478 enterococcu
640	7	1.4	721	16	Q9KS15	Q9ks15 vibrio chol
641	7	1.4	722	3	Q10668	Q10668 schizosacch
642	7	1.4	725	2	O68081	O68081 rhodobacter
643	7	1.4	732	10	Q94HA5	Q94ha5 oryza sativ
644	7	1.4	741	2	Q9XAU3	Q9xau3 pseudomonas
645	7	1.4	748	6	P79370	P79370 cryctolagus
646	7	1.4	758	11	Q99J52	Q99j52 mus musculu
647	7	1.4	770	4	Q8TET3	Q8tet3 homo sapien
648	7	1.4	779	10	Q8W0Q5	Q8w0q5 sorghum bic
649	7	1.4	784	16	Q8YAJ5	Q8ya'j5 listeria mo
650	7	1.4	788	16	Q9PFA1	Q9pfai xylella fas
651	7	1.4	797	4	Q9BYB0	Q9byb0 homo sapien
652	7	1.4	802	10	Q38802	Q38802 arabidopsis
653	7	1.4	813	12	Q9LDT8	Q9ldt8 oryza sativ
654	7	1.4	813	12	Q91IN8	Q91in8 hepatitis b
655	7	1.4	830	17	Q27158	Q27158 methanobact
656	7	1.4	832	10	Q9SA75	Q9sa75 arabidopsis
657	7	1.4	843	12	Q91524	Q91524 hepatitis b
658	7	1.4	843	12	Q91IP1	Q91ip1 hepatitis b
659	7	1.4	854	5	Q9NDZ8	Q9ndz8 leishmania
660	7	1.4	873	2	Q9S4K0	Q9s4k0 streptococc
661	7	1.4	880	16	Q9A1M8	Q9aim8 streptococc
662	7	1.4	881	16	Q91537	Q91537 pseudomonas
663	7	1.4	882	11	Q9R0S1	Q9r0s1 mus musculu
664	7	1.4	887	5	Q19428	Q19428 caenorhabdi
665	7	1.4	893	10	Q8S615	Q8s615 oryza sativ
666	7	1.4	902	5	Q9VSA5	Q9vsas drosophila
667	7	1.4	907	16	Q9L248	Q9l248 streptomyce
668	7	1.4	911	16	Q9RNU9	Q9rnus streptomyce
669	7	1.4	912	16	Q9K3Y2	Q9k3y2 streptomyce
670	7	1.4	923	2	Q9S3T2	Q9s3t2 streptococc
671	7	1.4	931	12	Q9QAP6	Q9qap6 rangiferine
672	7	1.4	933	16	Q8XE39	Q8xe39 escherichia

674	7	1.4	934	11	Q924X9	Q924x9 mus musculu	747	6	1.2	24	9	Q9T0Q7	Q9t0q7 bacterioph
675	7	1.4	939	16	Q8YQR3	Q8yqr3 anabaena sp	748	6	1.2	25	12	Q9WMG7	Q9wmq7 sigma virus
676	7	1.4	952	16	Q988M2	Q988m2 rhizobium l	749	6	1.2	28	11	Q925E3	Q925e3 phodopus su
677	7	1.4	964	16	Q8YFR7	Q8yfr7 brucella me	750	6	1.2	30	7	Q31234	Q31234 mus musculu
678	7	1.4	967	2	Q54123	Q54123 staphylococ	751	6	1.2	31	2	Q32325	Q32325 clostridium
679	7	1.4	968	2	Q9F848	Q9f848 streptomyce	752	6	1.2	33	4	Q16148	Q16148 homo sapien
680	7	1.4	970	16	Q92KJ8	Q92kj8 rhizobium m	753	6	1.2	33	8	Q95A09	Q95a09 synaphobran
681	7	1.4	971	16	Q8UH99	Q8uh99 agrobacteri	754	6	1.2	35	4	Q9UHK5	Q9uhk5 homo sapien
682	7	1.4	991	4	Q15043	Q15043 homo sapien	755	6	1.2	39	5	Q16984	Q16984 acheta dome
683	7	1.4	993	5	Q9VXM6	Q9vxm6 drosophila	756	6	1.2	40	10	Q9SSK6	Q9sek6 arabisdopsis
684	7	1.4	994	11	Q9QVY4	Q9qvy4 mus sp. neu	757	6	1.2	40	16	Q8VJ52	Q8vj52 mycobacteri
685	7	1.4	1015	2	Q93T50	Q93t50 streptococc	758	6	1.2	44	4	Q13013	Q13013 homo sapien
686	7	1.4	1015	4	Q14572	Q14572 homo sapien	759	6	1.2	45	4	Q12847	Q12847 homo sapien
687	7	1.4	1026	5	Q8SY90	Q8sy90 drosophila	760	6	1.2	45	4	Q8TD77	Q8td77 homo sapien
688	7	1.4	1027	2	Q93T51	Q93t51 streptococc	761	6	1.2	45	6	Q9GK71	Q9gk71 bos taurus
689	7	1.4	1039	16	Q9KEQ8	Q9keq8 bacillus ha	762	6	1.2	46	4	Q96J56	Q96js6 homo sapien
690	7	1.4	1042	4	Q9H4G6	Q9h4g6 homo sapien	763	6	1.2	46	11	Q9R1N8	Q9rln8 mus musculu
691	7	1.4	1062	4	Q9NSW2	Q9nsw2 homo sapien	764	6	1.2	46	11	Q9WVP4	Q9wvp4 mus spretus
692	7	1.4	1082	11	Q8VIT75	Q8vi75 mus musculu	765	6	1.2	46	11	Q9WTK9	Q9wtk9 mus musculu
693	7	1.4	1130	4	Q9H1V5	Q9h1v5 homo sapien	766	6	1.2	47	12	Q91FM8	Q91fm8 chilo iride
694	7	1.4	1131	16	Q8YT43	Q8yt43 anabaena sp	767	6	1.2	49	2	Q9EVP1	Q9evp1 escherichia
695	7	1.4	1133	17	Q96XX7	Q96xx7 sulfolobus	768	6	1.2	49	13	Q42578	Q42578 xenopus lae
696	7	1.4	1142	16	Q97J24	Q97j24 clostridium	769	6	1.2	52	16	Q9A041	Q9a041 streptococc
697	7	1.4	1153	5	Q9U2G5	Q9u2g5 caenorhabdi	770	6	1.2	54	4	Q13807	Q13807 homo sapien
698	7	1.4	1163	16	Q92P24	Q92p24 rhizobium m	771	6	1.2	56	2	P97248	P97248 escherichia
699	7	1.4	1166	11	Q9QVN4	Q9qvn4 rattus sp.	772	6	1.2	56	5	Q9UAC6	Q9uac6 mesobuthus
700	7	1.4	1172	16	Q9ZBY5	Q9zbys streptomyc	773	6	1.2	57	9	Q8SDV2	Q8sdv2 bacterioph
701	7	1.4	1177	16	Q8Y054	Q8y054 ralstonia s	774	6	1.2	58	4	Q969L1	Q969l1 homo sapien
702	7	1.4	1194	16	O53645	O53645 mycobacteri	775	6	1.2	59	3	Q9U067	Q9u067 schizosacch
703	7	1.4	1215	11	P97686	P97686 rattus norv	776	6	1.2	59	6	Q28715	Q28715 oryctolagus
704	7	1.4	1235	4	Q9UL54	Q9ul54 homo sapien	777	6	1.2	59	16	Q9L720	Q9l720 caulobacter
705	7	1.4	1235	11	Q9JLS3	Q9jls3 rattus norv	778	6	1.2	60	3	Q12711	Q12711 trichoderma
706	7	1.4	1236	2	Q9JPA4	Q9jpa4 rhodocyclus	779	6	1.2	60	9	Q38487	Q38487 bacterioph
707	7	1.4	1241	16	O8VKP9	O8vkp9 mycobacteri	780	6	1.2	61	2	O52860	O52860 bacillus su
708	7	1.4	1253	10	Q9SA04	Q9sa04 arabisdopsis	781	6	1.2	62	5	P82170	P82170 locusta mig
709	7	1.4	1269	5	O43993	O43993 dictyosteli	782	6	1.2	63	5	Q9BPF4	Q9bpf4 conus penna
710	7	1.4	1324	10	Q94GQ7	Q94gq7 oryza sativ	783	6	1.2	64	2	Q44855	Q44855 borrelia bu
711	7	1.4	1330	6	O97961	O97961 vulpes vulp	784	6	1.2	64	8	Q36146	Q36146 thamnophis
712	7	1.4	1379	5	Q9VNG9	Q9vng9 drosophila	785	6	1.2	65	16	Q9K2D5	Q9k2d5 chlamydia p
713	7	1.4	1379	5	Q9TY11	Q9tyl1 drosophila	786	6	1.2	67	4	Q9P1B8	Q9p1b8 homo sapien
714	7	1.4	1411	2	Q9AJ93	Q9aj93 actinomyc	787	6	1.2	67	5	Q9VPA4	Q9vpa4 drosophila
715	7	1.4	1429	4	Q9YST6	Q9yst6 homo sapien	788	6	1.2	67	16	Q92EM1	Q92em1 listeria in
716	7	1.4	1433	11	O07563	O07563 mus musculu	789	6	1.2	67	16	Q927S6	Q927s6 listeria in
717	7	1.4	1437	5	Q9QG51	Q9qg51 dictyosteli	790	6	1.2	67	16	Q8Y9V4	O8y9v4 listeria mo
718	7	1.4	1513	16	P66901	P66901 mycobacteri	791	6	1.2	68	10	Q8RYJ4	Q8ryj4 oryza sativ
719	7	1.4	1628	4	Q9P2F2	Q9p2f2 homo sapien	792	6	1.2	68	16	Q9CGB6	Q9cgb6 lactococcus
720	7	1.4	1630	16	Q8RHH7	Q8rhh7 fusobacteri	793	6	1.2	69	10	Q9AUF7	Q9auf7 brassica na
721	7	1.4	1690	16	O86821	O86821 streptomyc	794	6	1.2	69	12	Q9WIT0	Q9wi10 canarypox v
722	7	1.4	1740	2	Q9KMY8	Q9kwy8 streptomyc	795	6	1.2	69	16	Q91723	Q91723 pseudomonas
723	7	1.4	1829	5	O8T2N7	O8t2n7 dictyosteli	796	6	1.2	70	10	Q9AUF6	Q9auf6 brassica na
724	7	1.4	1886	5	Q9NKU5	Q9nkus leishmania	797	6	1.2	70	10	Q9AUF5	Q9auf5 brassica ol
725	7	1.4	1937	2	O8RJY2	O8rjy2 stigmateila	798	6	1.2	70	10	Q9AUF4	Q9auf4 brassica ca
726	7	1.4	2014	5	Q22774	Q22774 caenorhabdi	799	6	1.2	71	2	Q9FCW3	Q9fcw3 escherichia
727	7	1.4	2025	10	Q9SHK4	Q9shk4 arabisdopsis	800	6	1.2	71	10	P93234	P93234 lycopersico
728	7	1.4	2042	5	Q9W1C5	Q9wic5 drosophila	801	6	1.2	71	12	Q8QUQ7	Q8quq7 infectious
729	7	1.4	2479	11	O63002	O63002 rattus norv	802	6	1.2	71	17	O8TZV7	O8tzv7 pyrococcus
730	7	1.4	2554	5	Q9NKT1	Q9nkt1 leishmania	803	6	1.2	72	10	O65618	O65618 arabisdopsis
731	7	1.4	2813	4	Q96JPE	Q96jp6 homo sapien	804	6	1.2	72	12	Q8VB96	Q8vb96 white spot
732	7	1.4	2813	4	O8WXQ6	O8wxq6 homo sapien	805	6	1.2	73	4	Q93067	Q93067 homo sapien
733	7	1.4	2817	4	Q96P79	Q96p79 homo sapien	806	6	1.2	73	8	Q9XOR3	Q9xqr3 pisum sativ
734	7	1.4	2862	16	O8R874	O8r874 thermoaer	807	6	1.2	73	8	Q35148	Q35148 nerodia ery
735	7	1.4	2894	17	Q58791	Q58791 methanococc	808	6	1.2	73	16	Q9A2N3	Q9a2n3 caulobacter
736	7	1.4	3010	12	O81760	O81760 hepaticitis c	809	6	1.2	74	16	Q8Y2X8	Q8y2x8 ralstonia s
737	7	1.4	3897	12	O09461	O09461 border dise	810	6	1.2	75	2	Q9EYZ7	Q9eyz7 photobacter
738	7	1.4	4340	2	O30764	O30764 streptomyc	811	6	1.2	75	2	P94765	P94765 erwania chr
739	7	1.4	4450	5	Q9UBZ8	Q9ubz8 caenorhabdi	812	6	1.2	75	16	O8XTM9	O8xtm9 ralstonia s
740	7	1.4	4706	10	Q9FN44	Q9fn44 arabisdopsis	813	6	1.2	76	8	O48083	O48083 eryx tatari
741	7	1.4	5953	16	O8XS39	O8xs39 ralstonia s	814	6	1.2	77	8	O99364	O99364 elaphe rufo
742	7	1.4	8243	5	O96554	O96554 cryptospori	815	6	1.2	77	8	Q9ZXV7	Q9zxv7 elaphe rufo
743	6	1.2	15	3	Q9UR72	Q9ur72 trichoderma	816	6	1.2	77	10	O9XIX4	O9xix4 oryza sativ
744	6	1.2	19	6	Q9BDX2	Q9bdx2 macaca mula	817	6	1.2	78	8	Q36087	Q36087 thamnophis
745	6	1.2	19	10	Q9S956	Q9s956 zea mays (m	818	6	1.2	78	8	Q36143	Q36143 thamnophis
746	6	1.2	22	11	Q9QWB6	Q9qwb6 mus sp. sgp	819	6	1.2	79	6	Q29452	Q29452 bos taurus

820	6	1.2	79	16	025333	025333 helicobacte	893	6	1.2	94	8	Q36145	Q36145 thamnophis
821	6	1.2	80	2	070028	070028 streptomyce	894	6	1.2	94	8	Q36094	Q36094 thamnophis
822	6	1.2	80	2	Q9R6M8	Q9r6m8 agrobacteri	895	6	1.2	94	16	Q9CJR0	Q9cjr0 pasteurella
823	6	1.2	80	8	Q99365	Q99365 elaphe bima	896	6	1.2	95	2	Q49154	Q49154 methylobact
824	6	1.2	80	10	Q49028	Q49028 gracilaria	897	6	1.2	95	8	Q36000	Q36000 thamnophis
825	6	1.2	81	8	Q99362	Q99362 elaphe taen	898	6	1.2	95	8	Q35147	Q35147 nerodia ery
826	6	1.2	81	8	Q99370	Q99370 dinodon ruf	899	6	1.2	95	10	Q9FTU0	Q9ftu0 oryza sativ
827	6	1.2	81	8	Q99371	Q99371 dinodon ruf	900	6	1.2	95	15	Q9INC6	Q9inc6 human immun
828	6	1.2	81	8	Q99372	Q99372 zaocys dhum	901	6	1.2	96	8	Q36001	Q36001 thamnophis
829	6	1.2	81	8	Q99373	Q99373 zaocys dhum	902	6	1.2	96	11	Q8R401	Q8r401 rattus norv
830	6	1.2	81	8	Q99374	Q99374 ptyas korro	903	6	1.2	96	12	Q8QP44	Q8qp44 dengue viru
831	6	1.2	81	8	Q99375	Q99375 ptyas korro	904	6	1.2	96	15	Q38190	Q38190 human immun
832	6	1.2	81	8	Q36138	Q36138 thamnophis	905	6	1.2	97	8	Q36051	Q36051 thamnophis
833	6	1.2	81	8	Q9ZXM5	Q9zxm5 zaocys dhum	906	6	1.2	97	8	Q36019	Q36019 thamnophis
834	6	1.2	81	8	Q9ZXR1	Q9zxr1 elaphe taen	907	6	1.2	97	8	Q36021	Q36021 thamnophis
835	6	1.2	81	12	055445	055445 sindbis vir	908	6	1.2	97	8	Q36029	Q36029 thamnophis
836	6	1.2	81	12	055447	055447 sindbis vir	909	6	1.2	97	8	Q35983	Q35983 thamnophis
837	6	1.2	81	12	055448	055448 sindbis vir	910	6	1.2	97	15	Q9YY65	Q9yy65 human immun
838	6	1.2	81	12	Q9W8F2	Q9w8f2 sindbis vir	911	6	1.2	98	5	Q8SYX2	Q8syx2 drosophila
839	6	1.2	81	16	Q9PA00	Q9pa00 xylella fas	912	6	1.2	98	8	Q36077	Q36077 thamnophis
840	6	1.2	81	16	Q9R1W6	Q9riw6 streptomyce	913	6	1.2	98	8	Q35982	Q35982 thamnophis
841	6	1.2	82	4	Q9Y5U9	Q9y5u9 homo sapien	914	6	1.2	98	8	Q21564	Q21564 sigmodon oc
842	6	1.2	82	5	Q8T2S0	Q8t2s0 dictyosteli	915	6	1.2	98	8	Q36028	Q36028 thamnophis
843	6	1.2	82	11	Q9CR20	Q9cr20 mus musculu	916	6	1.2	98	9	Q80282	Q80282 xanthomonas
844	6	1.2	82	12	055446	055446 sindbis vir	917	6	1.2	99	8	Q36124	Q36124 thamnophis
845	6	1.2	83	4	Q9H3B2	Q9h3b2 homo sapien	918	6	1.2	99	8	Q9G435	Q9g435 thamnophis
846	6	1.2	84	4	Q36106	Q36106 thamnophis	919	6	1.2	99	8	Q36024	Q36024 thamnophis
847	6	1.2	84	12	Q8VB94	Q8vb94 white spot	920	6	1.2	99	12	P88822	P88822 saimirine
848	6	1.2	84	16	Q92S15	Q92s15 rhizobium m	921	6	1.2	99	12	Q73557	Q73557 lassa virus
849	6	1.2	85	4	Q8TE25	Q8tez5 homo sapien	922	6	1.2	99	15	Q71241	Q71241 human immun
850	6	1.2	85	5	Q9W5T0	Q9w5t0 drosophila	923	6	1.2	99	15	Q71241	Q92y38 rhizobium m
851	6	1.2	85	8	Q48086	Q48086 eryx tatari	924	6	1.2	99	16	Q92Y38	Q8yyu5 anabaena sp
852	6	1.2	85	15	Q909R4	Q909r4 human immun	925	6	1.2	99	16	Q8YYN5	Q8yep8 natrix natr
853	6	1.2	85	17	Q9HJF0	Q9hjf0 chermoplasm	926	6	1.2	100	8	Q9TEP7	Q9tep7 elaphe long
854	6	1.2	88	2	085938	085938 sphingomona	927	6	1.2	100	8	Q36144	Q36144 thamnophis
855	6	1.2	88	8	Q36141	Q36141 thamnophis	928	6	1.2	100	8	Q36025	Q36025 thamnophis
856	6	1.2	88	10	Q8RWS1	Q8rws1 arabadopsis	929	6	1.2	100	8	Q36027	Q36027 thamnophis
857	6	1.2	88	16	Q25107	Q25107 helicobacte	930	6	1.2	100	8	Q36003	Q36003 thamnophis
858	6	1.2	88	16	Q92K13	Q92k13 rhizobium m	931	6	1.2	100	8	Q35150	Q35150 nerodia fas
859	6	1.2	88	16	Q9F2U8	Q9f2u8 streptomyce	932	6	1.2	100	10	Q23329	Q23329 arabadopsis
860	6	1.2	89	8	Q36122	Q36122 thamnophis	933	6	1.2	100	12	Q91FS4	Q91fs4 chilo iride
861	6	1.2	89	8	Q95888	Q95888 peromyscus	934	6	1.2	100	13	Q90393	Q90393 cyprinodon
862	6	1.2	89	10	Q9AR36	Q9ar36 oryza sativ	935	6	1.2	100	16	Q92Y12	Q92y12 rhizobium m
863	6	1.2	89	11	Q9WUG8	Q9wug8 mus musculu	936	6	1.2	101	2	Q46552	Q46552 bacteroides
864	6	1.2	89	16	Q9CHR8	Q9chr8 lactococcus	937	6	1.2	101	3	Q96U48	Q96u48 neurospora
865	6	1.2	89	16	Q92SB3	Q92sb3 rhizobium m	938	6	1.2	101	8	Q36083	Q36083 thamnophis
866	6	1.2	90	4	Q9UQV8	Q9uqv8 homo sapien	939	6	1.2	101	8	Q952Q4	Q952q4 euphorbia p
867	6	1.2	90	8	Q36745	Q36745 epicrantes s	940	6	1.2	101	10	Q8S2M7	Q8s2m7 oryza sativ
868	6	1.2	90	8	Q8WEQ7	Q8weq7 sanzinia ma	941	6	1.2	101	12	Q84519	Q84519 paramecium
869	6	1.2	90	8	Q8WEQ6	Q8weg6 boa constri	942	6	1.2	101	16	Q9HVC1	Q9hvc1 pseudomonas
870	6	1.2	90	8	Q8WEQ5	Q8weg5 candoia bib	943	6	1.2	101	16	Q8YDB6	Q8ydb6 brucella me
871	6	1.2	90	8	Q8WEQ4	Q8weg4 candoia bib	944	6	1.2	101	17	Q9Y9N7	Q9y9n7 aeropyrum p
872	6	1.2	90	8	Q8WEQ3	Q8weg4 candoia car	945	6	1.2	102	8	Q9G1Z1	Q9g1z1 thamnophis
873	6	1.2	90	8	Q8WEQ2	Q8weg2 candoia car	946	6	1.2	102	8	Q9G1W2	Q9g1w2 thamnophis
874	6	1.2	90	8	Q8WEQ1	Q8weg1 candoia car	947	6	1.2	102	8	Q9G1V3	Q9g1v3 thamnophis
875	6	1.2	90	8	Q8W7U6	Q8w7u6 candoia bib	948	6	1.2	102	8	Q9G1T7	Q9g1t7 thamnophis
876	6	1.2	90	8	Q8W7N8	Q8w7n8 candoia asp	949	6	1.2	102	8	Q36078	Q36078 thamnophis
877	6	1.2	90	8	Q8W7N7	Q8w7n7 candoia asp	950	6	1.2	102	8	Q36022	Q36022 thamnophis
878	6	1.2	90	8	Q8W7N6	Q8w7n6 candoia asp	951	6	1.2	102	8	Q36023	Q36023 thamnophis
879	6	1.2	90	12	Q99CY8	Q99cy8 bovine herp	952	6	1.2	102	8	Q9B8P0	Q9b8p0 philodryas
880	6	1.2	90	13	Q91063	Q91063 jordanelia	953	6	1.2	102	8	Q9B8N9	Q9b8n9 philodryas
881	6	1.2	90	13	Q90XJ1	Q90xj1 acipenser s	954	6	1.2	102	8	Q9B8N8	Q9b8n8 philodryas
882	6	1.2	90	13	Q90XI5	Q90xi5 amia calva	955	6	1.2	102	8	Q9B8N7	Q9b8n7 philodryas
883	6	1.2	90	16	P71926	P71926 mycobacteri	956	6	1.2	102	8	Q9B8N6	Q9b8n6 philodryas
884	6	1.2	90	16	Q9K3G8	Q9k3g8 streptomyce	957	6	1.2	102	8	Q9B8N3	Q9b8n3 tropidodrya
885	6	1.2	90	17	Q8U1Q7	Q8u1q7 pyrococcus	958	6	1.2	102	8	Q9B8N1	Q9b8n1 oxyrhopus g
886	6	1.2	91	12	Q9PYT8	Q9pyt8 xestia c-ni	959	6	1.2	102	8	Q9G436	Q9g436 thamnophis
887	6	1.2	92	2	Q52631	Q52631 escherichia	960	6	1.2	102	8	Q9G434	Q9g434 thamnophis
888	6	1.2	92	2	Q52632	Q52632 escherichia	961	6	1.2	102	8	Q9G432	Q9g432 thamnophis
889	6	1.2	92	8	Q36123	Q36123 thamnophis	962	6	1.2	102	12	P88824	P88824 saimirine
890	6	1.2	92	16	Q8YBA0	Q8yba0 brucella me	963	6	1.2	102	16	Q8X798	Q8x798 escherichia
891	6	1.2	93	13	Q91251	Q91251 profundulus	964	6	1.2	102	16	Q8YJN7	Q8yjn7 brucella me
892	6	1.2	93	17	Q8TW6	Q8twe6 methanopyru	965	6	1.2	103	8	Q9TB05	Q9tb05 azemlops fe

966	6	1.2	103	8	Q9TB04	Q9tb04 agkistrodon
967	6	1.2	103	8	Q9TB03	Q9tb03 agkistrodon
968	6	1.2	103	8	Q9TB02	Q9tb02 gloydius br
969	6	1.2	103	8	Q9TB01	Q9tb01 agkistrodon
970	6	1.2	103	8	Q9TB00	Q9tb00 gloydius st
971	6	1.2	103	8	Q9TAZ9	Q9ta29 gloydius sa
972	6	1.2	103	8	Q9TAZ8	Q9ta28 gloydius sh
973	6	1.2	103	8	Q9TAZ7	Q9ta27 gloydius st
974	6	1.2	103	8	Q9TAZ6	Q9ta26 agkistrodon
975	6	1.2	103	8	Q9TAZ5	Q9ta25 ovophis mon
976	6	1.2	103	8	Q9TAZ4	Q9ta24 trimeresuru
977	6	1.2	103	8	Q9TAZ3	Q9ta23 trimeresuru
978	6	1.2	103	10	Q8S737	Q8s737 oryza sativ
979	6	1.2	103	11	Q9CUI3	Q9cul3 mus musculu
980	6	1.2	103	13	Q90224	Q90224 aplocheilic
981	6	1.2	103	13	Q90312	Q90312 crenichthys
982	6	1.2	103	13	Q91991	Q91991 zoogoneticu
983	6	1.2	103	16	Q9RX39	Q9rx39 deinococcus
984	6	1.2	103	16	Q98P21	Q98p21 rhizobium 1
985	6	1.2	103	16	Q84895	Q84895 salmonella
986	6	1.2	104	6	Q29169	Q29169 sus scrofa
987	6	1.2	104	13	Q90242	Q90242 aplocheilic
988	6	1.2	104	13	Q91536	Q91536 xenotoca ei
989	6	1.2	104	17	Q9UZM9	Q9uzm9 pyrococcus
990	6	1.2	105	3	Q9P8L3	Q9p8l3 botrytis ci
991	6	1.2	105	4	Q9P1P1	Q9p1p1 homo sapien
992	6	1.2	105	10	Q943N0	Q943n0 oryza sativ
993	6	1.2	105	16	Q99S11	Q99s11 staphylococ
994	6	1.2	105	16	Q8YH98	Q8yh98 brucella me
995	6	1.2	106	8	Q9B1R1	Q9b1r1 croctalus ho
996	6	1.2	106	8	Q9B4Z6	Q9b4z6 croctalus ho
997	6	1.2	106	8	Q21102	Q21102 homo sapien
998	6	1.2	106	12	Q9YK02	Q9yk02 dengue viru
999	6	1.2	107	2	Q05626	Q05626 streptomyce
1000	6	1.2	107	2	Q9XAT7	Q9xat7 rhodococcus

ALIGNMENTS

RESULT 1
Q9H2V8 PRELIMINARY; PRT; 439 AA.
AC Q9H2V8; 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CDAL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PHROCHROMOCYTOMA;
RA Li Y., Huang Q., Peng, Y, Song H., Yu Y., Xu S., Ren S., Chen Z.,
RA Han Z.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF21252; AAG41783.1; -.
DR HSSP; P00797; 2REN.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 439 AA; 48275 MW; 02EC0E0E50F11602 CRC64;

Query Match 84.7%; Score 439; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 MVDNLQDSDGRGYLLEMLIGTPPKQLILVDTGSSNFAVAGTPHSHYIDTYFDTERSTYR 139
|||||

Db	1	MVDNLQDSDGRGYLLEMLIGTPPKQLILVDTGSSNFAVAGTPHSHYIDTYFDTERSTYR	60
QY	140	SKGFDVTVKYTTQSGSWTGFVGEDLVITPKGFNTSFLVNIATIFESSENFPLGKWNGLGL	199
Db	61	SKGFDVTVKYTTQSGSWTGFVGEDLVITPKGFNTSFLVNIATIFESSENFPLGKWNGLGL	120
QY	200	AYATLAKPSSSLETFRDSLVTQANIPNVFSMQCGAGLPVAGSGTNGSLVLGIEPSLY	259
Db	121	AYATLAKPSSSLETFRDSLVTQANIPNVFSMQCGAGLPVAGSGTNGSLVLGIEPSLY	180
QY	260	KGDIWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKAIVDSGTTLLRLPKVFDV	319
Db	181	KGDIWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKAIVDSGTTLLRLPKVFDV	240
QY	320	VEAVARASLIPFSDGFWTGSQLACWTNSETPWSYFPKISYLRDENSRSFRITILPOL	379
Db	241	VEAVARASLIPFSDGFWTGSQLACWTNSETPWSYFPKISYLRDENSRSFRITILPOL	300
QY	380	YIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYVIFDRAQKRVGFASPCAEITAGA	439
Db	301	YIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYVIFDRAQKRVGFASPCAEITAGA	360
QY	440	AVSEISGPFSTEDVASNCPAQSLSEPIIIVSYALMSVCGAIIIVLIVLLLPFCQR	499
Db	361	AVSEISGPFSTEDVASNCPAQSLSEPIIIVSYALMSVCGAIIIVLIVLLLPFCQR	420
QY	500	PRDPEVNDSSLVHRWK 518	
Db	421	PRDPEVNDSSLVHRWK 439	

RESULT 2
Q9NZL1 PRELIMINARY; PRT; 396 AA.
AC Q9NZL1; 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; Pubmed=10965118;
RA Solans A., Estivill X., de la Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL CytoGenet. Cell Genet. 89:177-184(2000).
DR EMBL; AF188277; AAF35836.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW protease.
SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match 73.0%; Score 378; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARAALLPLLAQWLRAPELAPAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
Db 1 MGALARAALLPLLAQWLRAPELAPAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAWDNLQDSDGRGYLLEMLIGTPPKQLILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAWDNLQDSDGRGYLLEMLIGTPPKQLILVDTGSSNFAVAG 120

QY 121 TPHSYIDTYFDTERSSTYRSKGFVDVTVKYTGSGWTFVGEDLVTI PKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSTYRSKGFVDVTVKYTGSGWTFVGEDLVTI PKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKMNGILGLAVATLAKPSSSLETFFPDSLVTQANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFLLPGIKMNGILGLAVATLAKPSSSLETFFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIIEILKLEIGGQSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPQ 378
DB 361 YLRDENSRSFRITILPQ 378

RESULT 3

Q9NZL2 PRELIMINARY; PRT; 468 AA.
AC Q9NZL2; 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de la Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL Cyogenet. Cell Genet. 89:177-184(2000).
DR EMBL; AF188276; AAF35835.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

Query Match 63.3%; Score 328; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 6.6e-318;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAABELAPAPFTLPLRVAATNRVAVPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLRAABELAPAPFTLPLRVAATNRVAVPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFVDVTVKYTGSGWTFVGEDLVTI PKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSTYRSKGFVDVTVKYTGSGWTFVGEDLVTI PKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKMNGILGLAVATLAKPSSSLETFFPDSLVTQANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFLLPGIKMNGILGLAVATLAKPSSSLETFFPDSLVTQANIPNVFSMOMCGAGLPVA 240

QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIIEILKLEIGGQSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVPDAVEAVARASL 328
DB 301 IVDSGTTLLRLPQKVPDAVEAVARASL 328

RESULT 4

Q9JL18 PRELIMINARY; PRT; 514 AA.
AC Q9JL18; 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Aspartyl protease 1.
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi D.K., Sugano S., Sakaki Y.;
RT "Molecular characterization of the mouse Aspl gene, a homolog of the
RT human Aspl (Down Syndrome Region aspartyl protease).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216310; AAF36599.1; -.
DR HSSP; P32329; 1YPS.
DR MEROPS; A01.041; -.
DR MGD; MGI:1860440; Bace2.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 514 AA; 55799 MW; A70725F2C1DF5B47 CRC64;

Query Match 11.4%; Score 59; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 8.8e-50;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 FSMOMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIIEILKLEIGGQ 286
DB 224 FSMOMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIIEILKLEIGGQ 282

RESULT 5

Q9R1P7 PRELIMINARY; PRT; 255 AA.
AC Q9R1P7; 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Aspartyl protease (Fragment).
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Accarino M., Fumagalli P., Taramelli R., Ottolenghi S.;
RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
RT transmembrane protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051150; AAD45964.1; -.
DR MEROPS; A01.041; -.
DR MGD; MGI:1860440; Bace2.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.

DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
KW Protease.
FT NON TER
SQ SEQUENCE 255 AA; 28685 MW; 53DE317815996D63 CRC64;

Query Match 7.3%; Score 38; DB 11; Length 255;
Best Local Similarity 100.0%; Pred. No. 4e-29;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 INLDREYNADKAIVDSGTTLRLPQKVFDAVVEAVAR 325
Db 25 INLDREYNADKAIVDSGTTLRLPQKVFDAVVEAVAR 62

RESULT 6

Q9BYB9 PRELIMINARY; PRT; 432 AA.

AC Q9BYB9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-432.

GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;
RX MEDLINE=21408467; PubMed=11516562;

RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
cleaving enzyme (BACE) and their effect on amyloid beta-peptide
production.";
RL Neurosci. Lett. 307:9-12(2001).
DR EMBL; AB050438; BAB40933.1; -.
DR HSSP; P32329; 1YPS.

DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPsin.

DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.

SQ SEQUENCE 432 AA; 48212 MW; 96FC81B6F0BED01B CRC64;

Query Match 2.3%; Score 12; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
Db 90 ILVDTGSSNFAV 101

RESULT 7

Q9BYC0 PRELIMINARY; PRT; 457 AA.

AC Q9BYC0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-457 (Beta-site APP cleaving enzyme
type C).
GN BACE.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;
RX MEDLINE=21408467; PubMed=11516562;

RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
cleaving enzyme (BACE) and their effect on amyloid beta-peptide
production.";
RL Neurosci. Lett. 307:9-12(2001).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=EXOCRINE PANCREAS;
RA Zaccchetti D., De Pietri Tonelli D., Schnurbus R.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
human pancreas.";
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB050437; BAB40932.1; -.

DR EMBL; AF338817; AAK38375.1; -.

DR HSSP; P32329; 1YPS.

DR InterPro; IPR001461; AspproteaseA1.

DR InterPro; IPR001969; Aspprotease_site.

DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPsin.

DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.

SQ SEQUENCE 457 AA; 51068 MW; C794C9A9E85FE7A2 CRC64;

Query Match 2.3%; Score 12; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
Db 90 ILVDTGSSNFAV 101

RESULT 8

Q9BYC1 PRELIMINARY; PRT; 476 AA.

AC Q9BYC1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-476.

GN BACE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;
RX MEDLINE=21408467; PubMed=11516562;

RA Tanahashi H., Tabira T.;

RT "Three novel alternatively spliced isoforms of the human beta-site APP
cleaving enzyme (BACE) and their effect on amyloid beta-peptide
production.";

RL Neurosci. Lett. 307:9-12(2001).

DR EMBL; AB050436; BAB40931.1; -.

DR HSSP; P32329; 1YPS.

DR InterPro; IPR001461; AspproteaseA1.

DR InterPro; IPR001969; Aspprotease_site.

DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPsin.

DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.

SQ SEQUENCE 476 AA; 52907 MW; 6C8C87F8A953AF66 CRC64;

Query Match 2.3%; Score 12; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
Db 90 ILVDTGSSNFAV 101

RESULT 9

Q9ULS1

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ID Q9ULS1 PRELIMINARY; PRT; 532 AA.
AC Q9ULS1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE KIAA1149 protein (Fragment).
GN KIAA1149.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=20039618; Pubmed=10574461;
RA Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
DR EMBL; AB032975; BAA86463.2; -.
DR HSSP; P56272; 1AM5.
DR MEROPS; A01.004; -.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
Db 121 ILVDTGSSNFAV 132

RESULT 10
Q9P0D2 PRELIMINARY; PRT; 213 AA.
AC Q9P0D2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE HSPC104 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORD BLOOD;
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161367; AAF28927.1; -.
DR InterPro; IPR001461; AsproteaseA1.
DR Pfam; PF00026; asp; 1.
FT NON TER 1
SQ SEQUENCE 213 AA; 24338 MW; EC9D3FA31CFA835C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 SFRITLPO 378
Db 119 SFRITLPO 127
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RESULT 11
Q9CUU5 PRELIMINARY; PRT; 266 AA.
AC Q9CUU5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme (Fragment).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRIN;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014390; BAB29317.1; -.
DR MEROPS; A01.004; -.
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; AsproteaseA1.
DR Pfam; PF00026; asp; 1.
FT NON TER 1
SQ SEQUENCE 266 AA; 30201 MW; B913FDA8ADAB4238 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 SFRITLPO 378
Db 121 SFRITLPO 129

RESULT 12
Q32940 PRELIMINARY; PRT; 319 AA.
AC Q32940;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Possible sugar transport protein (Probable ABC-transport protein,
DE inner membrane component).
GN ML1426 OR MLCB2052.28.
GN Mycobacterium leprae.
OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; Pubmed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
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RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.,
RT "Massive gene decay in the leprosy bacillus."
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL; Z98604; CAB11326.1; -.
DR EMBL; AL583922; CAC30377.1; -.
DR Leproma; ML1426; -.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
DR PROSITE; PS00402; BPD_TRANS_P_NN_MEMBER; 1.
KW Sugar transport; Transmembrane; Transport; Complete proteome.
SQ SEQUENCE 319 AA; 34868 MW; D1FD52DBE850DFC7 CRC64;

Query Match 1.7%; Score 9; DB 16; Length 319;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 AILVLIVL 489
Db 294 AILVLIVL 302

RESULT 13
Q9PCW3 PRELIMINARY; PRT; 863 AA.
AC Q9PCW3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein Xf1641.
GN Xf1641.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Midanis J., Setubal J.C.,
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL; AE003991; AAF84450.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 863 AA; 95838 MW; 4FC65FC0A020876C CRC64;

Query Match 1.7%; Score 9; DB 16; Length 863;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GLALALEPA 67
Db 153 GLALALEPA 161

RESULT 14
Q99MX8 PRELIMINARY; PRT; 1121 AA.
AC Q99MX8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Macrophage hemoglobin scavenger receptor CD163 precursor.
GN CD163.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21243729; PubMed=11345593;
RA Schaefer D.J., Boretli F.S., Hongegger A., Poehler D., Linnscheid P.,
RA Staeger H., Muller C., Schoedon G., Schaffner A.,
RT "Molecular cloning and characterization of the mouse CD163 homologue,
RT a highly glucocorticoid-inducible member of the scavenger receptor
RT cysteine-rich family."
RL Immunogenetics 53:170-177(2001).
DR EMBL; AF274883; AAK16065.1; -.
DR MGI; MGI:2135946; Cdl63.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00530; SRCR; 9.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SMO0202; SR; 9.
DR PROSITE; PS00420; SRCR_1; UNKNOWN_3.
DR PROSITE; PS50287; SRCR_2; 9.
KW Receptor; Signal.
FT SIGNAL 1
SQ SEQUENCE 1121 AA; 120889 MW; 04428DF18AD26187 CRC64;

Query Match 1.7%; Score 9; DB 11; Length 1121;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 VCGAILLVL 486
Db 1051 VCGAILLVL 1059

RESULT 15
O07312 PRELIMINARY; PRT; 94 AA.
AC O07312;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Hypothetical 9.6 kDa protein.
GN URF6 OR URF3.
OS Rhodobacter capsulatus (Rhodopsseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;

OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97363217; PubMed=9219542;
RA Herter S.M., Schiltz E., Drews G.;
RT "Protein and gene structure of the NADH-binding fragment of
Rhodobacter capsulatus NADH:ubiquinone oxidoreductase.";
RL Eur. J. Biochem. 246:800-808(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B10;
RA Dupuis A., Issartel J.P.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y09884; CAA71015.1; -.
DR EMBL; AF029365; AAC24993.1; -.
KW Hypothetical protein.
SQ SEQUENCE 94 AA; 9613 MW; 0BAF868376A8F044 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RALLPLL 13
|||
Db 2 RALLPLL 9

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OM protein - protein search, using sw model

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Gapop 60.0 , Gapext 60.0

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	406	100.0	413	22	AAE10658	Acid-processed hu-
2	406	100.0	413	22	AAE02610	Human acid-process
3	406	100.0	413	23	ABB78619	Asp-IdeltaTM(his)6
4	406	100.0	475	22	AAE10657	Secreted recombin
5	406	100.0	475	22	AAE02609	Human secreted asp
6	406	100.0	475	23	ABB78618	Secreted recombin
7	406	100.0	481	22	AAG75592	Human colon cancer
8	406	100.0	518	19	AAW61362	Aspartic proteinas
9	406	100.0	518	20	AAV41714	Human PRO852 prote
10	406	100.0	518	20	AAV22239	Human CSP56, aspar

★1	406	100.0	518	20	AAV13799	Human aspartyl pro
12	406	100.0	518	21	AAE44270	Human PRO852 (UNQ4
13	406	100.0	518	21	AAV88424	Human aspartyl pro
14	406	100.0	518	22	AAE10628	Human aspartyl pro
15	406	100.0	518	22	AAE10656	Human-Asp 1 protei
16	406	100.0	518	22	AAU29059	Human PRO polypept
17	406	100.0	518	22	AAE06858	Human aspartyl pro
18	406	100.0	518	22	AAU06602	Human aspartyl pro
19	406	100.0	518	22	AAU07201	Human aspartyl pro
20	406	100.0	518	22	AAE02580	Human aspartyl pro
21	406	100.0	518	22	AAE02608	Human Aspartyl pro
22	406	100.0	518	23	ABB78589	Human Asp-1 protei
23	406	100.0	518	23	ABB78617	Human Asp-IdeltaTM
24	406	100.0	518	23	ABB06531	Human aspartyl pro
25	406	100.0	518	23	ABB07453	Human BACE2 amino
26	389	95.8	439	23	ABB90365	Human polypeptide
27	373	91.9	423	22	AAE04796	Human aspartyl pro
28	294	72.4	355	22	AAE93925	Human protein sequ
29	235	57.9	423	22	AAE88479	Human membrane or
30	59	14.5	514	22	AAE84204	Amino acid sequenc
31	50	12.3	50	22	AAE18665	Peptide #5099 enco
32	15	3.7	89	22	AAE25497	Human protein sequ
33	12	3.0	62	22	AAU23633	Novel human enzyme
34	12	3.0	387	22	AAU23068	Novel human enzyme
35	12	3.0	390	22	AAU23069	Novel human enzyme
36	12	3.0	415	21	AAE07899	Amino acid sequenc
37	12	3.0	425	21	AAV88437	Human Asp2 amino a
38	12	3.0	425	22	AAE10641	T7-Caspase-Caspase
39	12	3.0	425	22	AAE06871	T7-Caspase-Caspase
40	12	3.0	425	22	AAU06615	T7-Caspase-caspase
41	12	3.0	425	22	AAU07214	T7-Caspase-caspase
42	12	3.0	425	22	AAE02593	T7-Caspase-Caspase
43	12	3.0	425	23	ABB78602	T7-caspase-caspase
44	12	3.0	427	22	AAE93866	Human polypeptide,
45	12	3.0	428	22	AAE10646	Human-Asp 2(b) pro
46	12	3.0	428	22	AAE06891	Human-Asp2(b) delt
47	12	3.0	428	22	AAU06620	Human-pro-Asp 2(b)
48	12	3.0	428	22	AAU07219	Human aspartyl pro
49	12	3.0	428	22	AAE02598	Human aspartyl pro
50	12	3.0	428	23	AAE02597	Human Asp-2(b) delt
51	12	3.0	433	21	AAV88433	Human-pro-Asp 2(a)
52	12	3.0	433	22	AAE10640	Human-pro-Asp 2(a)
53	12	3.0	433	22	AAE06870	Human-pro-Asp2(a)
54	12	3.0	433	22	AAU06614	Human-pro-Asp2(a)
55	12	3.0	433	22	AAU07213	T7-human aspartyl
56	12	3.0	433	22	AAE02592	Human-pro-Asp 2(a)
57	12	3.0	433	23	ABB78601	Human-pro-Asp-2(a)
58	12	3.0	434	22	AAE10647	Human-Asp 2(b) pro
59	12	3.0	434	22	AAE06892	Human-Asp2(b) delt
60	12	3.0	434	22	AAU06621	Human-pro-Asp 2(b)
61	12	3.0	434	22	AAU07220	Human aspartyl pro
62	12	3.0	434	22	AAE02599	Human aspartyl pro
63	12	3.0	434	23	AAE02599	Human Asp-2(b) delt
64	12	3.0	446	21	AAV88431	T7-caspase-human-p
65	12	3.0	446	22	AAE10638	T7-Human-pro-Asp 2
66	12	3.0	446	22	AAE06868	T7-Human-pro-Asp2(
67	12	3.0	446	22	AAU06612	Human T7-Human-pro
68	12	3.0	446	22	AAU07211	T7-human aspartyl
69	12	3.0	446	22	AAE02590	T7-Human-pro-Asp-2
70	12	3.0	446	23	ABB78599	T7-human-pro-Asp-2
71	12	3.0	453	21	AAV88438	Modified human asp
72	12	3.0	453	22	AAE10642	Human-Asp 2(a) pro
73	12	3.0	453	22	AAE06872	Human-Asp2(a) delt
74	12	3.0	453	22	AAU06616	Human-pro-Asp 2(a)
75	12	3.0	453	22	AAU07215	Human aspartyl pro
76	12	3.0	453	22	AAE02594	Human-Asp-2(a) del
77	12	3.0	453	23	ABB78603	Human-Asp-2(a) delt
78	12	3.0	456	21	AAV07897	Active enzyme port
79	12	3.0	459	21	AAV88432	T7-caspase-human-p
80	12	3.0	459	21	AAV88439	Modified human asp
81	12	3.0	459	22	AAE10639	T7-Caspase-human-p
82	12	3.0	459	22	AAE10643	Human-Asp 2(a) pro
83	12	3.0	459	22	AAE06869	T7-Caspase-Human-p

84	12	3.0	459	22	AAE06873	Human-Asp2(a) delt	157	8	2.0	592	22	ABB62801	Drosophila melanog
85	12	3.0	459	22	AAU06613	Human T7-Caspase-H	158	8	2.0	592	22	ABB67339	Drosophila melanog
86	12	3.0	459	22	AAU06617	Human-pro-Asp 2(a)	159	7	1.7	25	22	ABB42277	Peptide #9783 enco
87	12	3.0	459	22	AAU07212	T7-caspase-human a	160	7	1.7	25	22	AAM63163	Human brain expres
88	12	3.0	459	22	AAU07216	Human aspartyl pro	161	7	1.7	25	22	AAM75977	Human bone marrow
89	12	3.0	459	22	AAE02591	T7-Caspase-human-p	162	7	1.7	25	22	AAM36085	Peptide #10122 enc
90	12	3.0	459	22	AAE02595	Human-Asp-2(a) del	163	7	1.7	34	21	AAB12350	Fragment of human
91	12	3.0	459	23	ABB78600	T7-caspase-human-p	164	7	1.7	34	21	AAG56900	Arabidopsis thalia
92	12	3.0	460	21	AAE07898	Human Asp-2(a)delt	165	7	1.7	41	22	ABB51187	Human secreted pro
93	12	3.0	476	21	AAV88426	Amino acid sequenc	166	7	1.7	47	22	AAU31051	Human secret
94	12	3.0	476	21	AAE10630	Human aspartyl pro	167	7	1.7	61	22	AAU42241	Proionibacterium
95	12	3.0	476	22	AAE06860	Human aspartyl pro	168	7	1.7	68	22	AAU20237	Human novel endocr
96	12	3.0	476	22	AAE06909	Human aspartyl pr	169	7	1.7	79	21	AAG56899	Arabidopsis thalia
97	12	3.0	476	22	AAU06604	Murine aspartyl pr	170	7	1.7	86	22	ABB51186	Human secreted pro
98	12	3.0	476	22	AAU07203	Human Aspartyl pro	171	7	1.7	88	22	AAO13578	Human polypeptide
99	12	3.0	476	22	AAE02582	Human aspartyl pro	172	7	1.7	90	22	AAU47158	Proionibacterium
100	12	3.0	476	22	AAE02619	Murine aspartyl pr	173	7	1.7	95	22	AAM00047	Plastidic trioseph
101	12	3.0	476	22	ABB78591	Human Asp-2(b) pro	174	7	1.7	105	23	ABP02682	Human ORFX protein
102	12	3.0	476	23	ABB06410	Human aspartyl pro	175	7	1.7	109	22	ABG11071	Novel human diagno
103	12	3.0	476	23	ABB06120	Human aspartyl pro	176	7	1.7	109	22	ABG23787	Novel human diagno
104	12	3.0	488	22	AAE06572	Human NS protein s	177	7	1.7	112	22	ABB67791	Drosophila melanog
105	12	3.0	488	22	AAE06572	Human memapsin 2.	178	7	1.7	115	22	AAM88647	Human immune/haema
106	12	3.0	488	22	AAE06572	Memapsin 2 protein	179	7	1.7	117	23	ABP33337	Human ORF2310 prot
107	12	3.0	488	23	AAU99488	Amino acid sequenc	180	7	1.7	120	21	AAG03247	Human secreted pro
108	12	3.0	501	19	AAW59807	Murine beta-secret	181	7	1.7	121	20	AAV12208	Human 5' EST secre
109	12	3.0	501	21	AAV94767	Murine beta-secret	182	7	1.7	126	22	AAM39144	Human polypeptide
110	12	3.0	501	21	AAV94768	Rat beta-secretase	183	7	1.7	130	22	AAO01648	Human polypeptide
111	12	3.0	501	21	AAV94769	Amino acid sequenc	184	7	1.7	139	22	AAM99857	Human excretory re
112	12	3.0	501	21	AAE07896	Human aspartyl pr	185	7	1.7	139	22	AAW42672	Human kidney relat
113	12	3.0	501	21	AAV88425	Human aspartyl pr	186	7	1.7	140	20	AAW93839	P. methanolica pep
114	12	3.0	501	21	AAE10629	Murine aspartyl pr	187	7	1.7	140	20	AAW93840	P. methanolica pep
115	12	3.0	501	22	AAE10631	Murine aspartyl pr	188	7	1.7	140	20	AAW93840	S. cerevisiae prot
116	12	3.0	501	22	AAE06859	Murine aspartyl pr	189	7	1.7	140	21	AAB19018	Amino acid sequenc
117	12	3.0	501	22	AAE06861	Human aspartyl pr	190	7	1.7	140	21	AAV51057	P. methanolica pep
118	12	3.0	501	22	AAU06603	Murine aspartyl pr	191	7	1.7	140	22	AAE05416	P. methanolica pep
119	12	3.0	501	22	AAU06603	Human Aspartyl pro	192	7	1.7	140	22	AAB67567	Amino acid sequenc
120	12	3.0	501	22	AAU06605	Mouse Aspartyl pro	193	7	1.7	140	22	AAB61993	P. methanolica PEP
121	12	3.0	501	22	AAU07202	Human aspartyl pro	194	7	1.7	140	22	AAV72372	P. methanolica PEP
122	12	3.0	501	22	AAU07204	Mouse aspartyl pro	195	7	1.7	140	22	AAB49227	P. methanolica PEP
123	12	3.0	501	22	AAE02581	Mouse aspartyl sec	196	7	1.7	140	23	AAO19974	Protein derived fr
124	12	3.0	501	22	AAE02583	Human aspartyl pro	197	7	1.7	145	22	ABB50641	Human secreted pro
125	12	3.0	501	22	AAE02583	Murine aspartyl pr	198	7	1.7	145	23	ABP34658	Human ORF3631 prot
126	12	3.0	501	23	ABB78590	Human Asp-2(a) pro	199	7	1.7	156	22	ABG22859	Novel human enzyme
127	12	3.0	501	23	ABB06409	Human aspartyl pro	200	7	1.7	157	22	AAU23445	Novel human diagno
128	12	3.0	503	22	AAB66573	Human pro-memapsin	201	7	1.7	166	23	ABP01194	Human ORFX protein
129	12	3.0	503	22	AAB61335	T7 promoter and ve	202	7	1.7	175	22	AAM17175	Peptide #3609 enco
130	12	3.0	503	22	AAU99489	Pro-memapsin 2 enc	203	7	1.7	175	22	AAM29668	Peptide #3705 enco
131	12	3.0	503	23	AAW52697	FLAG-tagged human	204	7	1.7	175	22	AAM40930	Human polypeptide
132	12	3.0	509	23	AAW59808	Partial amino acid	205	7	1.7	175	22	AAW40930	Peptide #3552 enco
133	12	3.0	790	19	AAW59808	Novel human diagno	206	7	1.7	209	21	AAG04117	Arabidopsis thalia
134	12	3.0	969	22	ABG09611	N terminus of 15KD	207	7	1.7	209	21	AAG11858	Arabidopsis thalia
135	9	2.2	45	23	AAU78524	Novel human diagno	208	7	1.7	209	21	AAG75438	Arabidopsis thalia
136	9	2.2	269	22	ABG18048	Novel human diagno	209	7	1.7	231	22	AAG75438	Human colon cancer
137	9	2.2	322	22	AAE04797	Human aspartyl pro	210	7	1.7	233	22	AAB61608	Human protein HP03
138	9	2.2	351	20	AAV35518	Extended human sec	211	7	1.7	235	20	AAV35512	Chlamydia pneumoni
139	8	2.0	67	23	ABP11020	Human ORFX protein	212	7	1.7	241	20	AAV37435	Amino acid sequenc
140	8	2.0	105	21	AAG45058	Arabidopsis thalia	213	7	1.7	253	22	AAE10135	Streptomyces nous
141	8	2.0	131	22	AAU23632	Novel human enzyme	214	7	1.7	261	22	AAU40710	Proionibacterium
142	8	2.0	239	22	ABG09608	Novel human diagno	215	7	1.7	262	21	AAB58184	Lung cancer associ
143	8	2.0	262	22	AAM41741	Human polypeptide	216	7	1.7	265	23	ABB72331	Rat protein isolat
144	8	2.0	285	21	AAE12862	Arabidopsis thalia	217	7	1.7	267	22	ABB64636	Drosophila melanog
145	8	2.0	287	23	ABB91441	Herbicidally activ	218	7	1.7	268	22	AAU69751	Escherichia coli e
146	8	2.0	307	21	AAE12861	Arabidopsis thalia	219	7	1.7	269	22	ABG07213	Novel human diagno
147	8	2.0	313	22	ABG09606	Novel human diagno	220	7	1.7	272	22	AAU49513	Proionibacterium
148	8	2.0	335	22	ABG18051	Novel human diagno	221	7	1.7	276	23	AAE14743	Human triacylglyce
149	8	2.0	341	20	AAV32039	Bovine pregnancy a	222	7	1.7	280	23	AAE14743	Human triacylglyce
150	8	2.0	380	20	AAV32041	Propionibacterium	223	7	1.7	289	21	AAG11857	Arabidopsis thalia
151	8	2.0	472	22	AAM39955	Human polypeptide	224	7	1.7	289	21	AAG54003	Arabidopsis thalia
152	8	2.0	473	22	ABB71149	Drosophila melanog	225	7	1.7	289	23	AAU77494	Human lipid metabo
153	8	2.0	475	23	ABB91454	Herbicidally activ	226	7	1.7	290	22	AAU63105	Propionibacterium
154	8	2.0	504	23	AAU84277	Human endometrial	227	7	1.7	306	22	AAG98408	Escherichia coli p
155	8	2.0	548	22	AAE08365	Escherichia coli p	228	7	1.7	320	15	AAR62044	Leptospira Ompl1.
156	8	2.0					229	7	1.7				

230	7	1.7	320	18	AAW14278	Leptospira alstoni
231	7	1.7	323	21	AAB12341	Fragment of human
232	7	1.7	326	22	AAB66589	Human pepsin. Hom
233	7	1.7	326	22	AAB61351	Pepsin protein. H
234	7	1.7	327	22	AAM00099	Plasticidic trioseph
235	7	1.7	339	22	ABG15392	Novel human diagno
236	7	1.7	346	23	ABB54038	Lactococcus lactis
237	7	1.7	354	17	AAW14463	Yeast glycoprotein
238	7	1.7	359	23	ABB90878	Herbicidally activ
239	7	1.7	363	18	AAW24256	Ammonifex histidin
240	7	1.7	369	22	ABG01477	Novel human diagno
241	7	1.7	373	21	AAG04115	Arabidopsis thalia
242	7	1.7	373	21	AAG11856	Arabidopsis thalia
243	7	1.7	373	21	AAG54002	Arabidopsis thalia
244	7	1.7	379	23	AAU72876	Human asparcyl pro
245	7	1.7	380	20	AAV32036	Bovine pregnancy a
246	7	1.7	380	20	AAV32048	Bovine pregnancy a
247	7	1.7	387	20	AAV32052	Bovine pregnancy a
248	7	1.7	388	20	AAV32058	Cat pregnancy asso
249	7	1.7	388	22	AAU27708	Human full-length
250	7	1.7	392	20	AAV32057	Bovine pregnancy a
251	7	1.7	395	23	AAE14744	Human triacylglyce
252	7	1.7	397	18	AAW31628	Aspergillus oryzae
253	7	1.7	397	23	AAE17308	Human lysosomal ac
254	7	1.7	399	22	AAG67513	Amino acid sequenc
255	7	1.7	399	23	AAU77496	Human lipid metabo
256	7	1.7	409	15	AAAR48060	Sequence of protea
257	7	1.7	410	13	AAAR28030	Pichia pastoris pr
258	7	1.7	420	21	ABB800665	Candida boidinii p
259	7	1.7	428	20	AAV09000	E. coli sura prote
260	7	1.7	433	21	AAG30824	Arabidopsis thalia
261	7	1.7	433	21	AAG31636	Arabidopsis thalia
262	7	1.7	450	21	AAV57041	Plasmodium vivax p
263	7	1.7	451	22	AAB66063	Murine protein: SE
264	7	1.7	456	21	AAV71062	Human membrane tra
265	7	1.7	456	22	AAW78336	Human protein sequ
266	7	1.7	460	22	AAAB94655	Human protein sequ
267	7	1.7	465	22	ABB66239	Drosophila melanog
268	7	1.7	470	22	AAAB66083	Murine TANGO 202.
269	7	1.7	489	22	ABB11767	Human membrane tra
270	7	1.7	489	22	AAW79320	Human protein sequ
271	7	1.7	506	21	AAAG17818	Arabidopsis thalia
272	7	1.7	508	21	AAAG31635	Arabidopsis thalia
273	7	1.7	513	21	AAAG45529	Arabidopsis thalia
274	7	1.7	522	21	AAAG17817	Arabidopsis thalia
275	7	1.7	525	23	ABP28514	Streptococcus poly
276	7	1.7	656	22	ABG26839	Novel human diagno
277	7	1.7	674	22	AAAB94461	Human protein sequ
278	7	1.7	674	22	AAAB95164	Human protein sequ
279	7	1.7	674	23	ABG66691	Human novel polype
280	7	1.7	692	22	ABG22381	Novel human diagno
281	7	1.7	702	23	ABP28373	Streptococcus poly
282	7	1.7	702	23	AAAM47575	Drosophila cell cy
283	7	1.7	726	22	AAAG66716	Human transcriptio
284	7	1.7	731	23	AAE14746	Human triacylglyce
285	7	1.7	773	23	ABB57374	Mouse ischaemic co
286	7	1.7	775	21	AAV67250	Mouse protein tyro
287	7	1.7	775	21	AAV67251	Mutant mouse PTP-P
288	7	1.7	784	23	ABBA77322	Listeria monocytog
289	7	1.7	802	17	AAAR90848	Gibberellin (GA1),
290	7	1.7	802	23	ABB92819	Herbicidally activ
291	7	1.7	863	22	ABB63583	Drosophila melanog
292	7	1.7	868	22	ABG24427	Novel human diagno
293	7	1.7	880	23	ABP27173	Streptococcus poly
294	7	1.7	896	22	ABG28532	Novel human diagno
295	7	1.7	925	22	ABG15391	Novel human diagno
296	7	1.7	933	23	ABP28348	Streptococcus poly
297	7	1.7	1133	22	ABG28516	Novel human diagno
298	7	1.7	1191	22	AAAM80219	Human protein sequ
299	7	1.7	1193	22	ABG18089	Novel human diagno
300	7	1.7	1379	22	ABB57823	Drosophila melanog
301	7	1.7	1429	20	AAW93941	Human brx protein.
302	7	1.7	1429	22	ABG05537	Novel human diagno
303	7	1.7	2042	22	ABB59689	Drosophila melanog
304	6	1.5	8	23	ABB06440	Beta-secretase rel
305	6	1.5	8	23	ABB07485	Theobroma cacao as
306	6	1.5	12	21	AAB09319	Hepatitis GB virus
307	6	1.5	12	22	AAB50475	Bacterial Aita pep
308	6	1.5	14	22	ABB55906	Vascular dementia-
309	6	1.5	14	22	AAB72296	-ADAMTS-R1 immunoge
310	6	1.5	15	22	AAG78131	Human actin 49 pep
311	6	1.5	15	23	ABB81892	Transcriptional ei
312	6	1.5	16	22	AAAM99379	Vaccine related MH
313	6	1.5	18	23	AAU78513	Human and mouse BA
314	6	1.5	19	18	AAW22374	S. pneumoniae HSP7
315	6	1.5	19	22	AAAB72292	ADAMTS-7 immunogen
316	6	1.5	20	9	AAAP82056	Pep-13 comprising
317	6	1.5	21	18	AAW10215	Endoglycoceramidas
318	6	1.5	24	15	AAAR47014	Cathepsin E positi
319	6	1.5	24	22	AAAM99380	Vaccine related MH
320	6	1.5	26	22	AAAG76928	Human colon cancer
321	6	1.5	27	23	AAAM49941	Human D40 associat
322	6	1.5	27	23	AAAM49967	Human D40 associat
323	6	1.5	30	23	AAAM49997	Human D40 associat
324	6	1.5	31	21	AAAB15670	Human D40 associat
325	6	1.5	31	21	AAV64997	Alpha V beta 3 rec
326	6	1.5	31	22	AAAG77180	Human 5' EST relat
327	6	1.5	32	22	ABBA2768	Human colon cancer
328	6	1.5	32	22	ABB26061	Peptide #10274 enc
329	6	1.5	32	22	AAAM63659	Protein #8060 enco
330	6	1.5	32	22	AAAM76473	Human brain.expres
331	6	1.5	32	22	AAAM20905	Human bone marrow
332	6	1.5	32	22	AAAM36581	Peptide #7339 enco
333	6	1.5	32	23	ABGA45734	Peptide #10618 enc
334	6	1.5	34	20	AAW92216	Human peptide enco
335	6	1.5	34	20	AAV03951	Analogue of parath
336	6	1.5	34	22	AAU20673	Human novel foetal
337	6	1.5	35	22	ABB30124	Peptide #2775 enco
338	6	1.5	35	22	ABB35296	Peptide #2802 enco
339	6	1.5	35	22	ABB39561	Peptide #7067 enco
340	6	1.5	35	22	ABB20738	Protein #2737 enco
341	6	1.5	35	22	ABBB24282	Protein #6281 enco
342	6	1.5	35	22	AAAM56125	Human brain expres
343	6	1.5	35	22	AAAM60260	Human brain expres
344	6	1.5	35	22	AAAM68497	Human bone marrow
345	6	1.5	35	22	AAAM72887	Human bone marrow
346	6	1.5	35	22	AAAM16303	Peptide #2737 enco
347	6	1.5	35	22	AAAM19767	Peptide #6201 enco
348	6	1.5	35	22	AAAM28796	Peptide #2833 enco
349	6	1.5	35	22	AAAM33118	Peptide #7155 enco
350	6	1.5	35	22	AAAM04039	Peptide #2721 enco
351	6	1.5	35	23	ABG38078	Human peptide enco
352	6	1.5	35	23	ABGA27221	Human peptide enco
353	6	1.5	36	22	ABB03311	Human musculoskele
354	6	1.5	40	10	AAAP90808	N-terminal sequenc
355	6	1.5	43	19	AAW74930	Human secreted pro
356	6	1.5	44	23	AAU78527	N terminus of 11kD
357	6	1.5	45	19	AAW79315	Staphylococcus aur
358	6	1.5	45	22	AAAM87000	Human immune/haema
359	6	1.5	45	22	AAAO13181	Human polypeptide
360	6	1.5	46	21	AAAG48490	Arabidopsis thalia
361	6	1.5	46	22	AAAM86213	Human immune/haema
362	6	1.5	47	22	ABB31222	Peptide #3873 enco
363	6	1.5	47	22	ABB36429	Peptide #3935 enco
364	6	1.5	47	22	AAAM57187	Human brain expres
365	6	1.5	47	22	AAAM69592	Human bone marrow
366	6	1.5	47	22	AAAM29928	Peptide #3965 enco
367	6	1.5	47	22	AAAM05091	Peptide #3773 enco
368	6	1.5	47	23	ABGA4108	Human peptide enco
369	6	1.5	48	23	ABGA4108	Human peptide enco
370	6	1.5	49	22	ABB29630	Peptide #2281 enco
371	6	1.5	49	22	ABB34808	Peptide #2314 enco
372	6	1.5	49	22	ABB50577	Human secreted pro
373	6	1.5	49	22	ABB20224	Protein #2223 enco
374	6	1.5	49	22	AAAM55610	Human brain expres
375	6	1.5	49	22	AAAM67995	Human bone marrow

376	6	1.5	49	22	AAM15811	Peptide #2245 enco	449	6	1.5	67	22	AAM16795	Peptide #3229 enco
377	6	1.5	49	22	AAM28321	Peptide #2358 enco	450	6	1.5	67	22	AAM29277	Peptide #3314 enco
378	6	1.5	49	22	AAM03549	Peptide #2231 enco	451	6	1.5	67	22	AAM04513	Peptide #3195 enco
379	6	1.5	49	23	ABG37527	Human peptide enco	452	6	1.5	67	23	ABG38553	Human peptide enco
380	6	1.5	50	22	AAU40556	Propionibacterium	453	6	1.5	68	21	AAV84596	Fragment of human
381	6	1.5	51	19	AAW71570	Hepatocyte nuclear	454	6	1.5	68	22	ABB31892	Peptide #4543 enco
382	6	1.5	51	22	AAU41435	Propionibacterium	455	6	1.5	68	22	ABB37130	Peptide #4636 enco
383	6	1.5	52	22	AAAM6713	Human immune/haema	456	6	1.5	68	22	ABB22441	Protein #4440 enco
384	6	1.5	52	22	AAO03436	Human polypeptide	457	6	1.5	68	22	AAM57849	Human brain expres
385	6	1.5	52	23	ABP26180	Streptococcus poly	458	6	1.5	68	22	AAM70267	Human bone marrow
386	6	1.5	52	23	ABP26181	Streptococcus poly	459	6	1.5	68	22	AAM18095	Peptide #4529 enco
387	6	1.5	53	22	AAU41231	Propionibacterium	460	6	1.5	68	22	AAM30604	Peptide #4641 enco
388	6	1.5	55	16	AAAR80193	Internal portion o	461	6	1.5	68	22	AAM05730	Peptide #4412 enco
389	6	1.5	55	19	AAW79444	Staphylococcus aur	462	6	1.5	68	23	ABG39911	Human peptide enco
390	6	1.5	55	21	AAAG02879	Human secreted pro	463	6	1.5	68	23	ABP07588	Human ORFX protein
391	6	1.5	55	22	ABG60250	Human ovarian anti	464	6	1.5	69	21	AAAG17411	Arabidopsis thalia
392	6	1.5	55	22	AAU64206	Propionibacterium	465	6	1.5	70	22	ABG18828	Novel human diagno
393	6	1.5	55	22	ABB39033	Peptide #6539 enco	466	6	1.5	70	22	AAW60973	Streptococcus pneu
394	6	1.5	55	22	ABBA0396	Peptide #7902 enco	467	6	1.5	71	21	AAAG25363	Arabidopsis thalia
395	6	1.5	55	22	ABBA23977	Protein #5976 enco	468	6	1.5	71	22	AAU45743	Propionibacterium
396	6	1.5	55	22	ABBA24768	Protein #6767 enco	469	6	1.5	72	23	AAU62168	Human ORFX protein
397	6	1.5	55	22	AAAM94384	Human reproductive	470	6	1.5	72	23	ABP05481	Human polypeptide
398	6	1.5	55	22	AAAM59687	Human brain expres	471	6	1.5	73	17	AAW04190	Peptide encoded by
399	6	1.5	55	22	AAAM61204	Human brain expres	472	6	1.5	73	17	AAW04190	Peptide encoded by
400	6	1.5	55	22	AAAM72263	Human bone marrow	473	6	1.5	73	17	AAW04199	Arabidopsis thalia
401	6	1.5	55	22	AAAM73923	Human bone marrow	474	6	1.5	73	21	AAAG43580	Novel human diagno
402	6	1.5	55	22	AAAM19522	Peptide #5956 enco	475	6	1.5	73	22	ABG03752	Human ORFX protein
403	6	1.5	55	22	AAAM20159	Peptide #6593 enco	476	6	1.5	73	23	ABP05087	Human ORFX protein
404	6	1.5	55	22	AAAM32522	Peptide #6559 enco	477	6	1.5	73	23	ABP10788	Human ORFX protein
405	6	1.5	55	22	AAAM34102	Peptide #8139 enco	478	6	1.5	74	22	AAU53361	Propionibacterium
406	6	1.5	55	23	ABG61721	Novel ovarian rela	479	6	1.5	74	22	AAO07082	Human polypeptide
407	6	1.5	55	23	ABG42078	Human peptide enco	480	6	1.5	75	22	AAAM99788	Human excretory re
408	6	1.5	55	23	ABG43811	Human peptide enco	481	6	1.5	75	22	AAAM42603	Human kidney relat
409	6	1.5	56	22	AAU47306	Propionibacterium	482	6	1.5	76	22	AAU67129	Propionibacterium
410	6	1.5	56	23	ABP34242	Human ORF3215 prot	483	6	1.5	77	22	AAAM90374	Human immune/haema
411	6	1.5	57	22	ABBA22299	Peptide #9805 enco	484	6	1.5	77	22	AAO10251	Human polypeptide
412	6	1.5	57	22	ABBA25802	Protein #7801 enco	485	6	1.5	77	23	ABP02872	Human ORFX protein
413	6	1.5	57	22	AAAM63185	Human brain expres	486	6	1.5	78	19	AAAM98260	H. pylori GHP 144
414	6	1.5	57	22	AAAM75999	Human bone marrow	487	6	1.5	78	21	AAAB33208	Pinus radiata tran
415	6	1.5	57	22	AAAM36107	Peptide #10144 enc	488	6	1.5	79	23	ABP00842	Human ORFX protein
416	6	1.5	57	23	ABG45406	Human peptide enco	489	6	1.5	80	22	ABG00065	Novel human diagno
417	6	1.5	58	20	AAV59754	Human normal ovari	490	6	1.5	80	22	ABG11887	Novel human diagno
418	6	1.5	58	22	AAU18640	Human lung antigen	491	6	1.5	80	22	AAAM85491	Human immune/haema
419	6	1.5	59	13	AAAR27732	SalP20.5R. Vaccin	492	6	1.5	81	22	ABP43203	Human polypeptide
420	6	1.5	59	14	AAAR43264	RGAI N-terminal.	493	6	1.5	81	22	AAO06868	Human glial fibril
421	6	1.5	59	22	AAU20680	Human novel foetal	494	6	1.5	82	19	AAV21011	Human polypeptide
422	6	1.5	59	22	AAAM94522	Human reproductive	495	6	1.5	82	21	AAAB28196	Human artemin neur
423	6	1.5	59	23	ABP02996	Human ORFX protein	496	6	1.5	82	22	ABB31944	Peptide #4595 enco
424	6	1.5	59	23	AAU09947	Caulobacter cresce	497	6	1.5	82	22	ABBA37183	Peptide #4689 enco
425	6	1.5	60	22	AAU54616	Propionibacterium	498	6	1.5	82	22	ABB22487	Protein #4486 enco
426	6	1.5	60	22	AAUG2553	Propionibacterium	499	6	1.5	82	22	AAAM57895	Human brain expres
427	6	1.5	60	22	AAAM87965	Human immune/haema	500	6	1.5	82	22	AAAM70313	Human bone marrow
428	6	1.5	60	22	AAAB69147	M. catarrhalis str	501	6	1.5	82	22	AAAM18511	Peptide #4585 enco
429	6	1.5	61	21	AAAG03465	Human secreted pro	502	6	1.5	82	22	AAAM25544	Human protein sequ
430	6	1.5	61	22	AAO10476	Human polypeptide	503	6	1.5	82	22	AAAM30654	Peptide #4691 enco
431	6	1.5	62	21	AAAG37069	Arabidopsis thalia	504	6	1.5	82	22	AAAM05777	Peptide #4459 enco
432	6	1.5	62	21	AAAY86274	Human secreted pro	505	6	1.5	82	23	ABG39957	Human peptide enco
433	6	1.5	62	22	AAAB63837	Human prostate can	506	6	1.5	83	22	AAU44883	Propionibacterium
434	6	1.5	62	23	ABP09488	Human ORFX protein	507	6	1.5	83	22	ABG28088	Novel human diagno
435	6	1.5	63	22	AAU50416	Propionibacterium	508	6	1.5	83	23	ABP01679	Human ORFX protein
436	6	1.5	63	22	AAU57838	Propionibacterium	509	6	1.5	84	13	AAAR21240	Human parathyroid
437	6	1.5	63	22	AAU59994	Propionibacterium	510	6	1.5	84	13	AAAR21179	Human parathyroid
438	6	1.5	64	21	AAAB38199	Human secreted pro	511	6	1.5	84	13	AAAR23516	Bovine parathyroid
439	6	1.5	65	21	AAAB45293	Protein fragment #	512	6	1.5	84	13	AAAR23323	Bovine parathyroid
440	6	1.5	65	21	AAAB45294	Human secreted pro	513	6	1.5	84	13	AAAR23455	Porcine parathyroi
441	6	1.5	65	21	AAAG00484	Human ORFX protein	514	6	1.5	84	22	AAU52779	Propionibacterium
442	6	1.5	65	23	ABP04162	Novel human diagno	515	6	1.5	84	22	AAU20156	Human novel endocr
443	6	1.5	67	22	ABG27225	Peptide #3266 enco	516	6	1.5	85	21	AAV42627	Zea mays protein f
444	6	1.5	67	22	ABB30615	Peptide #3285 enco	517	6	1.5	85	21	AAV44773	Protein-1 compri
445	6	1.5	67	22	ABB35779	Peptide #3201 enco	518	6	1.5	85	22	ABB66327	Drosophila melanog
446	6	1.5	67	22	ABB21202	Protein #3201 enco	519	6	1.5	85	22	AAU55013	Propionibacterium
447	6	1.5	67	22	AAAM56587	Human brain expres	520	6	1.5	85	22	ABG15570	Novel human diagno
448	6	1.5	67	22	AAAM68968	Human bone marrow	521	6	1.5	85	22	AAAM84225	Human immune/haema

522	6	1.5	86	21	AA026123	Zea mays protein f	595	6	1.5	119	22	AA007689	Human polypeptide
523	6	1.5	86	22	AAU47872	Propionibacterium	596	6	1.5	120	20	AAW97368	Murine growth horm
524	6	1.5	86	22	AAM90093	Human immune/haema	597	6	1.5	121	23	ABP42309	Human ovarian anti
525	6	1.5	86	23	ABP06241	Human ORFX protein	598	6	1.5	121	23	ABP29062	Streptococcus poly
526	6	1.5	86	23	AAM49087	Human p34cdc2-rela	599	6	1.5	122	21	AA051931	Arabidopsis thalia
527	6	1.5	89	23	ABBS3965	Lactococcus lactis	600	6	1.5	122	22	AAU23079	Novel human enzyme
528	6	1.5	90	21	AA091528	Human secreted pro	601	6	1.5	122	22	AAU32987	Novel human secret
529	6	1.5	90	22	ABG09609	Novel human diagno	602	6	1.5	123	20	AA013491	S. aureus IgG-bind
530	6	1.5	90	22	AAU29662	Novel human secret	603	6	1.5	123	21	AA044772	wheat serine O-ace
531	6	1.5	91	16	AA069587	Non-specific lipid	604	6	1.5	124	20	AA035862	Chlamydia pneumoni
532	6	1.5	92	20	AAW90173	Human heart muscle	605	6	1.5	124	20	AAW97371	Murine/porcine chi
533	6	1.5	92	21	AA038067	Arabidopsis thalia	606	6	1.5	124	22	ABG16821	Novel human diagno
534	6	1.5	92	23	ABP31398	Human transport pr	607	6	1.5	125	22	AA091635	C glutamicum prote
535	6	1.5	93	22	AAU87348	Novel central nerv	608	6	1.5	126	20	AA035836	Chlamydia pneumoni
536	6	1.5	94	8	AA070567	Product of ORF 9 f	609	6	1.5	126	21	AA038066	Arabidopsis thalia
537	6	1.5	94	23	AAU75733	M. Sativa cyclin b	610	6	1.5	126	21	AA056294	Arabidopsis thalia
538	6	1.5	95	20	AAW86822	Human tumour antig	611	6	1.5	126	21	AA074774	Neisseria gonorrhoe
539	6	1.5	95	22	AAU44604	Propionibacterium	612	6	1.5	126	21	AA074774	Neisseria meningit
540	6	1.5	95	22	AAU67642	Propionibacterium	613	6	1.5	126	22	AAU23696	Novel human enzyme
541	6	1.5	96	22	AAU45975	Propionibacterium	614	6	1.5	126	22	AAU17488	Novel signal trans
542	6	1.5	96	23	ABP00399	Human ORFX protein	615	6	1.5	126	22	AAU21848	Novel human neopla
543	6	1.5	97	21	AA053531	Human colon cancer	616	6	1.5	128	22	AAU44649	Propionibacterium
544	6	1.5	98	22	ABG13902	Human human diagno	617	6	1.5	130	20	AA011561	Human 5' EST secre
545	6	1.5	99	22	ABG20720	Novel human diagno	618	6	1.5	130	21	AA025177	Eucalyptus grandis
546	6	1.5	100	22	AAU29661	Novel human secret	619	6	1.5	130	21	AA000573	Human secreted pro
547	6	1.5	101	21	AA043039	Human ORFX ORF2803	620	6	1.5	130	21	AA000573	Human secreted pro
548	6	1.5	101	22	ABG25580	Novel human diagno	621	6	1.5	130	22	AA081535	S. epidermidis ope
549	6	1.5	102	21	AA032715	Zea mays protein f	622	6	1.5	130	22	AA000855	Sunflower Blight A
550	6	1.5	103	21	AA001742	Human secreted pro	623	6	1.5	131	22	AA001967	Human polypeptide
551	6	1.5	103	23	ABG60203	Human DITHP polype	624	6	1.5	131	23	AB053213	Human ORF119 prote
552	6	1.5	103	23	ABP32558	Human glycoprotein	625	6	1.5	132	22	AA003503	Human polypeptide
553	6	1.5	104	21	AA001771	Simian immunodefic	626	6	1.5	132	23	AB047865	Listeria monocytog
554	6	1.5	104	21	AA014790	Human Zsig67, a no	627	6	1.5	133	21	AA041267	Human ORFX ORF1031
555	6	1.5	105	21	AA033677	Arabidopsis thalia	628	6	1.5	133	21	AA007905	Arabidopsis thalia
556	6	1.5	105	22	ABG02738	Novel human diagno	629	6	1.5	133	22	AA012302	Human secreted pro
557	6	1.5	105	22	ABG16142	Novel human diagno	630	6	1.5	133	22	AA005039	Human polypeptide
558	6	1.5	105	22	AAW88385	Human immune/haema	631	6	1.5	134	22	AB011292	Human HSP-124 pro
559	6	1.5	105	23	ABP34337	Human kinase-like	632	6	1.5	134	22	AA006644	Human polypeptide
560	6	1.5	107	21	AA040186	Arabidopsis thalia	633	6	1.5	134	22	AA081720	S. epidermidis ope
561	6	1.5	107	21	AA084598	Fragment of human	634	6	1.5	135	22	AAU30249	Novel human secret
562	6	1.5	107	22	ABG12998	Novel human diagno	635	6	1.5	135	20	AA013003	Human secreted pro
563	6	1.5	108	19	AAW74953	Human secreted pro	636	6	1.5	136	22	ABG19495	Novel human diagno
564	6	1.5	108	21	AA009968	Arabidopsis thalia	637	6	1.5	137	21	AA040578	Human ORFX ORF342
565	6	1.5	108	21	AA040185	Propionibacterium	638	6	1.5	137	22	AAU67542	Propionibacterium
566	6	1.5	108	22	AA048674	Human transport pr	639	6	1.5	137	23	ABP07284	Human ORFX protein
567	6	1.5	108	23	ABP34346	Human colon cancer	640	6	1.5	138	21	AA015943	E. coli proliferat
568	6	1.5	109	22	AA076057	Human bone marrow	641	6	1.5	138	22	AAU48920	Propionibacterium
569	6	1.5	110	22	AAU71946	SIB 134 intestinal	642	6	1.5	139	22	AA082949	S. epidermidis ope
570	6	1.5	111	12	AA012604	S. pneumoniae deri	643	6	1.5	140	13	AA025864	HCV polypeptide 11
571	6	1.5	111	19	AA085920	Novel human secret	644	6	1.5	140	14	AA041742	Hepatitis C virus
572	6	1.5	111	22	AAU29683	Human polypeptide	645	6	1.5	141	21	AA008706	Arabidopsis thalia
573	6	1.5	111	22	AA002691	Staphylococcus aur	646	6	1.5	141	21	AA042719	Arabidopsis thalia
574	6	1.5	112	19	AAW79423	Arabidopsis thalia	647	6	1.5	142	21	AA037788	Arabidopsis thalia
575	6	1.5	112	21	AA005248	Propionibacterium	648	6	1.5	142	23	ABP42390	Human ovarian anti
576	6	1.5	112	21	AA009967	Novel human diagno	649	6	1.5	143	21	AA032914	Pinus radiata tran
577	6	1.5	112	22	AAU60191	Novel human connec	650	6	1.5	143	22	ABG29743	Novel human diagno
578	6	1.5	113	22	AAU86909	Novel human diagno	651	6	1.5	144	21	AA030702	Arabidopsis thalia
579	6	1.5	113	22	ABG02741	Human breast speci	652	6	1.5	145	21	AA044766	Arabidopsis thalia
580	6	1.5	113	23	ABG65559	C glutamicum prote	653	6	1.5	145	22	AAU56954	Corn serine O-acet
581	6	1.5	114	22	AA090032	Propionibacterium	654	6	1.5	145	22	AA085561	Propionibacterium
582	6	1.5	115	22	AAU61434	Novel human diagno	655	6	1.5	145	23	ABG64721	Human secreted pro
583	6	1.5	115	22	AAU65123	Novel human secret	656	6	1.5	146	23	AB089479	Human albumin fusi
584	6	1.5	115	22	AAU33001	Zea mays protein f	657	6	1.5	147	21	AA044111	Human polypeptide
585	6	1.5	116	21	AA027159	Novel human diagno	658	6	1.5	148	22	AAU30940	Arabidopsis thalia
586	6	1.5	116	22	ABG21772	Human reproductive	659	6	1.5	148	22	AA005046	Novel human secret
587	6	1.5	116	22	AA065687	Human polypeptide	660	6	1.5	149	22	ABG03013	Human polypeptide
588	6	1.5	116	22	AA004858	Group B Streptococ	661	6	1.5	150	22	ABG17930	Novel human diagno
589	6	1.5	116	22	AAU03684	Peptide CS4 from d	662	6	1.5	151	22	AA002623	Human polypeptide
590	6	1.5	117	18	AAW17913	Human immune/haema	663	6	1.5	151	22	AA003607	Human polypeptide
591	6	1.5	117	22	AAW89871	Human colon cancer	664	6	1.5	151	22	AA041423	Human polypeptide
592	6	1.5	118	22	AA075718	Human human diagno	665	6	1.5	151	23	AB053951	Lactococcus lactis
593	6	1.5	119	22	ABG16822	Novel human diagno	666	6	1.5	151	23	AA024037	Arabidopsis thalia
594	6	1.5	119	22	AA000450	Human polypeptide	667	6	1.5	153	22	AA067120	Cat mammary tumour

814	6	1.5	207	22	AAE03655	Human extracellula	887	6	1.5	235	20	AAV05674	Maize diphenyl oxi
815	6	1.5	207	23	AAU83629	Human PRO protein,	888	6	1.5	236	22	AAW94238	Human reproductive
816	6	1.5	208	21	AAG08705	Arabidopsis thalia	889	6	1.5	237	20	AAV02654	Human secreted pro
817	6	1.5	208	21	AAG42718	Arabidopsis thalia	890	6	1.5	237	21	AAV84585	Alternatively spli
818	6	1.5	208	23	AAU79290	Rat FGF-related pr	891	6	1.5	237	21	AAV92037	Human artemin (GDN
819	6	1.5	208	23	ABB93083	Herbicidally activ	892	6	1.5	237	21	AAV87321	Human signal pepti
820	6	1.5	209	18	AAV11177	S. pneumoniae N-(5	893	6	1.5	237	21	AAV68706	A human neublastin
821	6	1.5	209	22	ABG17441	Novel human diagno	894	6	1.5	237	21	AAV66721	Membrane-bound pro
822	6	1.5	210	21	AAB18636	Amino acid sequenc	895	6	1.5	237	22	ABG05288	Novel human diagno
823	6	1.5	210	22	AAB68416	Amino acid sequenc	896	6	1.5	237	22	AAU29134	Human PRO polypept
824	6	1.5	210	22	AAU00958	Murine Fibroblast	897	6	1.5	237	22	AAB65244	Human PRO511 (UNQ5
825	6	1.5	210	23	AAE24375	Human FGF-21 prote	898	6	1.5	237	23	ABG30699	Human artemin poly
826	6	1.5	211	21	AAG36629	Arabidopsis thalia	899	6	1.5	239	21	AAG05704	Arabidopsis thalia
827	6	1.5	211	23	AAU76144	Ralstonia solanace	900	6	1.5	239	21	AAG29617	Arabidopsis thalia
828	6	1.5	212	21	AAG26292	Arabidopsis thalia	901	6	1.5	239	21	AAG45610	Arabidopsis thalia
829	6	1.5	212	22	ABG29278	Novel human diagno	902	6	1.5	239	22	ABB64172	Drosophila melanog
830	6	1.5	212	22	AAB99966	Hordeum vulgare AG	903	6	1.5	239	22	AAU58883	Propionibacterium
831	6	1.5	213	21	AAG09106	Arabidopsis thalia	904	6	1.5	239	22	AAU97500	Human DNA polymera
832	6	1.5	213	21	AAG25232	Arabidopsis thalia	905	6	1.5	240	22	AAB94913	Human protein sequ
833	6	1.5	213	21	AAG26291	Arabidopsis thalia	906	6	1.5	240	23	AAU74427	Mouse protein sequ
834	6	1.5	214	20	AAV34657	C. pneumoniae prot	907	6	1.5	241	9	AAV80597	Cv-sis gene encode
835	6	1.5	214	21	AAB53324	Human colon cancer	908	6	1.5	241	14	AAV40967	CV-sis gene produc
836	6	1.5	215	21	AAV96096	Actinobacillus ple	909	6	1.5	241	15	AAV63472	Recombinant plate1
837	6	1.5	215	21	AAV97897	Actinobacillus ple	910	6	1.5	241	21	AAB54090	Human pancreatic c
838	6	1.5	215	22	AAV23663	Human EST encoded	911	6	1.5	241	22	ABB70112	Drosophila melanog
839	6	1.5	217	20	AAV34785	Amino acid sequenc	912	6	1.5	241	22	AAV99134	Putative P. abyssi
840	6	1.5	217	22	ABG22862	Novel human diagno	913	6	1.5	241	22	AAV93374	Human polypeptide,
841	6	1.5	218	22	AAG90916	C glutamicum prote	914	6	1.5	241	22	AAV83027	S. epidermidis ope
842	6	1.5	218	23	AAO18235	Aeropyrum pernix e	915	6	1.5	243	22	AAU41710	Propionibacterium
843	6	1.5	220	21	AAV84583	Amino acid sequenc	916	6	1.5	243	22	AAU31720	Novel human secret
844	6	1.5	220	21	AAV44776	Short splice varia	917	6	1.5	244	18	AAV22443	Mouse neurogenic d
845	6	1.5	220	21	AAV68710	A human pre-pro-ne	918	6	1.5	244	19	AAV80804	Amino acid sequenc
846	6	1.5	220	22	AAB50978	Human PRO3562 prot	919	6	1.5	244	19	AAV71019	Murine neuroD3 pro
847	6	1.5	220	23	ABG30698	Human artemin poly	920	6	1.5	244	19	AAV54943	Murine neurogenin 1 p
848	6	1.5	220	23	ABB95581	Human angiogenesis	921	6	1.5	244	19	AAV54944	Mouse neurogenin 1
849	6	1.5	220	23	AAU86158	Human PRO3562 poly	922	6	1.5	244	20	AAV95053	Myrothecium verruc
850	6	1.5	220	23	ABB84975	Human PRO3562 prot	923	6	1.5	244	21	AAV70565	Rat neurogenin-1 (
851	6	1.5	221	22	AAB63772	Human prostate can	924	6	1.5	244	21	AAV70566	Murine neurogenin-
852	6	1.5	222	20	AAV37759	Amino acid sequenc	925	6	1.5	244	22	ABG00011	Novel human diagno
853	6	1.5	222	22	AAU35175	Enterococcus faeca	926	6	1.5	244	22	AAV93260	Human polypeptide,
854	6	1.5	223	20	AAV97845	Human truncated bo	927	6	1.5	245	18	AAV25783	Anti-T3 antibody d
855	6	1.5	223	21	AAB36473	Human LMP-1 amino	928	6	1.5	247	21	AAV43617	Arabidopsis thalia
856	6	1.5	224	20	AAV06931	C. albicans antiige	929	6	1.5	247	22	AAE05353	Mouse high affinity
857	6	1.5	224	22	ABG16138	Novel human diagno	930	6	1.5	247	23	ABB72363	Murine protein iso
858	6	1.5	225	13	AAV29646	AMEPV Spheroidin a	931	6	1.5	248	19	AAV72906	Mycobacterium tube
859	6	1.5	225	15	AAV55573	AMEPV spheroidin G	932	6	1.5	248	20	AAV21923	Amino acid sequenc
860	6	1.5	225	19	AAV41298	AMEPV entomopoxvir	933	6	1.5	248	22	ABG18105	Novel human diagno
861	6	1.5	225	20	AAV30166	Protein encoded by	934	6	1.5	248	22	AAU78814	Bacillus sp. Autoi
862	6	1.5	225	21	AAV42241	Human ORFX ORF2005	935	6	1.5	249	22	AAV96195	Putative P. abyssi
863	6	1.5	225	21	AAB22119	Maize glutathione-	936	6	1.5	250	21	AAV43383	Human ORFX ORF3147
864	6	1.5	226	13	AAV22673	v-sis protein p28s	937	6	1.5	250	21	AAV08893	Arabidopsis thalia
865	6	1.5	227	21	AAV09105	Arabidopsis thalia	938	6	1.5	250	21	AAV44830	Zea mays protein f
866	6	1.5	227	23	ABB19125	Herbicidally activ	939	6	1.5	250	22	ABB60669	Drosophila melanog
867	6	1.5	227	23	ABB48599	Listeria monocytog	940	6	1.5	250	22	AAB50476	Listeria sp. strai
868	6	1.5	228	21	AAV93559	A human GDNF-relat	941	6	1.5	250	23	AAV78804	Autoinducer inacti
869	6	1.5	228	21	AAV44775	Long splice varian	942	6	1.5	250	23	AAV78805	Autoinducer inacti
870	6	1.5	228	22	ABB63150	Drosophila melanog	943	6	1.5	250	23	AAV78806	Autoinducer inacti
871	6	1.5	230	22	ABB60542	Drosophila melanog	944	6	1.5	250	23	AAV78807	Autoinducer inacti
872	6	1.5	230	22	ABG23889	Novel human diagno	945	6	1.5	250	23	AAV78808	Autoinducer inacti
873	6	1.5	230	22	AAV40569	Human polypeptide	946	6	1.5	250	23	AAV78809	Autoinducer inacti
874	6	1.5	230	23	ABP28496	Streptococcus poly	947	6	1.5	250	23	AAV78810	Autoinducer inacti
875	6	1.5	231	21	AAV97009	S. cerevisiae esse	948	6	1.5	250	23	AAV78811	Autoinducer inacti
876	6	1.5	231	22	ABG07188	Novel human diagno	949	6	1.5	250	23	AAV78812	Autoinducer inacti
877	6	1.5	231	22	ABG29059	Novel human diagno	950	6	1.5	251	18	AAV20277	H. pylori surface
878	6	1.5	231	22	AAV25880	Human protein sequ	951	6	1.5	251	22	AAV25293	Human protein sequ
879	6	1.5	232	22	ABB67478	Drosophila melanog	952	6	1.5	252	18	AAV28247	Amino acid sequenc
880	6	1.5	233	22	ABB68857	Drosophila melanog	953	6	1.5	252	21	AAV22060	Arabidopsis thalia
881	6	1.5	234	18	AAV10509	Soluble fused MHC	954	6	1.5	252	22	AAV39891	Propionibacterium
882	6	1.5	234	21	AAV08704	Arabidopsis thalia	955	6	1.5	252	22	AAV59819	Propionibacterium
883	6	1.5	234	21	AAV42717	Arabidopsis thalia	956	6	1.5	253	22	ABG16451	Novel human diagno
884	6	1.5	234	22	AAV0290	Propionibacterium	957	6	1.5	253	23	ABP41998	Human ovarian anti
885	6	1.5	234	23	ABP26911	Streptococcus poly	958	6	1.5	254	21	AAV22059	Arabidopsis thalia
886	6	1.5	235	20	AAV35400	Amino acid sequenc	959	6	1.5	254	21	AAV32612	Arabidopsis thalia

960	6	1.5	254	22	ABB64503	Drosophila melanog
961	6	1.5	256	22	AAG92545	C glutamicum prote
962	6	1.5	257	22	AAB96285	Putative P. abyssi
963	6	1.5	258	22	ABB65793	Drosophila melanog
964	6	1.5	258	23	ABP38691	Staphylococcus epi
965	6	1.5	259	22	AAU36010	Helicobacter pylor
966	6	1.5	259	22	AAB46975	H. pylori Murp pro
967	6	1.5	260	22	AAU17427	Novel signal trans
968	6	1.5	260	22	AAB79890	Corynebacterium gl
969	6	1.5	260	22	AAU21802	Novel human neopla
970	6	1.5	261	22	AAU41917	Human polypeptide
971	6	1.5	262	21	AAB42498	Human ORFX ORF2262
972	6	1.5	262	22	AAB85539	Human secreted pro
973	6	1.5	262	22	AAG73661	Human colon cancer
974	6	1.5	262	23	ABG64720	Human albumin fusi
975	6	1.5	263	21	AAG17344	Arabidopsis thalia
976	6	1.5	264	16	AAR81425	Hepatitis GB virus
977	6	1.5	264	21	AAB09032	Hepatitis GB virus
978	6	1.5	264	21	AAV44702	Wheat dwarf virus
979	6	1.5	264	21	AAV44703	Wheat dwarf virus
980	6	1.5	266	21	AAG06098	Arabidopsis thalia
981	6	1.5	266	21	AAG49376	Arabidopsis thalia
982	6	1.5	266	22	AAU38887	C. pneumoniae CT13
983	6	1.5	266	22	AAG89903	C glutamicum prote
984	6	1.5	266	23	ABB49459	Listeria monocytog
985	6	1.5	267	18	AAW21027	H. pylori putative
986	6	1.5	268	20	AAW88210	Pseudomonas aerugi
987	6	1.5	269	21	AAG49398	Arabidopsis thalia
988	6	1.5	270	22	AAU39394	Human polypeptide
989	6	1.5	270	22	AAB28795	Human hydrolase-li
990	6	1.5	271	9	AAP80595	Recombinant platel
991	6	1.5	271	14	AAR40963	PDGF Bv-bis. Simi
992	6	1.5	271	15	AAR63468	Recombinant platel
993	6	1.5	271	22	ABB58271	Drosophila melanog
994	6	1.5	271	23	ABB47658	Listeria monocytog
995	6	1.5	272	13	AAR25590	RING10 proteasome
996	6	1.5	272	17	AAW06437	Human proteasome s
997	6	1.5	272	22	ABB58995	Drosophila melanog
998	6	1.5	273	22	AAU40181	Propionibacterium
999	6	1.5	273	22	AAG90638	C glutamicum prote
1000	6	1.5	274	21	AAB43146	Human ORFX ORF2910

ALIGNMENTS

RESULT 1
AAE10658 standard; Protein; 413 AA.

XX	AC	AAE10658;
XX	DT	10-DEC-2001 (first entry)
XX	DE	Acid-processed hu-Asp 1 lacking TM domain and containing (His) 6 tag.
XX	KW	Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;
KW	Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;	
KW	amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective	
XX	OS	Homo sapiens.
OS	Synthetic.	
XX	PN	GB2357767-A.
XX	PD	04-JUL-2001.
XX	PF	22-SEP-2000; 2000GB-0023315.
XX	PR	23-SEP-1999; 99US-0155493.
PR	23-SEP-1999; 99US-0404133.	
PR	23-SEP-1999; 99WO-US20881.	
PR	13-OCT-1999; 99US-0416901.	

PR	06-DEC-1999;	99US-0169232.
XX	(PHAA) PHARMACIA & UPJOHN CO.	
PA	Bienkowski MJ, Gurney M;	
PI	WPI; 2001-444208/48.	
XX		
DR		
XX		
PT	Polypeptide comprising fragments of human aspartyl protease with	
PT	amyloid precursor protein processing activity and alpha-secretase	
PT	activity, for identifying modulators useful in treating Alzheimer's	
PT	disease -	
XX		
PS	Example 14; Page 158; 187pp; English.	
XX		
CC	The patent discloses human aspartyl protease 1 (hu-Aspl) or modified	
CC	Aspl proteins which lack transmembrane domain or amino terminal	
CC	domain or cytoplasmic domain and retains alpha-secretase activity	
CC	and amyloid protein precursor (APP) processing activity. The proteins	
CC	of the invention are useful for assaying hu-Aspl alpha-secretase	
CC	activity, which in turn is useful for identifying modulators of	
CC	hu-Aspl alpha-secretase activity, where modulators that increase	
CC	hu-Aspl alpha-secretase activity are useful for treating Alzheimer's	
CC	disease (AD) which causes progressive dementia with consequent	
CC	formation of amyloid plaques, neurofibrillary tangles, gliosis and	
CC	neuronal loss. Hu-Aspl protease substrate is useful for assaying	
CC	hu-Aspl proteolytic activity, by contacting hu-Aspl protein with	
CC	the substrate under acidic conditions and determining the level	
CC	of hu-Aspl proteolytic activity. The present sequence is the acid-	
CC	processed form of human Asp 1 protein lacking a transmembrane (TM)	
CC	domain and containing (His)6 tag.	
XX		
SQ	Sequence 413 AA;	
	Query Match 100.0%; Score 406; DB 22; Length 413;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNPAVAGTP 60	
Db	1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNPAVAGTP 60	
QY	61 HSYIDTYFDTERSSSTRSGKFDVTWKYTGSGWTFVGEDLVITPKGFNTSFLVNATIFE 120	
Db	61 HSYIDTYFDTERSSSTRSGKFDVTWKYTGSGWTFVGEDLVITPKGFNTSFLVNATIFE 120	
QY	121 SENFPLPGIKMNGILGLAVATLAKPSSSLETFFDSLVTOANIPNVFSMOMCGAGLPVAGS 180	
Db	121 SENFPLPGIKMNGILGLAVATLAKPSSSLETFFDSLVTOANIPNVFSMOMCGAGLPVAGS 180	
QY	181 GTNGSLVLGIEPSLYKEDIWYTPIKEWYQIEILKLEIGGOSLNLDCREYNADKAIV 240	
Db	181 GTNGSLVLGIEPSLYKEDIWYTPIKEWYQIEILKLEIGGOSLNLDCREYNADKAIV 240	
QY	241 DSGTLLRLRPQKVFDAVVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISITL 300	
Db	241 DSGTLLRLRPQKVFDAVVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISITL 300	
QY	301 RDENSSRSFRITILPOLYIQPMWGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360	
Db	301 RDENSSRSFRITILPOLYIQPMWGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360	
QY	361 QKRVGFASPCAEIAGAASEISGFSTEDVASNCVPAOSLSEPI 406	
Db	361 QKRVGFASPCAEIAGAASEISGFSTEDVASNCVPAOSLSEPI 406	
XX		
RESULT 2		
ID	AAE02610 standard; Protein; 413 AA.	
XX		
AC	AAE02610;	
XX		

DT 10-AUG-2001 (first entry)
XX
DE Human acid-processed form of aspartyl protease-1 deltatM (His)6 protein.
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;
KW beta-secretase; acid-processed Asp-1 deltatM (His)6 protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US26080.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI; 2001-290516/30.
XX
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease -
XX
XX Example 14; Page 186-187; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human acid-processed form of
CC Aspartyl protease-1 (Asp-1) deltatM (His)6 protein which is used for the
CC expression of pre-pro-human-Aspartyl protease 1 (Aspl). The protein is
CC obtained by replacing C-terminal transmembrane and cytoplasmic domains
CC with a hexahistidine purification tag in the human Aspartyl protease 1.
XX
SQ Sequence 413 AA;

Query Match 100.0%; Score 406; DB 22; Length 413;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALBPALASPAGANFLAMVDNIQDSDGRGYLEMLIGTPPQKIQLVDTGSSNFAVAGTP 60
Db 1 ALBPALASPAGANFLAMVDNIQDSDGRGYLEMLIGTPPQKIQLVDTGSSNFAVAGTP 60
QY 61 HSYIDTYFDTERSSSTRSKGPDVTVKYTGQSWTGFVGEDLVTIIPKGFNTSFLVNIATIFE 120
Db 61 HSYIDTYFDTERSSSTRSKGPDVTVKYTGQSWTGFVGEDLVTIIPKGFNTSFLVNIATIFE 120
QY 121 SENFFLPGIKMGILGLAVATLAKPSSSLETFFDLSLVTOANI PNVSQMCGAGLPVAGS 180
Db 121 SENFFLPGIKMGILGLAVATLAKPSSSLETFFDLSLVTOANI PNVSQMCGAGLPVAGS 180
QY 181 GTNGGSLVLGGIEPSLYKGDIMWTYPIKEEWYQIEILKLEIGGOSLNLDCREYNADKATV 240
Db 181 GTNGGSLVLGGIEPSLYKGDIMWTYPIKEEWYQIEILKLEIGGOSLNLDCREYNADKATV 240
QY 241 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQILACWTNSETPWSYFPKISITL 300
Db 241 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQILACWTNSETPWSYFPKISITL 300
QY 301 RDNSSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSITNALVIGATVMEGFYVIFDRA 360
Db 301 RDNSSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSITNALVIGATVMEGFYVIFDRA 360

QY 361 QKRVGFAASPCAIEIAGAVSEISGPFSTEDVASNCVPAQSLSEPI L 406
Db 361 QKRVGFAASPCAIEIAGAVSEISGPFSTEDVASNCVPAQSLSEPI L 406

RESULT 3
ABB78619
ID ABB78619 standard; Protein; 413 AA.
XX
AC ABB78619;
XX
DT 16-JUL-2002 (first entry)
XX
DE Asp-1deltatM(his)6 acid-processed form SEQ ID NO:68.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW proteolytic; chromosome 21.
XX
OS Homo sapiens.
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI; 2002-396337/43.
XX
XX Example 14; Page 158-159; 182pp; English.

The present invention describes a human aspartyl protease 1 (hu-Aspl)
substrate (I) which comprises a peptide of no more than 50 amino acids,
and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
Glu-Pro. Also described are: (1) a method (II) for assaying hu-Aspl
proteolytic activity, comprising: (a) contacting a hu-Aspl protein with
(I) under acidic conditions; and (b) determining the level of hu-Aspl
proteolytic activity; (2) a purified polynucleotide (III) comprising a
nucleotide sequence that hybridises under stringent conditions to the
non-coding strand complementary to a defined 1804 nucleotide sequence
(see AB152456) where the nucleotide sequence encodes a polypeptide having
Aspl proteolytic activity and lacks nucleotides encoding a transmembrane
domain); (3) a purified polynucleotide (III') comprising a sequence that
hybridises under stringent conditions to (III) (the nucleotide sequence
encodes a polypeptide further lacking a pro-peptide domain corresponding
to amino acids 23-62 of hu-Aspl (see AB178589)); (4) a vector (IV)
comprising (III) or (III') and (5) a host cell (V) transformed or
transfected with (III), (III') and/or (IV). The hu-Aspl protease
substrate (I) may be used as an enzyme substrate in assays to detect
aspartyl protease activity, (II) and therefore diagnose diseases
associated with aberrant hu-Aspl expression and activity such as
Alzheimer's disease. Hu-Aspl has been localised to chromosome 21, while
hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
sequence represents the Asp-1deltatM(his)6 acid-processed form amino acid
sequence, which is used in an example from the present invention.

Sequence 413 AA;

	Query Match	100.0%;	Score 406;	DB 23;	Length 413;								
	Best Local Similarity	100.0%;	Pred. No. 0;										
	Matches 406;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;								
QY	1	ALEPALASPAGAA	NFLAMVDNLQD	SGRGYLL	EMLIGTPPOKLQILVD	TGSSNFAVAGTP 60							
DB	1	ALEPALASPAGAA	NFLAMVDNLQD	SGRGYLL	EMLIGTPPOKLQILVD	TGSSNFAVAGTP 60							
QY	61	HSYIDTYFDTERS	STYRSKGF	VDVTKYTQGS	WTFVGEDLV	TI PKGFNTSFLVNIA	TI FE 120						
DB	61	HSYIDTYFDTERS	STYRSKGF	VDVTKYTQGS	WTFVGEDLV	TI PKGFNTSFLVNIA	TI FE 120						
QY	121	SENFFLPGIKW	NGILGLAYAT	LAKPSS	LETF	FDSLVTQANI	PNVFSMONGAGL	LPVAGS 180					
DB	121	SENFFLPGIKW	NGILGLAYAT	LAKPSS	LETF	FDSLVTQANI	PNVFSMONGAGL	LPVAGS 180					
QY	181	GTNGGSLVLG	GIEPSLYKGD	IWYTPPIKE	WYQI	EILKLEIGGQSL	NLD	CREYNADKAI	V 240				
DB	181	GTNGGSLVLG	GIEPSLYKGD	IWYTPPIKE	WYQI	EILKLEIGGQSL	NLD	CREYNADKAI	V 240				
QY	241	DSGTTLLRL	POKVFDAV	VEAVARAS	LIP	ESDGF	WTSQ	LACW	TNSE	TEP	WSP	FKIS	IYL 300
DB	241	DSGTTLLRL	POKVFDAV	VEAVARAS	LIP	ESDGF	WTSQ	LACW	TNSE	TEP	WSP	FKIS	IYL 300
QY	301	RDENSSRS	FRITIL	PQLYIQ	PMMGAG	LN	VECYR	FGIS	PST	NALVIGAT	WMEGF	YVIF	DR 360
DB	301	RDENSSRS	FRITIL	PQLYIQ	PMMGAG	LN	VECYR	FGIS	PST	NALVIGAT	WMEGF	YVIF	DR 360
QY	361	QKRVGFAAS	PCAEIAGA	AVSEIS	GF	PST	ED	VASNC	VPAQ	SL	SEP	IL 406	
DB	361	QKRVGFAAS	PCAEIAGA	AVSEIS	GF	PST	ED	VASNC	VPAQ	SL	SEP	IL 406	

Accession	Protein Name	Length (AA)	Source	Notes
AAE10657	standard; Protein;	475	AA.	
AAE10657				
10-DEC-2001	(first entry)			
Secreted recombinant hu-Asp 1 with (His) ₆ tag and lacking TM domain.				
Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;				
Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;				
amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.				
Homo sapiens.				
Synthetic.				
GB2357767-A.				
04-JUL-2001.				
22-SEP-2000;	2000GB-0023315.			
23-SEP-1999;	99US-0155493.			
23-SEP-1999;	99US-0404133.			
23-SEP-1999;	99WO-US20881.			
13-OCT-1999;	99US-0416901.			
06-DEC-1999;	99US-0169232.			
(PHAA) PHARMACIA & UPJOHN CO.				
Bienkowski MJ, Gurney M;				
WPI; 2001-444208/48.				
Polypeptide comprising fragments of human aspartyl protease with				
amyloid precursor protein processing activity and alpha-secretase				
activity, for identifying modulators useful in treating Alzheimer's				
disease -				

PS Example 14; Page 156-158; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level
CC of hu-Asp1 proteolytic activity. The present sequence is secreted
CC recombinant human Asp 1 protein lacking a transmembrane (TM) domain
CC and containing a (His)6 tag. This sequence is generated from human
CC Asp 1 protein by the deletion of its C-terminal TM domain and addition
CC of hexa-histidine tag at its C-terminus.

XX

SO Sequence 475 AA;

Query Match	100.0%;	Score 406;	DB 22;	Length 475;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 406;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY 1	ALPEALASPAGAAFLAMVDNLQGSGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60		
Db 63	ALPEALASPAGAAFLAMVDNLQGSGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122		
QY 61	HSYIDTYFDTERSSTYRSKGFVDVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIAITFE	120		
Db 123	HSYIDTYFDTERSSTYRSKGFVDVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIAITFE	182		
QY 121	SENFLEPGIKWNGILGLAYATLAKPSSSLETFDLSLVTOANI PNVSQMCGAGLPVAGS	180		
Db 183	SENFLEPGIKWNGILGLAYATLAKPSSSLETFDLSLVTOANI PNVSQMCGAGLPVAGS	242		
QY 181	GTNGGSLVLGIEPSLYKGDIMWTPPIKEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	240		
Db 243	GTNGGSLVLGIEPSLYKGDIMWTPPIKEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	302		
QY 241	DSGTTLLRLPQKVFDAVVEAVARASLIPEPSDGFWTGSQLACWTNSETPMSYFPKISITL	300		
Db 303	DSGTTLLRLPQKVFDAVVEAVARASLIPEPSDGFWTGSQLACWTNSETPMSYFPKISITL	362		
QY 301	RDENSRSRFRITILPOLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA	360		
Db 363	RDENSRSRFRITILPOLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA	422		
QY 361	QKRVGFAASPCAEIAAGAVSEISGPFSTEDVASNCVPAQSLSEPII 406			
Db 423	QKRVGFAASPCAEIAAGAVSEISGPFSTEDVASNCVPAQSLSEPII 468			

RESULT 5	
AAE02609	
ID	AAE02609 standard; Protein; 475 AA.
XX	
AC	AAE02609;
XX	
DT	10-AUG-2001 (first entry)
XX	
DE	Human secreted aspartyl protease-1 (Asp-1) deltaTM (His)6 protein.
XX	
KW	Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW	Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;
KW	beta-secretase; secreted Asp-1 deltaTM (His)6 protein.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	

PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US26080.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI; 2001-290516/30.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease -
XX
PS Example 14; Page 184-186; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human secreted recombinant
CC Aspartyl protease-1 (Asp-1) deltaTM (His)6 protein which is used for the
CC expression of pre-pro-human-Aspartyl protease 1 (Asp1). The protein is
CC obtained by replacing C-terminal transmembrane and cytoplasmic domains
CC with a hexahistidine purification tag in the human Aspartyl protease 1.
XX
SQ Sequence 475 AA;

Query Match 100.0%; Score 406; DB 22; Length 475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFGVEDLVITIPKGFNTSFLVNIAITFE 120
Db 123 HSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFGVEDLVITIPKGFNTSFLVNIAITFE 182
QY 121 SENFFLPGIKMGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMGAGLPVAGS 180
Db 183 SENFFLPGIKMGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMGAGLPVAGS 242
QY 181 GTNCGSLVLGGIEPSLYKGDWYTPIKEWYYQIEILKLEIGQSILNDCREYNADKATV 240
Db 243 GTNCGSLVLGGIEPSLYKGDWYTPIKEWYYQIEILKLEIGQSILNDCREYNADKATV 302
QY 241 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISITL 300
Db 303 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISITL 362
QY 301 RDNSSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDNSSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFASPACAIAGAASEISGPFSTEDVASNCVPAQISSEPII 406
Db 423 QKRVGFASPACAIAGAASEISGPFSTEDVASNCVPAQISSEPII 468

RESULT 6
ABB78618
ID ABB78618 standard; Protein; 475 AA.
XX
AC ABB78618;

XX
DT 16-JUL-2002 (first entry)
XX
DE Secreted recombinant Asp-1deltaTM(his)6 amino acid SEQ ID NO:67.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW proteolytic; chromosome 21.
XX
OS Homo sapiens.
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI; 2002-396337/43.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect
PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT disease -
XX
PS Example 14; Page 156-158; 182pp; English.
XX

The present invention describes a human aspartyl protease 1 (hu-Asp1) substrate (I) which comprises a peptide of no more than 50 amino acids, and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1 proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with (I) under acidic conditions; and (b) determining the level of hu-Asp1 proteolytic activity; (2) a purified polynucleotide (III) comprising a nucleotide sequence that hybridises under stringent conditions to the non-coding strand complementary to a defined 1804 nucleotide sequence (see AB152456) where the nucleotide sequence encodes a polypeptide having Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane domain; (3) a purified polynucleotide (III') comprising a sequence that hybridises under stringent conditions to (III) (the nucleotide sequence encodes a polypeptide further lacking a pro-peptide domain corresponding to amino acids 23-62 of hu-Asp1 (see AB178589)); (4) a vector (IV) comprising (III) or (III'); and (5) a host cell (V) transformed or transfected with (III), (III') and/or (IV). The hu-Asp1 protease substrate (I) may be used as an enzyme substrate in assays to detect aspartyl protease activity, (II) and therefore diagnose diseases associated with aberrant hu-Asp1 expression and activity such as Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present sequence represents a secreted recombinant Asp-1deltaTM(his)6 amino acid sequence, which is used in an example from the present invention.

Query Match 100.0%; Score 406; DB 23; Length 475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFGVEDLVITIPKGFNTSFLVNIAITFE 120
Db 123 HSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFGVEDLVITIPKGFNTSFLVNIAITFE 182

QY 121 SENFPLGIKNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
| | | | |
Db 183 SENFPLGIKNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAIV 240
| | | | |
Db 243 GTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAIV 302
QY 241 DSGTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 300
| | | | |
Db 303 DSGTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 362
QY 301 RDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPTNALVIGATWMEGFYIFDRA 360
| | | | |
Db 363 RDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPTNALVIGATWMEGFYIFDRA 422
QY 361 QKRVGFASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPI L 406
| | | | |
Db 423 QKRVGFASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPI L 468

RESULT 7

AAG75592
ID AAG75592 standard; Protein; 481 AA.
XX AAG75592;
AC AAG75592;
XX 03-SEP-2001 (first entry)
DT
XX
DE Human colon cancer antigen protein SEQ ID NO:6356.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 21.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR N-PSDB; AAH34997.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 11; Page 7815-7817; 9803pp; English.
XX
XX

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
cancer-associated nucleic acid molecules (N) and proteins (P), where
the proteins are collectively known as colon cancer antigens. The colon
cancer antigens have cytostatic activity and can be used in gene
therapy and vaccine production. N and P may be used in the prevention,
diagnosis and treatment of diseases associated with inappropriate P
expression. For example, N and P may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of P by expressing
inactive proteins or to supplement the patients own production of P.
Additionally, N may be used to produce the colon cancer-associated Ps,
by inserting the nucleic acids into a host cell and culturing the cell
to express the proteins. N and P can be used in the prevention, diagnosis
and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
and AAB77789 represent sequences used in the exemplification of the

CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX

SQ Sequence 481 AA;

Query Match 100.0%; Score 406; DB 22; Length 481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSGRGYILEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
| | | | |
Db 26 ALEPALASPAGANFLAMVDNLQDSGRGYILEMLIGTPPQKLQILVDTGSSNFAVAGTP 85
QY 61 HSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFGEDLVITPKGFNTSFLVNIAITFE 120
| | | | |
Db 86 HSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFGEDLVITPKGFNTSFLVNIAITFE 145
QY 121 SENFPLGIKNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
| | | | |
Db 146 SENFPLGIKNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 205
QY 181 GTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAIV 240
| | | | |
Db 206 GTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAIV 265
QY 241 DSGTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 300
| | | | |
Db 266 DSGTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 325
QY 301 RDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPTNALVIGATWMEGFYIFDRA 360
| | | | |
Db 326 RDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPTNALVIGATWMEGFYIFDRA 385
QY 361 QKRVGFASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPI L 406
| | | | |
Db 386 QKRVGFASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPI L 431

RESULT 8

AAW61362
ID AAW61362 standard; Protein; 518 AA.
XX
XX AAW61362;
AC AAW61362;
XX
DT 25-SEP-1998 (first entry)
XX
DE Aspartic proteinase ASP1.
XX
KW ASP1; Aspartic proteinase; Alzheimer's disease; cancer; melanoma.
XX
OS Homo sapiens.
XX
PN EP848062-A2.
XX
PD 17-JUN-1998.
XX
XX

01-DEC-1997; 97EP-0309648.
XX
XX 14-DEC-1996; 96GB-0026022.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Chapman CG, Evans JR, Powell DJ, Southan C;
XX
XX

WPI; 1998-314477/28.
DR N-PSDB; AAV27962.
XX
PT New isolated polynucleotide encodes Aspartic protease polypeptide -
PT used to diagnosis, treat and vaccinate against Alzheimer's disease,
cancer and melanoma

XX Claim 11; Page 7; 19pp; English.
PS
XX
CC The human ASP1 protein is structurally related to other proteins of the
CC Aspartic proteinase family. ASP 1 polypeptides and polynucleotides can
CC be used to diagnosis, treat and vaccinate against Alzheimer's disease,
CC cancer and melanoma.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 406; DB 19; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSDRGYLEMLIGTPPKLOILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGANFLAMVDNLQDSDRGYLEMLIGTPPKLOILVDTGSSNFAVAGTP 122

QY 61 HSYIDTYFDTERSTYRSKGFVTVYKTTQGSWTGFGVEDLVTPKGFNTSFLVNIATIFE 120
Db 123 HSYIDTYFDTERSTYRSKGFVTVYKTTQGSWTGFGVEDLVTPKGFNTSFLVNIATIFE 182

QY 121 SENFFLPGIKWNIGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCGAGLPVAGS 180
Db 183 SENFFLPGIKWNIGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCGAGLPVAGS 242

QY 181 GTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGQSINLDCREYNADKAIV 240
Db 243 GTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGQSINLDCREYNADKAIV 302

QY 241 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISIVL 300
Db 303 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISIVL 362

QY 301 RDENSSRSFRITILPOLYIQPMWAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDENSSRSFRITILPOLYIQPMWAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422

QY 361 QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPII 406
Db 423 QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPII 468

RESULT 9
AA41714
ID AAY41714 standard; Protein; 518 AA.
XX
AC AAY41714;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO852 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX 16-SEP-1999.
PD
XX
PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.

396

PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.

PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.

XX (GETH) GENENTECH INC.

XX PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX DR WPI; 1999-551358/46.

DR N-PSDB; AAZ34056.

XX PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -

XX PS Claim 12; Fig 73; 530pp; English.

XX CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.

XX SQ Sequence 518 AA;

Query Match 100.0%; Score 406; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGAAFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGAAFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTVKYTGQSWTGFVGEDLVTIPKGFNTSFLVNIAITFE 120
Db 123 HSYIDTYFDTERSSSTYRSKGFDTVKYTGQSWTGFVGEDLVTIPKGFNTSFLVNIAITFE 182
QY 121 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKAIV 240
Db 243 GTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKAIV 302
QY 241 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITYL 300
Db 303 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITYL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 406
Db 423 QKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 468

RESULT 10
AAY22239
ID AAY22239 standard; Protein; 518 AA.
XX AC AAY22239;

XX DT 20-SEP-1999 (first entry)
XX DE Human CSP56, aspartyl-type protease, protein sequence.
XX KW Metastatic marker protein; human; cancer metastasis; breast cancer;
KW colon cancer; diagnosis; therapy; tumour; metastatic potential;
KW CSP56; aspartyl-type protease.

XX OS Homo sapiens.

XX PN ~~MO9934004-A2.~~

XX PD 08-JUL-1999.

XX PF 24-DEC-1998; 98WO-US27608.

XX PR 31-DEC-1997; 97US-0070112.

XX PA (CHIR) CHIRON CORP.

XX PI Giese K, Xin H;

XX DR WPI; 1999-430248/36.

DR N-PSDB; AAX84708.

XX PT New polynucleotides associated with cancer metastasis

XX PS Claim 4; Page 78-80; 80pp; English.

XX CC This sequence represents a polypeptide of the invention, and is
CC an aspartyl-type protease, designated CSP56. The polynucleotides (PNs) of
CC the invention encode metastatic marker protein variants. The PNs and
CC polypeptides can be used as markers for cancer metastasis. The products
CC can be used for identifying metastatic tissue or metastatic potential of
CC a tissue, e.g. breast or colon tissue. They can also be used for
CC screening test compounds for the ability to suppress the metastatic
CC potential of a tumour. The products can be used for developing products
CC for the therapy of cancers, particularly breast or colon cancer.

XX SQ Sequence 518 AA;

Query Match 100.0%; Score 406; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGAAFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGAAFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTVKYTGQSWTGFVGEDLVTIPKGFNTSFLVNIAITFE 120
Db 123 HSYIDTYFDTERSSSTYRSKGFDTVKYTGQSWTGFVGEDLVTIPKGFNTSFLVNIAITFE 182
QY 121 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKAIV 240
Db 243 GTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKAIV 302
QY 241 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITYL 300
Db 303 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITYL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 406
Db 423 QKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 468

BACKFILE-DAILY PRODUCTION REPORT
EFFICIENCY SHEET

Application # : 09668314

Date: 12/10/03

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Team #: 29

QC'er Name: _____

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Team Leader Sampler Name: _____ Team: # _____

Remark: _____

RESULT 11
ID AAY13799 standard; Protein; 518 AA.
XX AAY13799;
AC AAY13799;
XX AAY13799;
DT 21-SEP-1999 (first entry)
XX 21-SEP-1999 (first entry)
DE Human aspartyl protease, CSP56.
XX CSP56; human; aspartyl protease; diagnosis; neoplasia; tumour;
KW breast tumour; colon tumour.
XX Homo sapiens.
OS Homo sapiens.
PN WO9933963-A1.
XX WO9933963-A1.
PD 08-JUL-1999.
XX 08-JUL-1999.
PF 14-DEC-1998; 98WO-US26547.
XX 14-DEC-1998; 98WO-US26547.
PR 31-DEC-1997; 97US-0070112.
XX 31-DEC-1997; 97US-0070112.
PA (CHIR) CHIRON CORP.
XX (CHIR) CHIRON CORP.
PI Giese KW, Xin H;
XX Giese KW, Xin H;
DR WPI; 1999-430240/36.
DR N-PSDB; AAX89297.
XX N-PSDB; AAX89297.
PT Human CSP56 protein for diagnosis of neoplasia
PS Claim 2; Fig 2A; 51pp; English.
XX Claim 2; Fig 2A; 51pp; English.
CC This represents a human CSP56 protein, a novel aspartyl protease. The
CC CSP56 protein can be used in methods for diagnosing neoplasia, for
CC determining the metastatic potential of a tumour, and for screening test
CC compounds for the ability to suppress the metastatic potential of a
CC tumour. The tumours are preferably from breast or colon.
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 406; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 423 QKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPII 468
|||||
RESULT 12
ID AAB44270 standard; Protein; 518 AA.
XX AAB44270;
AC AAB44270;
XX AAB44270;
DT 08-FEB-2001 (first entry)
XX 08-FEB-2001 (first entry)
DE Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.
XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
PN WO200053756-A2.
XX WO200053756-A2.
PD 14-SEP-2000.
XX 14-SEP-2000.
PF 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04341.
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX (GETH) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78500.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Claim 12; Fig 73; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.

[illegible]

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RESULT 13
ID AAY88424 standard; Protein; 518 AA.
AC AAY88424;
DT 03-AUG-2000 (first entry)
DE Human aspartyl protease 1 (Asp1) amino acid sequence.
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;
KW Alzheimer's disease; beta secretase site.
XX Homo sapiens.
XX OS
XX WO200017369-A2.
XX PN
XX 30-MAR-2000.
XX PD
XX 23-SEP-1999; 99WO-US20881.
XX PF
XX 24-SEP-1998; 98US-0101594.
XX PR
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX PA
XX Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;
XX PI
XX WPI; 2000-303209/26.
XX DR
XX N-PSDB; AAA15661.
XX DR
XX
XX New enzyme designated human aspartase useful in research into
XX PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at
XX PT the beta secretase site to produce amyloid beta peptide -
XX PT
XX Claim 54; Fig 1; 183pp; English.
XX PS
XX
XX This sequence represents the human aspartyl protease amino acid sequence.
XX The invention relates to a protease capable of cleaving the beta
CC

```

secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DTG and a sequence encoding DSG or DTG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal transmembrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying inhibitors of the protease, are useful in the treatment of and research in to Alzheimer's disease.

Query Match	100.0%;	Score 406;	DB 21;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 406;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	ALPALASPAGAAFLAVNDLQGDSDGRGYLLEMLIGTPQKLQILVDTGSSNFAVAGTP	60		
DB 63	ALPALASPAGAAFLAVNDLQGDSDGRGYLLEMLIGTPQKLQILVDTGSSNFAVAGTP	122		
QY 61	HSYIDTYFDTERSSTYRSKGFVDTVKTYTQGSWTFVGEDLVTIPIKGFNTSFLVNIAITFE	120		
DB 123	HSYIDTYFDTERSSTYRSKGFVDTVKTYTQGSWTFVGEDLVTIPIKGFNTSFLVNIAITFE	182		
QY 121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS	180		
DB 183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS	242		
QY 181	GTNGGSLVLGGIEPSLYKGDIMWYTPIKEEMWYQIEILKLEIGGQSLNLDCREYNADKAIY	240		
DB 243	GTNGGSLVLGGIEPSLYKGDIMWYTPIKEEMWYQIEILKLEIGGQSLNLDCREYNADKAIY	302		
QY 241	DSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSOLA CWTNSETPWSYFPKISIYL	300		
DB 303	DSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSOLA CWTNSETPWSYFPKISIYL	362		
QY 301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSINALVIGATVMEGFYVIFDRA	360		
DB 363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSINALVIGATVMEGFYVIFDRA	422		
QY 361	QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAOSLSEPII 406			
DB 423	QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAOSLSEPII 468			

RESULT 14	
AAE10628	
ID	AAE10628 standard; Protein; 518 AA.
XX	
AC	AAE10628;
XX	
DT	10-DEC-2001 (first entry)
XX	
DE	Human aspartyl protease 1 (hu-Asp1) protein.
XX	
KM	Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KM	Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KM	amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
XX	chromosome 21.
OS	
XX	Homo sapiens.
FH	
Key	location/Qualifiers
Peptide	1..20
FT	/label= Signal_peptide
FT	21..518
Protein	/note= "Mature human aspartyl protease 1"
FT	469..492
Domain	/label= Transmembrane domain
FT	

XX	
PN	GB2357767-A.
XX	
PD	04-JUL-2001.
XX	
PF	22-SEP-2000; 2000GB-0023315.
XX	
PR	23-SEP-1999; 99US-0155493.
PR	23-SEP-1999; 99US-0404133.
PR	23-SEP-1999; 99WO-US20881.
PR	13-OCT-1999; 99US-0416901.
PR	06-DEC-1999; 99US-0169232.
XX	
PA	(PHAA) PHARMACIA & UPJOHN CO.
XX	
PI	Bienkowski MJ, Gurney M;
XX	
DR	WPI: 2001-444208/48.
	DR -PSDB; AAD17864.

PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
PS Claim 36; Fig 1; 187pp; English.

CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is Asp1 protein
CC from human. Asp1 gene is localised on chromosome 21.

SQ Sequence 518 AA;

Query Match	100.0%;	Score 406;	DB 22;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 406; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY 1 ALEPALSPAGANFLAMVDNLQDSDGRGYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
|||||
63 ALEPALSPAGANFLAMVDNLQDSDGRGYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy	61	HSYIDTYFDTERSS	TYRSKGF	VDVTKY	TQGSMTG	FVGED	LV	TPKGF	NTS	FL	VNI	AT	IF	120
Db	123	HSYIDTYFDTERSS	TYRSKGF	VDVTKY	TQGSMTG <td>FVGED <td>LV <td>TPKGF <td>NTS</td> <td>FL <td>VNI <td>AT <td>IF</td> <td>182</td> </td></td></td></td></td></td>	FVGED <td>LV <td>TPKGF <td>NTS</td> <td>FL <td>VNI <td>AT <td>IF</td> <td>182</td> </td></td></td></td></td>	LV <td>TPKGF <td>NTS</td> <td>FL <td>VNI <td>AT <td>IF</td> <td>182</td> </td></td></td></td>	TPKGF <td>NTS</td> <td>FL <td>VNI <td>AT <td>IF</td> <td>182</td> </td></td></td>	NTS	FL <td>VNI <td>AT <td>IF</td> <td>182</td> </td></td>	VNI <td>AT <td>IF</td> <td>182</td> </td>	AT <td>IF</td> <td>182</td>	IF	182

[illegible][illegible][illegible]

Qy	301	RDENSSRSFRITILPOLYIQPMGAGLNEYCRFGISPS	TNALVIGATWMEGFYI	FDRA	360
Db	363	RDENSSRSFRITILPOLYIQPMGAGLNEYCRFGISPS <td>TNALVIGATWMEGFYI <td>FDRA</td> <td>422</td> </td>	TNALVIGATWMEGFYI <td>FDRA</td> <td>422</td>	FDRA	422

QY		361	QKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db		423	QKRVGFAASPCAEIIAGAASEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 15
AAE10656
ID AAE10656 standard; Protein; 518 AA.

AC AAE10656;

DT 10-DEC-2001 (first entry)

DE Human-Asp 1 protein lacking TM domain and containing (His)6 tag.

KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

OS Homo sapiens.

✕✕

XX

PR 23-SEP-1999; 99US-0404133.

PR 13-OCT-1999; 99US-0416901.

XX

PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -

PS Example 14; Page 155-156; 187pp; English.

The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1 proteins which lack transmembrane domain or amino terminal domain or cytoplasmic domain and retains alpha-secretase activity and amyloid protein precursor (APP) processing activity. The proteins of the invention are useful for assaying hu-Asp1 alpha-secretase activity, which in turn is useful for identifying modulators of hu-Asp1 alpha-secretase activity, where modulators that increase hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's disease (AD) which causes progressive dementia with consequent formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with the substrate under acidic conditions and determining the level of hu-Asp1 proteolytic activity. The present sequence is human Asp 1 protein lacking a transmembrane (TM) domain and containing (His)6 tag. This sequence is generated from human Asp 1 protein by the deletion of its C-terminal TM domain and addition of hexa-histidine tag at its C-terminus.

SQ Sequence 518 AA;

Query Match	100.0%;	Score 406;	DB 22;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 406; Conservative	0;	Mismatches	0;	Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQGDSSGRGYLLEMLIGTPQKLQILVDTGSSNFAVAGTP 60

Db	63	ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
QY	61	HSYIDTYFDTERSSSTYRSKGFVDVTVKYTGGSWTGFVGEDLVTI PKGFNTSFLVNIAITFE	120
Db	123	HSYIDTYFDTERSSSTYRSKGFVDVTVKYTGGSWTGFVGEDLVTI PKGFNTSFLVNIAITFE	182
QY	121	SENFLEPGIKMNGILGLAYATLAKPSSSLETFEFDLSLVTOANI PNVSFMOGAGLPVAGS	180
Db	183	SENFLEPGIKMNGILGLAYATLAKPSSSLETFEFDLSLVTOANI PNVSFMOGAGLPVAGS	242
QY	181	GTNGSLVLGCIIEPSLYKGDIMWTP IKEENYQIEILKLEIGGOSLNLDCREYNADKAIV	240
Db	243	GTNGSLVLGCIIEPSLYKGDIMWTP IKEENYQIEILKLEIGGOSLNLDCREYNADKAIV	302
QY	241	DSGTTILRLPQKVFDAVEAVARASLIPESDGFWTGSQACWNTSETPMSYFPKISITL	300
Db	303	DSGTTILRLPQKVFDAVEAVARASLIPESDGFWTGSQACWNTSETPMSYFPKISITL	362
QY	301	RDENSRSFRITTLPOLYIQPMMGAGLNEYCRFGISPTNALVIGATWMEGFYVIFDRA	360
Db	363	RDENSRSFRITTLPOLYIQPMMGAGLNEYCRFGISPTNALVIGATWMEGFYVIFDRA	422
QY	361	QKRVGFAASPCAETIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL	406
Db	423	QKRVGFAASPCAETIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL	468

Search completed: April 1, 2003, 11:51:27
Job time : 53 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:50:50 ; Search time 18 Seconds
(without alignments)
663.650 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 segs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
& and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	406	100.0	518	4	US-09-434-427-2 Sequence 2, Appli
3	406	100.0	518	4	US-09-548-372D-2 Sequence 2, Appli
4	406	100.0	518	4	US-09-548-367D-2 Sequence 2, Appli
5	59	14.5	514	4	US-09-717-432-2 Sequence 2, Appli
6	59	14.5	514	4	US-09-912-484-2 Sequence 2, Appli
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94	6	1.5	171	4	US-09-134-001C-5205 Sequence 5205, Ap
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266	6	1.5	431	2	US-08-484-434C-14	Sequence 14, Appl	339	6	1.5	579	4	US-09-171-710-4	Sequence 4, Appli
267	6	1.5	431	5	PCT-US91-04036-2	Sequence 2, Appli	340	6	1.5	579	4	US-09-171-710-6	Sequence 6, Appli
268	6	1.5	431	5	PCT-US91-04036-4	Sequence 4, Appli	341	6	1.5	581	2	US-08-989-386-7	Sequence 7, Appli
269	6	1.5	431	5	PCT-US94-05275-2	Sequence 2, Appli	342	6	1.5	584	2	US-08-928-692-13	Sequence 13, Appl
270	6	1.5	431	5	PCT-US94-05275-4	Sequence 4, Appli	343	6	1.5	584	4	US-09-339-972-13	Sequence 13, Appl
271	6	1.5	433	4	US-09-705-448-3	Sequence 3, Appli	344	6	1.5	586	4	US-09-504-358-20	Sequence 20, Appl
272	6	1.5	437	4	US-09-353-332-2	Sequence 2, Appli	345	6	1.5	586	4	US-09-954-314-20	Sequence 44, Appl
273	6	1.5	445	4	US-08-974-691-6	Sequence 6, Appli	346	6	1.5	591	4	US-09-352-159-44	Sequence 46, Appl
274	6	1.5	451	4	US-08-974-691-2	Sequence 2, Appli	347	6	1.5	591	4	US-09-352-159-46	Sequence 42, Appl
275	6	1.5	452	1	US-08-275-488A-2	Sequence 2, Appli	348	6	1.5	598	4	US-09-352-159-42	Sequence 36, Appl
276	6	1.5	452	1	US-08-275-490-2	Sequence 2, Appli	349	6	1.5	600	4	US-09-352-159-36	Sequence 38, Appl
277	6	1.5	452	1	US-08-446-380-2	Sequence 2, Appli	350	6	1.5	600	4	US-09-352-159-38	Sequence 13, Appl
278	6	1.5	452	1	US-08-446-374-2	Sequence 2, Appli	351	6	1.5	600	4	US-09-423-468A-13	Sequence 42, Appl
279	6	1.5	452	1	US-08-446-382-2	Sequence 2, Appli	352	6	1.5	601	4	US-09-398-395A-42	Sequence 95, Appl
280	6	1.5	452	1	US-08-445-801-2	Sequence 2, Appli	353	6	1.5	604	1	US-08-224-657-84	Sequence 84, Appl
281	6	1.5	452	1	US-08-275-487-2	Sequence 15, Appli	354	6	1.5	604	1	US-08-224-657-95	Sequence 98, Appl
282	6	1.5	452	4	US-09-323-872A-15	Sequence 2, Appli	355	6	1.5	604	1	US-08-224-657-98	Sequence 84, Appl
283	6	1.5	452	5	PCT-US95-08919-2	Sequence 12, Appl	356	6	1.5	604	4	US-09-354-138-84	Sequence 95, Appl
284	6	1.5	453	1	US-08-275-488A-12	Sequence 12, Appl	357	6	1.5	604	4	US-09-354-138-95	Sequence 98, Appl
285	6	1.5	453	1	US-08-446-380-12	Sequence 12, Appl	358	6	1.5	607	2	US-08-472-534-5	Sequence 5, Appli
286	6	1.5	453	1	US-08-446-380-12	Sequence 12, Appl	359	6	1.5	607	4	US-09-271-778-1	Sequence 1, Appli
287	6	1.5	453	1	US-08-446-382-12	Sequence 12, Appl	360	6	1.5	609	4	US-09-788-871-1	Sequence 6, Appli
288	6	1.5	453	1	US-08-445-801-12	Sequence 12, Appl	361	6	1.5	609	4	US-09-821-717B-6	Sequence 11, Appl
289	6	1.5	453	1	US-08-275-487-12	Sequence 12, Appl	362	6	1.5	610	1	US-08-119-262B-6	Sequence 6, Appli
290	6	1.5	453	5	PCT-US95-08919-12	Sequence 1, Appli	363	6	1.5	610	1	US-08-135-929A-11	Sequence 11, Appl
291	6	1.5	457	4	US-09-124-238A-1	Sequence 10, Appl	364	6	1.5	610	1	US-08-234-265A-11	Sequence 5, Appli
292	6	1.5	457	4	US-09-124-238A-10	Sequence 3838, Ap	365	6	1.5	612	4	US-09-516-914-5	Sequence 33, Appl
293	6	1.5	457	4	US-09-134-001C-3838	Sequence 1, Appli	366	6	1.5	629	1	US-08-250-740-33	Sequence 2, Appli
294	6	1.5	457	4	US-09-721-975-1	Sequence 10, Appl	367	6	1.5	629	1	US-07-695-472B-2	Sequence 13, Appl
295	6	1.5	457	4	US-09-721-975-10	Sequence 3, Appli	368	6	1.5	668	4	US-09-149-879-13	Sequence 264, App
296	6	1.5	461	1	US-08-672-571A-3	Sequence 25, Appl	369	6	1.5	672	1	US-07-841-651-2	Sequence 3, Appli
297	6	1.5	461	4	US-09-102-528-25	Sequence 18, Appl	370	6	1.5	672	1	US-08-204-656B-10	Sequence 10, Appl
298	6	1.5	462	2	US-08-299-351-1	Sequence 10, Appl	371	6	1.5	687	1	US-08-470-702-10	Sequence 10, Appl
299	6	1.5	462	2	US-08-371-377-18	Sequence 2, Appli	372	6	1.5	687	1	US-08-467-831-10	Sequence 75, Appl
300	6	1.5	462	4	US-09-309-572-10	Sequence 2, Appli	373	6	1.5	687	1	US-08-947-965-75	Sequence 12, Appl
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302	6	1.5	470	1	US-08-471-496-2	Sequence 2, Appli	375	6	1.5	687	1	US-09-308-179B-1	Sequence 5, Appli
303	6	1.5	470	2	US-08-894-840-2	Sequence 2, Appli	376	6	1.5	687	1	US-07-716-827C-5	Sequence 23, Appl
304	6	1.5	470	3	US-09-139-675-2	Sequence 2, Appli	377	6	1.5	687	1	US-08-380-182-23	Sequence 11, Appl
305	6	1.5	470	3	US-08-583-318-5	Sequence 5, Appli	378	6	1.5	718	2	US-08-677-734A-12	Sequence 12, Appl
306	6	1.5	479	1	US-09-305-681-2	Sequence 2, Appli	379	6	1.5	775	4	US-09-097-053-12	Sequence 9, Appli
307	6	1.5	480	4	US-09-444-728-2	Sequence 4, Appli	380	6	1.5	795	1	US-08-677-734A-9	Sequence 9, Appli
308	6	1.5	488	4	US-09-986-536-2	Sequence 2, Appli	381	6	1.5	820	2	US-09-097-053-10	Sequence 10, Appl
309	6	1.5	489	4	US-08-672-571A-1	Sequence 4, Appli	382	6	1.5	831	4	US-08-677-734A-11	Sequence 11, Appl
310	6	1.5	490	1	US-08-275-490-4	Sequence 4, Appli	383	6	1.5	831	4	US-08-677-734A-12	Sequence 12, Appl
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312	6	1.5	494	1	US-08-446-382-4	Sequence 4, Appli	385	6	1.5	834	2	US-09-097-053-10	Sequence 10, Appl
313	6	1.5	494	1	US-08-445-801-4	Sequence 4, Appli	386	6	1.5	834	4	US-08-867-129-2	Sequence 2, Appli
314	6	1.5	494	1	US-08-275-487-4	Sequence 4, Appli	387	6	1.5	843	2	PCT-US95-08919-4	Sequence 4, Appli
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413	6	1.5	933	4	US-09-271-438A-9	Sequence 9, Appli
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423	6	1.5	1097	2	US-08-680-326-39	Sequence 39, Appl
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428	6	1.5	1220	2	US-08-843-530B-36	Sequence 36, Appl
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457	6	1.5	1638	4	US-09-071-035-262	Sequence 262, App
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463	6	1.5	2013	2	US-08-384-616-12	Sequence 12, Appl
464	6	1.5	2013	2	US-08-904-686A-12	Sequence 12, Appl
465	6	1.5	2013	4	US-09-315-850-12	Sequence 12, Appl
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488	6	1.5	2887	4	US-08-462-467B-8	Sequence 8, Appli
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493	6	1.5	3010	2	US-08-384-616-14	Sequence 2, Appli
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511	5	1.2	5	6	5276016-17	Patent No. 5276016
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538	5	1.2	9	2	US-08-340-283-174	Sequence 174, App
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543	5	1.2	9	3	US-09-231-797-81	Sequence 81, Appl
544	5	1.2	9	3	US-08-422-093-20	Sequence 20, Appl
545	5	1.2	9	3	US-08-934-224-81	Sequence 81, Appl
546	5	1.2	9	3	US-08-933-843-81	Sequence 81, Appl
547	5	1.2	9	3	US-08-422-112-20	Sequence 20, Appl
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564	5	1.2	11	4	US-08-875-309-12	Sequence 12, Appl
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835	5	1.2	34	1	US-08-174-745A-12	Sequence 12, Appl	908	5	1.2	38	1	US-08-189-331-109	Sequence 109, App
836	5	1.2	34	1	US-08-449-500-2	Sequence 2, Appli	909	5	1.2	38	2	US-08-471-939-109	Sequence 109, App
837	5	1.2	34	1	US-08-449-500-23	Sequence 23, Appl	910	5	1.2	38	2	US-08-471-800-109	Sequence 109, App
838	5	1.2	34	1	US-08-449-500-24	Sequence 24, Appl	911	5	1.2	38	2	US-08-471-068-109	Sequence 109, App
839	5	1.2	34	1	US-08-449-500-35	Sequence 35, Appl	912	5	1.2	38	2	US-08-378-548-13	Sequence 13, Appl
840	5	1.2	34	1	US-08-449-500-36	Sequence 36, Appl	913	5	1.2	39	4	US-09-149-476-538	Sequence 538, App
841	5	1.2	34	1	US-08-449-500-37	Sequence 37, Appl	914	5	1.2	40	1	US-07-868-353A-3	Sequence 3, Appli
842	5	1.2	34	1	US-08-449-500-61	Sequence 61, Appl	915	5	1.2	40	2	US-08-407-804-3	Sequence 3, Appli
843	5	1.2	34	1	US-08-449-500-79	Sequence 79, Appl	916	5	1.2	40	3	US-08-124-807-3	Sequence 3, Appli
844	5	1.2	34	1	US-08-449-317A-2	Sequence 2, Appli	917	5	1.2	41	1	US-08-122-520C-2	Sequence 2, Appli
845	5	1.2	34	1	US-08-449-317A-23	Sequence 23, Appl	918	5	1.2	41	2	US-08-640-847C-35	Sequence 35, Appl
846	5	1.2	34	1	US-08-449-317A-24	Sequence 24, Appl	919	5	1.2	41	4	US-08-858-207A-294	Sequence 294, App
847	5	1.2	34	1	US-08-449-317A-35	Sequence 35, Appl	920	5	1.2	41	5	PCT-US93-08744-3	Sequence 3, Appli
848	5	1.2	34	1	US-08-449-317A-36	Sequence 36, Appl	921	5	1.2	42	1	US-08-293-778-13	Sequence 13, Appl
849	5	1.2	34	1	US-08-449-317A-37	Sequence 37, Appl	922	5	1.2	42	1	US-08-293-778-14	Sequence 14, Appl
850	5	1.2	34	1	US-08-449-317A-61	Sequence 61, Appl	923	5	1.2	42	2	US-08-143-311B-4	Sequence 4, Appli
851	5	1.2	34	1	US-08-449-317A-79	Sequence 79, Appl	924	5	1.2	42	4	US-09-131-750-27	Sequence 27, Appl
852	5	1.2	34	2	US-08-477-022-2	Sequence 2, Appli	925	5	1.2	42	4	US-08-753-851-4	Sequence 4, Appli
853	5	1.2	34	2	US-08-477-022-23	Sequence 23, Appl	926	5	1.2	43	1	US-07-998-003A-30	Sequence 30, Appl
854	5	1.2	34	2	US-08-477-022-24	Sequence 24, Appl	927	5	1.2	43	1	US-08-453-274B-30	Sequence 30, Appl
855	5	1.2	34	2	US-08-477-022-35	Sequence 35, Appl	928	5	1.2	43	1	US-08-453-695A-30	Sequence 30, Appl
856	5	1.2	34	2	US-08-477-022-36	Sequence 36, Appl	929	5	1.2	43	1	US-08-268-161A-30	Sequence 30, Appl
857	5	1.2	34	2	US-08-477-022-37	Sequence 37, Appl	930	5	1.2	43	2	US-08-488-161-53	Sequence 53, Appl
858	5	1.2	34	2	US-08-477-022-61	Sequence 61, Appl	931	5	1.2	43	2	US-08-453-702A-30	Sequence 30, Appl
859	5	1.2	34	2	US-08-477-022-79	Sequence 79, Appl	932	5	1.2	43	3	US-09-273-685-53	Sequence 53, Appl
860	5	1.2	34	2	US-08-195-947-12	Sequence 12, Appl	933	5	1.2	43	3	US-09-099-639-30	Sequence 30, Appl
861	5	1.2	34	2	US-08-449-447-2	Sequence 2, Appli	934	5	1.2	43	5	PCT-US93-12588-30	Sequence 30, Appl
862	5	1.2	34	2	US-08-449-447-23	Sequence 23, Appl	935	5	1.2	43	5	PCT-US95-08071-30	Sequence 30, Appl
863	5	1.2	34	2	US-08-449-447-24	Sequence 24, Appl	936	5	1.2	43	5	PCT-US95-11934-53	Sequence 53, Appl
864	5	1.2	34	2	US-08-449-447-35	Sequence 35, Appl	937	5	1.2	44	6	5188961-4	Patent No. 5188961
865	5	1.2	34	2	US-08-449-447-36	Sequence 36, Appl	938	5	1.2	45	1	US-08-237-418-1	Sequence 1, Appli
866	5	1.2	34	2	US-08-449-447-37	Sequence 37, Appl	939	5	1.2	45	2	US-08-472-244-7	Sequence 7, Appli
867	5	1.2	34	2	US-08-449-447-61	Sequence 61, Appl	940	5	1.2	45	4	US-08-602-999A-41	Sequence 41, Appl
868	5	1.2	34	2	US-08-433-885-12	Sequence 12, Appl	941	5	1.2	45	4	US-08-468-337-1	Sequence 1, Appli
869	5	1.2	34	2	US-08-184-328-2	Sequence 2, Appli	942	5	1.2	45	4	US-08-227-865-41	Sequence 41, Appl
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871	5	1.2	34	2	US-08-184-328-24	Sequence 24, Appl	944	5	1.2	45	4	US-09-227-357-262	Sequence 262, App
872	5	1.2	34	2	US-08-184-328-35	Sequence 35, Appl	945	5	1.2	46	4	US-09-261-855-27	Sequence 27, Appl
873	5	1.2	34	2	US-08-184-328-36	Sequence 36, Appl	946	5	1.2	46	4	US-08-469-260A-256	Sequence 256, App
874	5	1.2	34	2	US-08-184-328-37	Sequence 37, Appl	947	5	1.2	48	1	US-08-548-540-98	Sequence 98, Appl
875	5	1.2	34	2	US-08-184-328-61	Sequence 61, Appl	948	5	1.2	48	6	5219996-4	Patent No. 5219996
876	5	1.2	34	2	US-08-184-328-79	Sequence 79, Appl	949	5	1.2	48	6	5219996-5	Patent No. 5219996
877	5	1.2	34	2	US-08-751-305-6	Sequence 6, Appli	950	5	1.2	48	6	5219996-7	Patent No. 5219996
878	5	1.2	34	2	US-08-433-908B-12	Sequence 12, Appl	951	5	1.2	48	6	5219996-8	Patent No. 5219996
879	5	1.2	34	2	US-08-521-097-2	Sequence 2, Appli	952	5	1.2	49	1	US-08-222-616-8	Sequence 8, Appli
880	5	1.2	34	2	US-08-521-097-23	Sequence 23, Appl	953	5	1.2	49	2	US-08-693-274A-13	Sequence 13, Appl
881	5	1.2	34	2	US-08-521-097-24	Sequence 24, Appl	954	5	1.2	49	2	US-08-876-882-4	Sequence 4, Appli
882	5	1.2	34	2	US-08-521-097-35	Sequence 35, Appl	955	5	1.2	49	3	US-09-020-299-1	Sequence 1, Appli
883	5	1.2	34	2	US-08-521-097-36	Sequence 36, Appl	956	5	1.2	49	3	US-09-020-299-2	Sequence 2, Appli
884	5	1.2	34	2	US-08-521-097-37	Sequence 37, Appl	957	5	1.2	49	4	US-09-155-107-9	Sequence 9, Appli
885	5	1.2	34	2	US-08-521-097-61	Sequence 61, Appl	958	5	1.2	49	4	US-09-155-107-10	Sequence 10, Appl
886	5	1.2	34	2	US-08-521-097-79	Sequence 79, Appl	959	5	1.2	49	4	US-09-155-107-11	Sequence 11, Appl
887	5	1.2	34	2	US-08-410-614-12	Sequence 12, Appl	960	5	1.2	49	4	US-09-155-107-12	Sequence 12, Appl
888	5	1.2	34	4	US-09-215-212-13	Sequence 13, Appl	961	5	1.2	49	4	US-08-446-648-8	Sequence 8, Appli
889	5	1.2	34	4	US-09-301-978C-25	Sequence 25, Appl	962	5	1.2	49	4	US-08-315-928-4	Sequence 4, Appli
890	5	1.2	34	4	PCT-US94-04361-52	Sequence 52, Appl	963	5	1.2	49	4	US-09-542-749A-4	Sequence 4, Appli
891	5	1.2	34	5	US-08-190-802A-255	Sequence 255, App	964	5	1.2	49	5	PCT-US95-04228-8	Sequence 8, Appli
892	5	1.2	35	1	US-08-477-346-255	Sequence 255, App	965	5	1.2	49	6	5252477-4	Patent No. 5252477
893	5	1.2	35	4	US-09-380-061B-10	Sequence 10, Appl	966	5	1.2	50	1	US-08-450-945-73	Sequence 73, Appl
894	5	1.2	35	4	US-08-473-089-255	Sequence 255, App	967	5	1.2	50	4	US-08-976-161-73	Sequence 73, Appl
895	5	1.2	35	4	US-08-487-072A-255	Sequence 255, App	968	5	1.2	51	2	US-08-821-619-3	Sequence 3, Appli
896	5	1.2	35	4	US-09-152-060-112	Sequence 112, App	969	5	1.2	52	1	US-08-294-189-17	Sequence 17, Appl
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898	5	1.2	36	1	US-08-411-098-15	Sequence 15, Appl	971	5	1.2	52	3	US-08-524-694A-5	Sequence 5, Appli
899	5	1.2	36	2	US-08-505-617-4	Sequence 4, Appli	972	5	1.2	52	3	US-08-725-459B-76	Sequence 76, Appl
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901	5	1.2	36	2	US-08-944-483-26	Sequence 26, Appl	974	5	1.2	52	4	US-09-655-270A-37	Sequence 37, Appl
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977	5	1.2	53	4	US-09-345-293-4	Sequence 4, Appli
978	5	1.2	53	4	US-09-149-476-439	Sequence 439, App
979	5	1.2	54	1	US-08-237-418-6	Sequence 6, Appli
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984	5	1.2	54	5	PCT-US95-04228-26	Sequence 26, Appli
985	5	1.2	55	4	US-08-858-207A-511	Sequence 511, App
986	5	1.2	55	4	US-08-469-260A-493	Sequence 493, App
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994	5	1.2	60	1	US-08-688-675-10	Sequence 10, Appli
995	5	1.2	60	3	US-08-477-860C-10	Sequence 11, Appli
996	5	1.2	60	3	US-08-468-011A-11	Sequence 3, Appli
997	5	1.2	60	4	US-08-468-337-3	Sequence 11, Appli
998	5	1.2	60	4	US-09-236-468A-11	Patent No. 518961
999	5	1.2	60	6	518961-1	Sequence 41, Appli
1000	5	1.2	61	2	US-08-867-087B-41	

ALIGNMENTS

RESULT 1
US-08-999-723-2
; Sequence 2, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-999-723-2

Query Match 100.0%; Score 406; DB 3; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	183	SENFPLPGIKWNGILGLAYATLAK	PSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS	242
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QY	241	DSGTTLLRLPQKVFDAV	EAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISITYL	300
DB	303	DSGTTLLRLPQKVFDAV	EAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISITYL	362

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DB	423	OKRVGFAASPCAIEIAGAV	SEISGPFSTEDVASNCVPAQSLSEPII	468

RESULT 2
US-09-434-427-2
; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; EARLIER FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-434-427-2

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	303	DSGTTLLRLPQKVFDAV	EAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISITYL	362
QY	301	RDENSSRSFRITILPOLYIQPM	GAGLNEYECYRFGISPTNALVIGATVMEGFYVIFDRA	360
DB	363	RDENSSRSFRITILPOLYIQPM	GAGLNEYECYRFGISPTNALVIGATVMEGFYVIFDRA	422
QY	361	OKRVGFAASPCAIEIAGAV	SEISGPFSTEDVASNCVPAQSLSEPII	406
DB	423	OKRVGFAASPCAIEIAGAV	SEISGPFSTEDVASNCVPAQSLSEPII	468

RESULT 3
US-09-548-372D-2
; Sequence 2, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-2

Query Match 100.0%; Score 406; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTP 122
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Db 363 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
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Db 423 QKRVGFAASPCAIEIAGAIVSEISGPFSTEDVASNCVPAQSLSEPII 468

RESULT 4
US-09-548-367D-2
; Sequence 2, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-2

Query Match 100.0%; Score 406; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 243 GTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIETLKLEIGGQSLNLDCREYNADKAIY 302
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Db 303 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIYL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFAASPCAIEIAGAIVSEISGPFSTEDVASNCVPAQSLSEPII 406
Db 423 QKRVGFAASPCAIEIAGAIVSEISGPFSTEDVASNCVPAQSLSEPII 468

RESULT 5
US-09-717-432-2
; Sequence 2, Application US/09717432
; Patent No. 6291223
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: CHRISTIE, GARY
; APPLICANT: POWELL, DAVID J.
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-717-432-2

Query Match 14.5%; Score 59; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 FSMOMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIETLKLEIGGQ 224
Db 224 FSMOMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIETLKLEIGGQ 282


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RESULT 6
US-09-912-484-2
; Sequence 2, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaotong
; APPLICANT: Powell, David J.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mAsp1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/717,432
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-912-484-2
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Query Match 14.5%; Score 59; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 224 FSMQMGAGLPVAGSGTNGSLVLGIEPSLYKGDIMWTPIKEEWYQIEILKLEIGGQ 282

RESULT 7
US-09-548-372D-28
; Sequence 28, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-28
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Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 45 ILVDTGSSNFAV 56
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Db 62 ILVDTGSSNFAV 73

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; Sequence 28, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-28

Query Match 3.0%; Score 12; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 45 ILVDTGSSNFAV 56
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Db 62 ILVDTGSSNFAV 73

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RESULT 9
US-09-548-372D-51
; Sequence 51, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-51
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Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 45 ILVDTGSSNFAV 56
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Db 90 ILVDTGSSNFAV 101

RESULT 10

US-09-548-367D-51
; Sequence 51, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-51

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
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Db 90 ILVDTGSSNFAV 101

RESULT 11
US-09-548-372D-26
; Sequence 26, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-26

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Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
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Db 70 ILVDTGSSNFAV 81

RESULT 12
US-09-548-367D-26
; Sequence 26, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-26

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QY 45 ILVDTGSSNFAV 56
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Db 70 ILVDTGSSNFAV 81

RESULT 13
US-09-548-372D-53
; Sequence 53, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-53

Query Match 3.0%; Score 12; DB 4; Length 434;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
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Db 90 ILVDTGSSNFAV 101

RESULT 14

US-09-548-367D-53
; Sequence 53, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-53

Query Match

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Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
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Db 90 ILVDTGSSNFAV 101

RESULT 15

US-09-548-372D-22
; Sequence 22, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-22

Query Match

3.0%; Score 12; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
|||
Db 83 ILVDTGSSNFAV 94

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Job time : 27 secs

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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	406	100.0	518	9	US-09-999-832A-196
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92	406	100.0	518	9	US-10-184-652-72	Sequence 72, Appl

239	406	100.0	518	9	US-10-197-694-72	Sequence 72, Appl	312	12	3.0	453	10	US-09-794-748-30	Sequence 30, Appl
240	406	100.0	518	9	US-10-197-697-72	Sequence 72, Appl	313	12	3.0	453	10	US-09-794-925-30	Sequence 30, Appl
241	406	100.0	518	9	US-10-197-707-72	Sequence 72, Appl	314	12	3.0	453	10	US-09-681-442-30	Sequence 30, Appl
242	406	100.0	518	9	US-10-199-303-72	Sequence 72, Appl	315	12	3.0	459	10	US-09-794-927-24	Sequence 24, Appl
243	406	100.0	518	9	US-10-199-318-72	Sequence 72, Appl	316	12	3.0	459	10	US-09-794-927-32	Sequence 32, Appl
244	406	100.0	518	9	US-10-199-458-72	Sequence 72, Appl	317	12	3.0	459	10	US-09-795-847-24	Sequence 24, Appl
245	406	100.0	518	9	US-10-199-462-72	Sequence 72, Appl	318	12	3.0	459	10	US-09-795-847-32	Sequence 32, Appl
246	406	100.0	518	9	US-10-201-324-72	Sequence 72, Appl	319	12	3.0	459	10	US-09-794-743-24	Sequence 24, Appl
247	406	100.0	518	9	US-10-201-328-72	Sequence 72, Appl	320	12	3.0	459	10	US-09-794-743-32	Sequence 32, Appl
248	406	100.0	518	9	US-10-201-527-72	Sequence 72, Appl	321	12	3.0	459	10	US-09-794-748-24	Sequence 24, Appl
249	406	100.0	518	9	US-10-201-528-72	Sequence 72, Appl	322	12	3.0	459	10	US-09-794-748-32	Sequence 32, Appl
250	406	100.0	518	9	US-10-201-529-72	Sequence 72, Appl	323	12	3.0	459	10	US-09-794-925-24	Sequence 24, Appl
251	406	100.0	518	9	US-10-201-530-72	Sequence 72, Appl	324	12	3.0	459	10	US-09-794-925-32	Sequence 32, Appl
252	406	100.0	518	9	US-10-202-408-72	Sequence 72, Appl	325	12	3.0	459	10	US-09-681-442-24	Sequence 24, Appl
253	406	100.0	518	9	US-10-202-409-72	Sequence 72, Appl	326	12	3.0	459	10	US-09-681-442-32	Sequence 32, Appl
254	406	100.0	518	9	US-10-202-411-72	Sequence 72, Appl	327	12	3.0	476	10	US-09-794-927-6	Sequence 6, Appl
255	406	100.0	518	9	US-10-202-472-72	Sequence 72, Appl	328	12	3.0	476	10	US-09-795-847-6	Sequence 6, Appl
256	406	100.0	518	9	US-10-205-502-72	Sequence 72, Appl	329	12	3.0	476	10	US-09-794-743-6	Sequence 6, Appl
257	406	100.0	518	9	US-10-205-507-72	Sequence 72, Appl	330	12	3.0	476	10	US-09-794-748-6	Sequence 6, Appl
258	406	100.0	518	9	US-10-205-511-72	Sequence 72, Appl	331	12	3.0	476	10	US-09-794-925-6	Sequence 6, Appl
259	406	100.0	518	9	US-10-205-902-72	Sequence 72, Appl	332	12	3.0	476	10	US-09-681-442-6	Sequence 6, Appl
260	406	100.0	518	9	US-10-205-907-72	Sequence 72, Appl	333	12	3.0	488	9	US-09-795-903A-2	Sequence 2, Appl
261	406	100.0	518	9	US-09-918-585A-196	Sequence 196, App	334	12	3.0	488	10	US-09-796-264-2	Sequence 2, Appl
262	406	100.0	518	9	US-10-194-456-72	Sequence 72, Appl	335	12	3.0	488	10	US-09-845-226-2	Sequence 2, Appl
263	406	100.0	518	9	US-10-196-758-72	Sequence 72, Appl	336	12	3.0	501	9	US-09-969-671A-2	Sequence 2, Appl
264	406	100.0	518	9	US-10-198-770-72	Sequence 72, Appl	337	12	3.0	501	10	US-09-794-927-4	Sequence 4, Appl
265	406	100.0	518	9	US-10-199-308-72	Sequence 72, Appl	338	12	3.0	501	10	US-09-794-927-8	Sequence 8, Appl
266	406	100.0	518	9	US-10-200-617-72	Sequence 72, Appl	339	12	3.0	501	10	US-09-795-847-4	Sequence 4, Appl
267	406	100.0	518	9	US-10-205-893-72	Sequence 72, Appl	340	12	3.0	501	10	US-09-795-847-8	Sequence 8, Appl
268	406	100.0	518	9	US-10-205-897-72	Sequence 72, Appl	341	12	3.0	501	10	US-09-794-743-4	Sequence 4, Appl
269	406	100.0	518	10	US-09-794-927-2	Sequence 2, Appl	342	12	3.0	501	10	US-09-794-743-8	Sequence 8, Appl
270	406	100.0	518	10	US-09-795-847-2	Sequence 2, Appl	343	12	3.0	501	10	US-09-794-748-4	Sequence 4, Appl
271	406	100.0	518	10	US-09-794-743-2	Sequence 2, Appl	344	12	3.0	501	10	US-09-794-748-8	Sequence 8, Appl
272	406	100.0	518	10	US-09-794-748-2	Sequence 2, Appl	345	12	3.0	501	10	US-09-794-925-4	Sequence 4, Appl
273	406	100.0	518	10	US-09-794-925-2	Sequence 2, Appl	346	12	3.0	501	10	US-09-794-925-8	Sequence 8, Appl
274	406	100.0	518	10	US-09-215-450-19	Sequence 19, Appl	347	12	3.0	501	10	US-09-681-442-4	Sequence 4, Appl
275	406	100.0	518	10	US-09-681-442-2	Sequence 2, Appl	348	12	3.0	501	10	US-09-681-442-8	Sequence 8, Appl
276	406	100.0	518	12	US-10-052-586-72	Sequence 72, Appl	349	12	3.0	503	9	US-09-795-903A-3	Sequence 3, Appl
277	373	91.9	423	9	US-09-470-954A-46	Sequence 46, Appl	350	12	3.0	503	10	US-09-796-264-3	Sequence 3, Appl
278	50	12.3	50	10	US-09-864-761-49075	Sequence 49075, A	351	12	3.0	503	10	US-09-845-226-3	Sequence 3, Appl
279	12	3.0	425	10	US-09-794-927-28	Sequence 28, Appl	352	12	3.0	774	9	US-09-969-671A-4	Sequence 4, Appl
280	12	3.0	425	10	US-09-795-847-28	Sequence 28, Appl	353	9	2.2	322	9	US-09-470-954A-47	Sequence 47, Appl
281	12	3.0	425	10	US-09-794-743-28	Sequence 28, Appl	354	9	2.2	401	9	US-09-924-340-24	Sequence 24, Appl
282	12	3.0	425	10	US-09-794-748-28	Sequence 28, Appl	355	9	2.2	401	9	US-09-992-600A-24	Sequence 24, Appl
283	12	3.0	425	10	US-09-794-925-28	Sequence 28, Appl	356	8	2.0	504	10	US-09-919-497-67	Sequence 67, Appl
284	12	3.0	425	10	US-09-681-442-28	Sequence 28, Appl	357	8	2.0	548	10	US-09-741-669-413	Sequence 413, App
285	12	3.0	428	10	US-09-794-927-51	Sequence 51, Appl	358	7	1.7	21	9	US-09-974-879-293	Sequence 293, App
286	12	3.0	428	10	US-09-795-847-51	Sequence 51, Appl	359	7	1.7	25	10	US-09-864-761-45398	Sequence 45398, A
287	12	3.0	428	10	US-09-794-743-51	Sequence 51, Appl	360	7	1.7	34	9	US-09-948-820-94	Sequence 94, Appl
288	12	3.0	428	10	US-09-794-748-51	Sequence 51, Appl	361	7	1.7	50	9	US-09-974-879-291	Sequence 291, App
289	12	3.0	428	10	US-09-794-925-51	Sequence 51, Appl	362	7	1.7	60	8	US-08-914-350-7	Sequence 7, Appl
290	12	3.0	428	10	US-09-681-442-51	Sequence 51, Appl	363	7	1.7	95	10	US-09-734-569-52	Sequence 52, Appl
291	12	3.0	433	10	US-09-794-927-26	Sequence 26, Appl	364	7	1.7	175	10	US-09-864-761-46612	Sequence 46612, A
292	12	3.0	433	10	US-09-795-847-26	Sequence 26, Appl	365	7	1.7	262	10	US-09-925-302-522	Sequence 522, App
293	12	3.0	433	10	US-09-794-743-26	Sequence 26, Appl	366	7	1.7	265	9	US-09-866-050A-655	Sequence 655, App
294	12	3.0	433	10	US-09-794-748-26	Sequence 26, Appl	367	7	1.7	306	10	US-09-741-669-456	Sequence 456, App
295	12	3.0	433	10	US-09-681-442-26	Sequence 26, Appl	368	7	1.7	320	8	US-08-914-350-2	Sequence 2, Appl
296	12	3.0	433	10	US-09-681-442-26	Sequence 26, Appl	369	7	1.7	323	9	US-09-948-820-85	Sequence 85, Appl
297	12	3.0	434	10	US-09-794-927-53	Sequence 53, Appl	370	7	1.7	326	9	US-09-795-903A-31	Sequence 31, Appl
298	12	3.0	434	10	US-09-795-847-53	Sequence 53, Appl	371	7	1.7	326	10	US-09-796-264-31	Sequence 31, Appl
299	12	3.0	434	10	US-09-794-743-53	Sequence 53, Appl	372	7	1.7	326	10	US-09-845-226-31	Sequence 31, Appl
300	12	3.0	434	10	US-09-794-748-53	Sequence 53, Appl	373	7	1.7	327	10	US-09-734-569-156	Sequence 156, App
301	12	3.0	434	10	US-09-794-925-53	Sequence 53, Appl	374	7	1.7	363	10	US-09-905-173-36	Sequence 36, App
302	12	3.0	434	10	US-09-681-442-53	Sequence 53, Appl	375	7	1.7	388	10	US-09-215-450-23	Sequence 23, Appl
303	12	3.0	446	10	US-09-794-927-22	Sequence 22, Appl	376	7	1.7	451	9	US-10-042-431-43	Sequence 43, Appl
304	12	3.0	446	10	US-09-795-847-22	Sequence 22, Appl	377	7	1.7	451	9	US-09-759-130B-413	Sequence 413, App
305	12	3.0	446	10	US-09-794-743-22	Sequence 22, Appl	378	7	1.7	470	9	US-10-042-431-69	Sequence 69, Appl
306	12	3.0	446	10	US-09-794-748-22	Sequence 22, Appl	379	7	1.7	470	9	US-09-759-130B-439	Sequence 439, App
307	12	3.0	446	10	US-09-794-925-22	Sequence 22, Appl	380	7	1.7	615	10	US-09-862-027-49	Sequence 49, Appl
308	12	3.0	446	10	US-09-681-442-22	Sequence 22, Appl	381	7	1.7	1429	9	US-09-953-407-1	Sequence 1, Appl
309	12	3.0	453	10	US-09-794-927-30	Sequence 30, Appl	382	6	1.5	12	8	US-08-424-550B-446	Sequence 446, App
310	12	3.0	453	10	US-09-795-847-30	Sequence 30, Appl	383	6	1.5	14	10	US-09-918-171A-28	Sequence 28, Appl
311	12	3.0	453	10	US-09-794-743-30	Sequence 30, Appl	384	6	1.5	19	10	US-09-918-171A-24	Sequence 24, Appl

385	6	1.5	31	9	US-09-996-069-12	Sequence 12, Appl	458	6	1.5	207	9	US-10-230-414-76	Sequence 76, Appl
386	6	1.5	32	10	US-09-864-761-41359	Sequence 41359, A	459	6	1.5	210	9	US-10-060-765-2	Sequence 2, Appl1
387	6	1.5	35	10	US-09-864-761-36036	Sequence 36036, A	460	6	1.5	210	9	US-10-090-983-7	Sequence 7, Appl1
388	6	1.5	35	10	US-09-864-761-39580	Sequence 39580, A	461	6	1.5	211	9	US-10-222-577-5	Sequence 5, Appl1
389	6	1.5	36	10	US-09-764-877-1258	Sequence 1258, Ap	462	6	1.5	211	9	US-10-222-578-5	Sequence 5, Appl1
390	6	1.5	38	10	US-09-873-106B-16	Sequence 16, Appl	463	6	1.5	211	10	US-09-790-045-5	Sequence 5, Appl1
391	6	1.5	43	9	US-09-809-391-524	Sequence 524, App	464	6	1.5	214	9	US-09-925-299-864	Sequence 864, App
392	6	1.5	47	10	US-09-864-761-43013	Sequence 43013, A	465	6	1.5	214	10	US-09-925-299-864	Sequence 864, App
393	6	1.5	48	10	US-09-864-761-48227	Sequence 48227, A	466	6	1.5	218	9	US-09-738-626-4670	Sequence 4670, Ap
394	6	1.5	49	10	US-09-864-761-35522	Sequence 35522, A	467	6	1.5	220	9	US-10-001-054-56	Sequence 56, Appl
395	6	1.5	55	10	US-09-908-711-80	Sequence 80, Appl1	468	6	1.5	220	10	US-09-220-920-26	Sequence 26, Appl
396	6	1.5	55	10	US-09-864-761-39275	Sequence 39275, A	469	6	1.5	220	10	US-09-804-615-9	Sequence 9, Appl1
397	6	1.5	55	10	US-09-864-761-40066	Sequence 40066, A	470	6	1.5	222	10	US-09-815-242-10768	Sequence 10768, A
398	6	1.5	57	10	US-09-864-761-41100	Sequence 41100, A	471	6	1.5	234	12	US-10-081-281-119	Sequence 119, App
399	6	1.5	58	9	US-10-079-854-191	Sequence 191, App	472	6	1.5	237	9	US-09-992-598-295	Sequence 295, App
400	6	1.5	58	10	US-09-764-878-191	Sequence 191, App	473	6	1.5	237	9	US-09-989-293A-295	Sequence 295, App
401	6	1.5	59	9	US-09-848-616-141	Sequence 141, App	474	6	1.5	237	9	US-09-989-735-295	Sequence 295, App
402	6	1.5	62	9	US-10-012-542-191	Sequence 191, App	475	6	1.5	237	9	US-09-990-444-295	Sequence 295, App
403	6	1.5	67	10	US-09-864-761-36500	Sequence 36500, A	476	6	1.5	237	9	US-09-989-730-295	Sequence 295, App
404	6	1.5	68	10	US-09-220-920-50	Sequence 50, Appl1	477	6	1.5	237	9	US-09-990-436-295	Sequence 295, App
405	6	1.5	68	10	US-09-864-761-37739	Sequence 37739, A	478	6	1.5	237	9	US-09-991-181-295	Sequence 295, App
406	6	1.5	78	10	US-09-881-752A-120	Sequence 120, App	479	6	1.5	237	9	US-09-993-687-295	Sequence 295, App
407	6	1.5	82	10	US-09-864-761-37785	Sequence 37785, A	480	6	1.5	237	9	US-09-989-734-295	Sequence 295, App
408	6	1.5	87	10	US-09-220-920-115	Sequence 115, App	481	6	1.5	237	9	US-09-997-653-295	Sequence 295, App
409	6	1.5	91	9	US-09-989-920-205	Sequence 205, App	482	6	1.5	237	9	US-10-174-590-222	Sequence 222, App
410	6	1.5	97	9	US-09-925-299-1071	Sequence 1071, Ap	483	6	1.5	237	9	US-10-176-758-222	Sequence 222, App
411	6	1.5	97	10	US-09-925-299-1071	Sequence 1071, Ap	484	6	1.5	237	9	US-10-175-737-222	Sequence 222, App
412	6	1.5	107	10	US-09-220-920-52	Sequence 52, Appl	485	6	1.5	237	9	US-09-983-802-154	Sequence 154, App
413	6	1.5	108	9	US-09-809-391-552	Sequence 552, App	486	6	1.5	237	9	US-09-993-667-295	Sequence 295, App
414	6	1.5	110	10	US-09-867-550-298	Sequence 298, App	487	6	1.5	237	9	US-10-173-706-222	Sequence 222, App
415	6	1.5	113	9	US-10-092-154-974	Sequence 974, App	488	6	1.5	237	9	US-10-175-738-222	Sequence 222, App
416	6	1.5	113	10	US-09-764-847-974	Sequence 974, App	489	6	1.5	237	9	US-10-175-752-222	Sequence 222, App
417	6	1.5	114	9	US-09-738-626-3786	Sequence 3786, Ap	490	6	1.5	237	9	US-10-176-482-222	Sequence 222, App
418	6	1.5	125	9	US-09-738-626-5389	Sequence 5389, Ap	491	6	1.5	237	9	US-10-176-757-222	Sequence 222, App
419	6	1.5	126	9	US-09-764-868-1053	Sequence 1053, Ap	492	6	1.5	237	9	US-10-176-913-222	Sequence 222, App
420	6	1.5	130	9	US-10-101-464A-496	Sequence 496, App	493	6	1.5	237	9	US-10-180-552-222	Sequence 222, App
421	6	1.5	138	10	US-09-912-020-300	Sequence 300, App	494	6	1.5	237	9	US-10-180-557-222	Sequence 222, App
422	6	1.5	142	9	US-09-839-894-38	Sequence 38, Appl	495	6	1.5	237	9	US-09-990-438-295	Sequence 295, App
423	6	1.5	144	9	US-10-076-785-50	Sequence 50, Appl	496	6	1.5	237	9	US-09-990-562-295	Sequence 295, App
424	6	1.5	145	10	US-09-915-582-88	Sequence 88, Appl	497	6	1.5	237	9	US-09-997-428-295	Sequence 295, App
425	6	1.5	154	10	US-09-867-550-646	Sequence 646, App	498	6	1.5	237	9	US-09-997-666-295	Sequence 295, App
426	6	1.5	157	9	US-09-981-286A-1	Sequence 1, Appl1	499	6	1.5	237	9	US-10-173-700-222	Sequence 222, App
427	6	1.5	157	9	US-09-809-391-350	Sequence 350, App	500	6	1.5	237	9	US-10-174-572-222	Sequence 222, App
428	6	1.5	163	10	US-09-867-550-522	Sequence 522, App	501	6	1.5	237	9	US-10-174-579-222	Sequence 222, App
429	6	1.5	165	9	US-09-839-894-33	Sequence 33, Appl	502	6	1.5	237	9	US-10-174-582-222	Sequence 222, App
430	6	1.5	165	9	US-09-981-286A-33	Sequence 33, Appl	503	6	1.5	237	9	US-10-174-588-222	Sequence 222, App
431	6	1.5	165	9	US-09-981-286A-34	Sequence 34, Appl	504	6	1.5	237	9	US-10-174-588-222	Sequence 222, App
432	6	1.5	167	9	US-09-764-868-953	Sequence 953, App	505	6	1.5	237	9	US-10-175-739-222	Sequence 222, App
433	6	1.5	167	9	US-09-839-894-4	Sequence 4, Appl1	506	6	1.5	237	9	US-10-175-740-222	Sequence 222, App
434	6	1.5	168	9	US-09-839-894-37	Sequence 37, Appl	507	6	1.5	237	9	US-10-176-488-222	Sequence 222, App
435	6	1.5	169	9	US-09-981-286A-7	Sequence 7, Appl1	508	6	1.5	237	9	US-10-176-492-222	Sequence 222, App
436	6	1.5	173	9	US-09-738-626-6034	Sequence 6034, Ap	509	6	1.5	237	9	US-10-176-747-222	Sequence 222, App
437	6	1.5	173	10	US-09-925-301-1425	Sequence 1425, Ap	510	6	1.5	237	9	US-10-176-750-222	Sequence 222, App
438	6	1.5	174	9	US-09-738-626-4376	Sequence 4376, Ap	511	6	1.5	237	9	US-10-176-985-222	Sequence 222, App
439	6	1.5	174	10	US-09-764-864-904	Sequence 904, App	512	6	1.5	237	9	US-10-176-987-222	Sequence 222, App
440	6	1.5	181	10	US-09-220-920-40	Sequence 40, Appl	513	6	1.5	237	9	US-10-176-991-222	Sequence 222, App
441	6	1.5	184	10	US-09-925-297-737	Sequence 737, App	514	6	1.5	237	9	US-10-176-992-222	Sequence 222, App
442	6	1.5	185	9	US-10-078-770-178	Sequence 178, App	515	6	1.5	237	9	US-10-176-993-222	Sequence 222, App
443	6	1.5	186	9	US-09-809-391-394	Sequence 394, App	516	6	1.5	237	9	US-10-184-658-222	Sequence 222, App
444	6	1.5	187	10	US-09-864-761-35716	Sequence 35716, A	517	6	1.5	237	9	US-09-990-711-295	Sequence 295, App
445	6	1.5	187	10	US-09-864-761-36096	Sequence 36096, A	518	6	1.5	237	9	US-10-173-695-222	Sequence 222, App
446	6	1.5	188	9	US-09-974-879-508	Sequence 508, App	519	6	1.5	237	9	US-10-173-697-222	Sequence 222, App
447	6	1.5	193	10	US-09-764-898-214	Sequence 214, App	520	6	1.5	237	9	US-10-173-705-222	Sequence 222, App
448	6	1.5	196	9	US-09-957-187-8	Sequence 8, Appl1	521	6	1.5	237	9	US-10-174-576-222	Sequence 222, App
449	6	1.5	196	12	US-10-081-281-109	Sequence 109, App	522	6	1.5	237	9	US-10-174-585-222	Sequence 222, App
450	6	1.5	196	12	US-10-081-281-117	Sequence 117, App	523	6	1.5	237	9	US-10-174-586-222	Sequence 222, App
451	6	1.5	200	9	US-09-738-626-4692	Sequence 4692, Ap	524	6	1.5	237	9	US-10-175-747-222	Sequence 222, App
452	6	1.5	200	10	US-09-804-615-2	Sequence 2, Appl1	525	6	1.5	237	9	US-10-176-481-222	Sequence 222, App
453	6	1.5	207	9	US-10-227-884-76	Sequence 76, Appl	526	6	1.5	237	9	US-10-176-485-222	Sequence 222, App
454	6	1.5	207	9	US-10-230-163-76	Sequence 76, Appl	527	6	1.5	237	9	US-10-176-487-222	Sequence 222, App
455	6	1.5	207	9	US-10-149-819-19	Sequence 19, Appl	528	6	1.5	237	9	US-10-176-493-222	Sequence 222, App
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457	6	1.5	207	9	US-10-230-338-76	Sequence 76, Appl	530	6	1.5	237	9	US-10-176-911-222	Sequence 222, App

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689	6	1.5	237	9	US-10-199-317-222	Sequence 222, App	762	6	1.5	237	10	US-09-989-727-295	Sequence 295, App
690	6	1.5	237	9	US-10-199-665-222	Sequence 222, App	763	6	1.5	237	10	US-09-989-732-295	Sequence 295, App
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695	6	1.5	237	9	US-10-201-855-222	Sequence 222, App	768	6	1.5	237	10	US-09-991-163-295	Sequence 295, App
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699	6	1.5	237	9	US-10-202-476-222	Sequence 222, App	772	6	1.5	237	12	US-10-052-586-222	Sequence 222, App
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701	6	1.5	237	9	US-10-202-935-222	Sequence 222, App	774	6	1.5	240	9	US-09-908-193-43	Sequence 43, Appl
702	6	1.5	237	9	US-10-202-936-222	Sequence 222, App	775	6	1.5	240	9	US-09-860-836B-15	Sequence 15, Appl
703	6	1.5	237	9	US-10-202-939-222	Sequence 222, App	776	6	1.5	241	10	US-09-925-297-542	Sequence 542, App
704	6	1.5	237	9	US-10-205-504-222	Sequence 222, App	777	6	1.5	242	9	US-10-042-141-101	Sequence 101, App
705	6	1.5	237	9	US-10-205-509-222	Sequence 222, App	778	6	1.5	242	10	US-09-726-643-101	Sequence 101, App
706	6	1.5	237	9	US-10-205-895-222	Sequence 222, App	779	6	1.5	244	1	US-08-722-570-1	Sequence 1, Appl
707	6	1.5	237	9	US-10-205-899-222	Sequence 222, App	780	6	1.5	247	9	US-09-866-050A-687	Sequence 687, App
708	6	1.5	237	9	US-10-205-900-222	Sequence 222, App	781	6	1.5	248	10	US-09-791-171-60	Sequence 60, Appl
709	6	1.5	237	9	US-10-205-909-222	Sequence 222, App	782	6	1.5	256	9	US-09-738-626-6299	Sequence 6299, Ap
710	6	1.5	237	9	US-09-990-443-295	Sequence 295, App	783	6	1.5	259	9	US-09-991-211-3	Sequence 3, Appl
711	6	1.5	237	9	US-09-990-726-295	Sequence 295, App	784	6	1.5	259	10	US-09-815-242-11603	Sequence 11603, A
712	6	1.5	237	9	US-09-997-559-295	Sequence 295, App	785	6	1.5	260	9	US-09-764-868-992	Sequence 992, App
713	6	1.5	237	9	US-09-997-601-295	Sequence 295, App	786	6	1.5	262	10	US-09-915-582-66	Sequence 66, Appl
714	6	1.5	237	9	US-10-183-002-222	Sequence 222, App	787	6	1.5	264	8	US-08-424-550B-76	Sequence 76, Appl
715	6	1.5	237	9	US-10-184-621-222	Sequence 222, App	788	6	1.5	266	9	US-09-738-626-3657	Sequence 3657, Ap
716	6	1.5	237	9	US-10-184-638-222	Sequence 222, App	789	6	1.5	266	12	US-10-007-693-66	Sequence 66, Appl
717	6	1.5	237	9	US-10-187-752-222	Sequence 222, App	790	6	1.5	273	9	US-09-738-626-4392	Sequence 4392, Ap
718	6	1.5	237	9	US-10-187-887-222	Sequence 222, App	791	6	1.5	274	9	US-09-738-626-6741	Sequence 6741, Ap
719	6	1.5	237	9	US-10-194-461-222	Sequence 222, App	792	6	1.5	276	10	US-09-925-300-11624	Sequence 11624, Ap
720	6	1.5	237	9	US-10-195-892-222	Sequence 222, App	793	6	1.5	277	10	US-09-925-300-1169	Sequence 1169, Ap
721	6	1.5	237	9	US-10-196-751-222	Sequence 222, App	794	6	1.5	281	10	US-09-801-368-278	Sequence 278, App
722	6	1.5	237	9	US-10-197-694-222	Sequence 222, App	795	6	1.5	283	10	US-09-908-711-95	Sequence 95, Appl
723	6	1.5	237	9	US-10-197-697-222	Sequence 222, App	796	6	1.5	284	9	US-09-738-626-3667	Sequence 3667, Ap
724	6	1.5	237	9	US-10-197-707-222	Sequence 222, App	797	6	1.5	289	9	US-10-151-832-6	Sequence 6, Appl
725	6	1.5	237	9	US-10-199-303-222	Sequence 222, App	798	6	1.5	289	9	US-10-151-832-8	Sequence 8, Appl
726	6	1.5	237	9	US-10-199-318-222	Sequence 222, App	799	6	1.5	294	9	US-10-151-832-7	Sequence 7, Appl
727	6	1.5	237	9	US-10-199-458-222	Sequence 222, App	800	6	1.5	302	9	US-10-125-540-421	Sequence 421, App
728	6	1.5	237	9	US-10-199-462-222	Sequence 222, App	801	6	1.5	302	10	US-09-764-870-421	Sequence 421, App
729	6	1.5	237	9	US-10-201-324-222	Sequence 222, App	802	6	1.5	303	10	US-09-854-122-48	Sequence 48, Appl
730	6	1.5	237	9	US-10-201-328-222	Sequence 222, App	803	6	1.5	303	10	US-09-733-569A-15	Sequence 15, Appl
731	6	1.5	237	9	US-10-201-527-222	Sequence 222, App	804	6	1.5	303	10	US-09-882-837-2	Sequence 2, Appl
732	6	1.5	237	9	US-10-201-528-222	Sequence 222, App	805	6	1.5	304	9	US-09-738-626-3743	Sequence 3743, Ap
733	6	1.5	237	9	US-10-201-529-222	Sequence 222, App	806	6	1.5	304	10	US-09-854-122-47	Sequence 47, Appl
734	6	1.5	237	9	US-10-201-530-222	Sequence 222, App	807	6	1.5	309	10	US-09-886-055-149	Sequence 149, App
735	6	1.5	237	9	US-10-202-408-222	Sequence 222, App	808	6	1.5	310	9	US-10-147-761-2	Sequence 2, Appl
736	6	1.5	237	9	US-10-202-409-222	Sequence 222, App	809	6	1.5	310	9	US-10-151-832-3	Sequence 3, Appl
737	6	1.5	237	9	US-10-202-411-222	Sequence 222, App	810	6	1.5	312	9	US-10-151-832-9	Sequence 9, Appl
738	6	1.5	237	9	US-10-202-472-222	Sequence 222, App	811	6	1.5	317	9	US-10-151-832-5	Sequence 5, Appl
739	6	1.5	237	9	US-10-205-502-222	Sequence 222, App	812	6	1.5	324	1	US-08-781-986A-5209	Sequence 5209, Ap
740	6	1.5	237	9	US-10-205-507-222	Sequence 222, App	813	6	1.5	324	10	US-09-854-122-18	Sequence 18, Appl
741	6	1.5	237	9	US-10-205-511-222	Sequence 222, App	814	6	1.5	324	10	US-09-815-242-5392	Sequence 5392, Ap
742	6	1.5	237	9	US-10-205-902-222	Sequence 222, App	815	6	1.5	326	10	US-09-815-242-12264	Sequence 12264, A
743	6	1.5	237	9	US-10-205-907-222	Sequence 222, App	816	6	1.5	328	9	US-09-738-626-5059	Sequence 5059, Ap
744	6	1.5	237	9	US-09-989-729A-295	Sequence 295, App	817	6	1.5	330	10	US-09-815-837-94	Sequence 94, Appl
745	6	1.5	237	9	US-09-990-440-295	Sequence 295, App	818	6	1.5	341	9	US-09-974-879-465	Sequence 465, App
746	6	1.5	237	9	US-09-991-854-295	Sequence 295, App	819	6	1.5	341	10	US-09-873-106B-2	Sequence 2, Appl
747	6	1.5	237	9	US-09-997-349-295	Sequence 295, App	820	6	1.5	342	10	US-09-991-258-10	Sequence 10, Appl
748	6	1.5	237	9	US-09-997-440-295	Sequence 295, App	821	6	1.5	343	8	US-08-424-550B-608	Sequence 608, App
749	6	1.5	237	9	US-09-997-628-295	Sequence 295, App	822	6	1.5	343	10	US-09-864-761-36084	Sequence 36084, A

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828	6	1.5	349	9	US-10-121-049-170	Sequence 170, App
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832	6	1.5	349	9	US-10-176-918-170	Sequence 170, App
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846	6	1.5	353	9	US-10-084-507B-17	Sequence 17, Appl
847	6	1.5	353	9	US-10-084-507B-22	Sequence 22, Appl
848	6	1.5	353	10	US-09-771-063-2	Sequence 2, Appli
849	6	1.5	353	10	US-09-771-063-4	Sequence 4, Appli
850	6	1.5	353	10	US-09-842-316-8	Sequence 8, Appli
851	6	1.5	353	10	US-09-731-030A-19	Sequence 19, Appl
852	6	1.5	353	12	US-10-037-616-23	Sequence 23, Appl
853	6	1.5	355	9	US-09-847-010-16	Sequence 16, Appl
854	6	1.5	355	10	US-09-815-242-13830	Sequence 13830, A
855	6	1.5	357	10	US-09-952-663-17	Sequence 17, Appl
856	6	1.5	361	9	US-10-114-893-88	Sequence 88, Appl
857	6	1.5	365	9	US-09-738-626-6336	Sequence 6336, Ap
858	6	1.5	376	10	US-09-815-242-10160	Sequence 10160, A
859	6	1.5	378	10	US-09-925-301-1208	Sequence 1208, Ap
860	6	1.5	382	9	US-09-738-626-5949	Sequence 5949, Ap
861	6	1.5	382	10	US-09-969-711-2	Sequence 2, Appli
862	6	1.5	386	10	US-09-975-901-4	Sequence 4, Appli
863	6	1.5	388	9	US-09-470-954A-48	Sequence 48, Appl
864	6	1.5	388	10	US-09-815-242-10684	Sequence 10684, A
865	6	1.5	388	10	US-09-215-450-24	Sequence 24, Appl
866	6	1.5	394	9	US-10-165-603-18	Sequence 18, Appl
867	6	1.5	395	9	US-10-094-080-3	Sequence 3, Appli
868	6	1.5	396	9	US-09-470-954A-49	Sequence 49, Appl
869	6	1.5	396	10	US-09-215-450-22	Sequence 22, Appl
870	6	1.5	396	10	US-09-953-956-13	Sequence 13, Appl
871	6	1.5	396	12	US-10-114-464-13	Sequence 13, Appl
872	6	1.5	398	9	US-10-215-211-2	Sequence 2, Appli
873	6	1.5	398	9	US-10-011-548-26	Sequence 26, Appl
874	6	1.5	398	9	US-10-199-209-2	Sequence 2, Appli
875	6	1.5	398	10	US-09-854-162-2	Sequence 2, Appli
876	6	1.5	398	10	US-09-912-020-304	Sequence 304, App
877	6	1.5	398	10	US-09-921-667-8	Sequence 8, Appli
878	6	1.5	398	10	US-09-840-707A-4	Sequence 4, Appli
879	6	1.5	403	9	US-09-976-059-23	Sequence 23, Appl
880	6	1.5	403	9	US-09-738-626-5159	Sequence 5159, Ap
881	6	1.5	403	10	US-09-826-508-30	Sequence 30, Appl
882	6	1.5	403	10	US-09-895-686-5	Sequence 5, Appli
883	6	1.5	404	10	US-09-864-761-36208	Sequence 36208, A
884	6	1.5	405	10	US-09-768-781-6	Sequence 6, Appli
885	6	1.5	406	10	US-09-215-450-26	Sequence 26, Appl
886	6	1.5	407	10	US-09-815-242-5348	Sequence 5348, Ap
887	6	1.5	408	9	US-09-804-625-6	Sequence 6, Appli
888	6	1.5	408	9	US-09-749-728B-69	Sequence 69, Appl
889	6	1.5	409	9	US-09-813-398-27	Sequence 27, Appl
890	6	1.5	409	9	US-10-081-051-18	Sequence 18, Appl
891	6	1.5	411	9	US-10-015-536-17	Sequence 17, Appl
892	6	1.5	412	10	US-09-215-450-25	Sequence 25, Appl
893	6	1.5	412	10	US-09-953-956-12	Sequence 12, Appl
894	6	1.5	412	12	US-10-114-464-12	Sequence 12, Appl
895	6	1.5	419	10	US-09-789-919-44	Sequence 44, Appl
896	6	1.5	419	10	US-09-784-911-2	Sequence 2, Appli
897	6	1.5	420	10	US-09-815-242-11001	Sequence 11001, A
898	6	1.5	420	10	US-09-804-073-2	Sequence 2, Appli
899	6	1.5	427	10	US-09-826-508-32	Sequence 32, Appl
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901	6	1.5	427	10	US-09-942-447-4	Sequence 4, Appli
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906	6	1.5	436	10	US-09-815-242-12846	Sequence 12846, A
907	6	1.5	437	9	US-09-738-626-3992	Sequence 3992, Ap
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909	6	1.5	437	12	US-10-016-358-2	Sequence 2, Appli
910	6	1.5	438	9	US-10-078-770-182	Sequence 182, App
911	6	1.5	441	9	US-09-738-626-5156	Sequence 5156, Ap
912	6	1.5	441	12	US-10-081-281-115	Sequence 115, App
913	6	1.5	444	10	US-09-815-242-12376	Sequence 12376, A
914	6	1.5	448	12	US-10-081-281-111	Sequence 111, App
915	6	1.5	454	10	US-09-767-041-30	Sequence 30, Appl
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917	6	1.5	459	10	US-09-815-242-11954	Sequence 11954, A
918	6	1.5	471	10	US-09-912-020-284	Sequence 284, App
919	6	1.5	485	9	US-10-191-398A-5	Sequence 5, Appli
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935	6	1.5	514	9	US-09-738-626-5869	Sequence 5869, Ap
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938	6	1.5	525	9	US-09-978-295A-301	Sequence 301, App
939	6	1.5	525	9	US-09-978-697-301	Sequence 301, App
940	6	1.5	525	9	US-09-978-192A-301	Sequence 301, App
941	6	1.5	525	9	US-09-999-832A-301	Sequence 301, App
942	6	1.5	525	9	US-09-978-189-301	Sequence 301, App
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944	6	1.5	525	9	US-10-176-758-436	Sequence 436, App
945	6	1.5	525	9	US-10-175-737-436	Sequence 436, App
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973	6	1.5	525	9	US-10-173-695-436	Sequence 436, App
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995	6	1.5	525	9	US-10-180-555-436	Sequence 436, App
996	6	1.5	525	9	US-10-180-559-436	Sequence 436, App
997	6	1.5	525	9	US-10-181-000-436	Sequence 436, App
998	6	1.5	525	9	US-10-183-010-436	Sequence 436, App
999	6	1.5	525	9	US-10-183-012-436	Sequence 436, App
1000	6	1.5	525	9	US-10-184-614-436	Sequence 436, App

ALIGNMENTS

RESULT 1
US-09-978-295A-196
; Sequence 196, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James J.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A

; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 HSYIDTYFDTERSSYRSKGFDTVKYTOGSGWTGFVGEDLVITPKGFNTSFLVNIATIFE 120
DB 123 HSYIDTYFDTERSSYRSKGFDTVKYTOGSGWTGFVGEDLVITPKGFNTSFLVNIATIFE 182
QY 121 SENFPLGIKWNGILGLAVATLAKPSSSLETFDLSLVTOANI PNVSQMCGAGLPVAGS 180
DB 183 SENFPLGIKWNGILGLAVATLAKPSSSLETFDLSLVTOANI PNVSQMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDIMWYPIKEWYQIEILKLEIGGOSLNLDCREYNADKATV 240
DB 243 GTNGSLVLGGIEPSLYKGDIMWYPIKEWYQIEILKLEIGGOSLNLDCREYNADKATV 302
QY 241 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFMTGSQILACWTNSETPWSYFPKISITYL 300
DB 303 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFMTGSQILACWTNSETPWSYFPKISITYL 362
QY 301 RDENSRSFRITILPOLYIQPMNGAGLNYECYRFGISPSNALVIGATVMEGFYVIFDRA 360
DB 363 RDENSRSFRITILPOLYIQPMNGAGLNYECYRFGISPSNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSUSEPIL 406
DB 423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSUSEPIL 468

RESULT 2
US-09-886-143-2
; Sequence 2, Application US/09886143
; Patent No. US20020159991A1
; GENERAL INFORMATION:
; APPLICANT: Cordell, Barbara
; APPLICANT: Schimmoller, Frauke
; APPLICANT: Liu, Yu-Wang
; TITLE OF INVENTION: Modulation of A Levels by
; TITLE OF INVENTION: Secretease BACE2
; FILE REFERENCE: SCIOS.022A
; CURRENT APPLICATION NUMBER: US/09/886,143
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/215,729
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

LENGTH: 518
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-143-2

Query Match 100.0%; Score 406; DB 9; length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 423 QKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 468

RESULT 3

US-09-978-697-196
Sequence 196, Application US/09978697
Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
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APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivarov, Ellen
APPLICANT: Fong, Sherman
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APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27

CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 123 HSYIDTYFDTERSSYRSKGFDTVKYTGQSWTGFVGEDLVTIIPKGFNTSFLVNIAIIFE 182
Qy 121 SENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
Qy 181 GTINGGSLVLGGIEPSLYKGDIIWYTPIKEEWYQIETLKLEIGGQSLNDCREYNADKAIV 240
Db 243 GTINGGSLVLGGIEPSLYKGDIIWYTPIKEEWYQIETLKLEIGGQSLNDCREYNADKAIV 302
Qy 241 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIVL 300
Db 303 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIVL 362
Qy 301 RDNSSRSFRITILPOLYIQPMWGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDNSSRSFRITILPOLYIQPMWGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
Qy 361 QKRVGFAASPCAEIAGAVSEISGPFSTEDVASNCVPAQSLSEPIIL 406
Db 423 QKRVGFAASPCAEIAGAVSEISGPFSTEDVASNCVPAQSLSEPIIL 468

RESULT 4
US-09-978-192A-196
; Sequence 196, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697

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Db 123 HSYIDTFDTERSTYRSKGFDTVKYTOGSWTGFVGEDLVITPKGNTSFLVNIATIFE 182
OY 121 SENFPLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTOANIENVESQMCGAGLPVAGS 180
Db 183 SENFPLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTOANIENVESQMCGAGLPVAGS 242
OY 181 GTNGGSLVLGGIEPSLYKGDIMWTPIKEWYVQIEILKLEIGGOSLNLDCREYNADKATV 240
Db 243 GTNGGSLVLGGIEPSLYKGDIMWTPIKEWYVQIEILKLEIGGOSLNLDCREYNADKATV 302
OY 241 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISTYL 300
Db 303 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISTYL 362
OY 301 RDNSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSITNALVIGATVMEGFYVIFDRA 360
Db 363 RDNSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSITNALVIGATVMEGFYVIFDRA 422
OY 361 QKRVGFAASPCAIEIAGAAVSEISGFSTEDVASNCVPAQSLSEPIIL 406
Db 423 QKRVGFAASPCAIEIAGAAVSEISGFSTEDVASNCVPAQSLSEPIIL 468

RESULT 5

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; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PlC63
; CURRENT APPLICATION NUMBER: US/09/999, 832A
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 406; DB 9; length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTRSKGFDVTVKYTOGSWTGFVGEDLVTIIPKGFNTSFLVNIAITFE 120
Db 123 HSYIDTYFDTERSSSTRSKGFDVTVKYTOGSWTGFVGEDLVTIIPKGFNTSFLVNIAITFE 182
QY 121 SENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GINGSLVLGIEPSLYKGDIIWYTPIKEWYYQIEILKLEIGQSLNLDCREYNADKAIV 240

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Db      243 GTNGGSLVLGGIEPSLYKGDWYTPIKEWYYQIEILKLEIGQSLNLDCREYNADKAIIV 302
QY      241 DSGTTLRLPQKVFDAVVEAARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISITYL 300
Db      303 DSGTTLRLPQKVFDAVVEAARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISITYL 362
QY      301 RDENSSRSFRITILPOLYIQPMWAGLNYECYRFGISPTNALVIGATVMEGFYVIFDRA 360
Db      363 RDENSSRSFRITILPOLYIQPMWAGLNYECYRFGISPTNALVIGATVMEGFYVIFDRA 422
QY      361 QKRVGFASPCAIEAGAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
Db      423 QKRVGFASPCAIEAGAVSEISGPFSTEDVASNCVPAQSLSEPIL 468
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RESULT 6

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US-09-978-189-196
; Sequence 196, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James J.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; PRIOR APPLICATION NUMBER: 2001-10-15
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
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; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
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; PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
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; PRIOR APPLICATION NUMBER: 60/082569
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; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
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;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
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;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392
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;; PRIOR APPLICATION NUMBER: 60/083496
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;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
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;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
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;; PRIOR APPLICATION NUMBER: 60/084441
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;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-5-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
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;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
DB 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

QY 61 HSYIDTYFDTERSSTYRSKGFVDTVKTYTQSGTWGTFVGEDLVITIPKGFNTSFLVNIAITFE 120
DB 123 HSYIDTYFDTERSSTYRSKGFVDTVKTYTQSGTWGTFVGEDLVITIPKGFNTSFLVNIAITFE 182

QY 121 SENFELPGIKWNGILGLAYATLAKPSSSLETFEDSLVTQANIPNVFSMQCGAGLPVAGS 180
DB 183 SENFELPGIKWNGILGLAYATLAKPSSSLETFEDSLVTQANIPNVFSMQCGAGLPVAGS 242

QY 181 GTNGGSLVLGGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGSLNLDREYNADKAIV 240
DB 243 GTNGGSLVLGGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGSLNLDREYNADKAIV 302

QY 241 DSGTTLRLPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYEPKISITL 300
DB 303 DSGTTLRLPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYEPKISITL 362

QY 301 RDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGRYVIFDRA 360
DB 363 RDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGRYVIFDRA 422

QY 361 QKRVGFAASPCAEIAGAIVSEISGPFSTEDVASNCVPAQSLSEPIL 406
DB 423 QKRVGFAASPCAEIAGAIVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 7

US-10-174-590-72
; Sequence 72, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRIOR application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-72

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
DB 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

QY 61 HSYIDTYFDTERSSTYRSKGFVDTVKTYTQSGTWGTFVGEDLVITIPKGFNTSFLVNIAITFE 120
DB 123 HSYIDTYFDTERSSTYRSKGFVDTVKTYTQSGTWGTFVGEDLVITIPKGFNTSFLVNIAITFE 182

QY 121 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDIMWTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKAIV 240
Db 243 GTNGSLVLGGIEPSLYKGDIMWTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKAIV 302
QY 241 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 300
Db 303 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 362
QY 301 RDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
Db 423 QKRVGFASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 8

US-10-176-758-72
; Sequence 72, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-72

Query Match 100.0%; Score 406; DB 9; length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTYVYKTYGSGWTGFGVEDLVITPKGFNTSFLVNIAITFE 120
Db 123 HSYIDTYFDTERSSSTYRSKGFDTYVYKTYGSGWTGFGVEDLVITPKGFNTSFLVNIAITFE 182
QY 121 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDIMWTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKAIV 240
Db 243 GTNGSLVLGGIEPSLYKGDIMWTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKAIV 302
QY 241 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 300
Db 243 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 362

Db 303 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 362
QY 301 RDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
Db 423 QKRVGFASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 9

US-10-175-737-72
; Sequence 72, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-72

Query Match 100.0%; Score 406; DB 9; length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTYVYKTYGSGWTGFGVEDLVITPKGFNTSFLVNIAITFE 120
Db 123 HSYIDTYFDTERSSSTYRSKGFDTYVYKTYGSGWTGFGVEDLVITPKGFNTSFLVNIAITFE 182
QY 121 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDIMWTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKAIV 240
Db 243 GTNGSLVLGGIEPSLYKGDIMWTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKAIV 302
QY 241 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 300
Db 303 DSGTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITL 362
QY 301 RDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
Db 363 RDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
Db 423 QKRVGFASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468


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RESULT 10
US-10-173-706-72
; Sequence 72, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-72
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Query Match      100.0%; Score 406; DB 9; length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTVKYTOGSGWTGFGVEDLVTIPKGFNTSFLVNIATIFE 120
Db 123 HSYIDTYFDTERSSSTYRSKGFDTVKYTOGSGWTGFGVEDLVTIPKGFNTSFLVNIATIFE 182
QY 121 SENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240
Db 243 GTNGSLVLGGIEPSLYKGDWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 302
QY 241 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITYL 300
Db 303 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITYL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIFDRA 360
Db 363 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIFDRA 422
QY 361 QKRVGFAASPCAIEIAGA VSEISGPFSTEDVASNCVPAQSLSEPI L 406
Db 423 QKRVGFAASPCAIEIAGA VSEISGPFSTEDVASNCVPAQSLSEPI L 468
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RESULT 11
US-10-175-738-72
; Sequence 72, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
```

```
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-72
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Query Match      100.0%; Score 406; DB 9; length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTP 60
Db 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTVKYTOGSGWTGFGVEDLVTIPKGFNTSFLVNIATIFE 120
Db 123 HSYIDTYFDTERSSSTYRSKGFDTVKYTOGSGWTGFGVEDLVTIPKGFNTSFLVNIATIFE 182
QY 121 SENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
Db 183 SENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240
Db 243 GTNGSLVLGGIEPSLYKGDWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 302
QY 241 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITYL 300
Db 303 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISITYL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIFDRA 360
Db 363 RDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIFDRA 422
QY 361 QKRVGFAASPCAIEIAGA VSEISGPFSTEDVASNCVPAQSLSEPI L 406
Db 423 QKRVGFAASPCAIEIAGA VSEISGPFSTEDVASNCVPAQSLSEPI L 468
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RESULT 12
US-10-175-752-72
; Sequence 72, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
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QY 181 GTNGSLVLGGIEPSLYKGDWYTPPIKEWYYQIEILKLEIGGQSLNDCREYNADKAIV 240
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Db 243 GTNGSLVLGGIEPSLYKGDWYTPPIKEWYYQIEILKLEIGGQSLNDCREYNADKAIV 302
QY 241 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITL 300
|
Db 303 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITL 362
QY 301 RDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
|
Db 363 RDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFASPCAEIIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
|
Db 423 QKRVGFASPCAEIIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 15
US-10-176-913-72
; Sequence 72, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C66
; CURRENT APPLICATION NUMBER: US/10/176,913
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-913-72

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDGSGRYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
|
Db 63 ALEPALASPAGANFLAMVDNLQDGSGRYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFGVEDLVITPKGFNTSFLVNIATIFE 120
|
Db 123 HSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFGVEDLVITPKGFNTSFLVNIATIFE 182
QY 121 SENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMOMCGAGLPVAGS 180
|
Db 183 SENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDWYTPPIKEWYYQIEILKLEIGGQSLNDCREYNADKAIV 240
|
Db 243 GTNGSLVLGGIEPSLYKGDWYTPPIKEWYYQIEILKLEIGGQSLNDCREYNADKAIV 302
QY 241 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITL 300
|
Db 303 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITL 362
QY 301 RDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
|

Db 363 RDENSSRSFRITILPOLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
QY 361 QKRVGFASPCAEIIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
Db 423 QKRVGFASPCAEIIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

Search completed: April 1, 2003, 12:01:46
Job time : 50 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:50:25 ; Search time 21 Seconds
(without alignments)
1858.599 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
Perfect score: 406
Sequence: 1 ALEPALASPAGANFLAMVD.....STEDVASNCVPAQSLSEPTL 406

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database : PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	12	3.0	501	2 A59090	aspartic proteinas
2	8	2.0	166	2 H64131	transcription regu
3	8	2.0	237	2 J00729	60K inner-membrane
4	8	2.0	287	2 G96659	protein F2K11.24 {
5	8	2.0	303	2 H75528	conserved hypothet
6	8	2.0	319	2 AG0742	high-affinity zinc
7	8	2.0	323	1 PRLJHD	proteinase (EC 3.4
8	8	2.0	327	2 T42999	ethanolamine-phosp
9	8	2.0	340	1 PEIKL	polyporopepsin (EC
10	8	2.0	352	2 C72748	probable sun prote
11	8	2.0	365	2 T37720	ethanolamine-phosp
12	8	2.0	449	2 E96676	hypothetical prote
13	8	2.0	472	2 JCT626	amino acid transpo
14	8	2.0	548	1 B65173	probable 60K inner
15	8	2.0	548	2 H91208	60 KD inner-membra
16	8	2.0	548	2 B86055	60 KD inner-membra
17	8	2.0	548	2 AF0957	probable membrane
18	8	2.0	637	2 T01961	hypothetical prote
19	8	2.0	904	2 C83030	exoribonuclease RN
20	8	2.0	1622	2 JE0378	DNA (cytosine-5-)-
21	7	1.7	88	2 PNO135	pepsin (EC 3.4.23.
22	7	1.7	115	2 TS1324	nickel-insertion a
23	7	1.7	128	1 UQDOR	ubiquitin / riboso
24	7	1.7	131	2 B90553	50S ribosomal prot
25	7	1.7	141	2 D83834	flagellar biosynth
26	7	1.7	180	2 G70912	hypothetical prote
27	7	1.7	206	2 B97594	50S ribosomal prot
28	7	1.7	206	2 AG2815	50S ribosomal prot
29	7	1.7	235	2 F86598	pseudouridine synt

30	7	1.7	235	2 H72025	probable pseudouri
31	7	1.7	235	2 G81515	ribosomal large ch
32	7	1.7	241	2 F71478	probable pseudouri
33	7	1.7	241	2 E81741	ribosomal large ch
34	7	1.7	244	2 AD3266	asparagine transpo
35	7	1.7	245	2 E87719	protein R119.3 [im
36	7	1.7	254	2 B87630	hypothetical prote
37	7	1.7	257	2 T44278	conserved hypothet
38	7	1.7	267	2 T00114	exodeoxyribonuclea
39	7	1.7	267	2 H64044	exodeoxyribonuclea
40	7	1.7	267	2 B83109	probable transcrip
41	7	1.7	268	1 NCECX3	exodeoxyribonuclea
42	7	1.7	268	2 G90935	exonuclease III [i
43	7	1.7	268	2 C85784	exonuclease III [i
44	7	1.7	270	2 H70690	hypothetical prote
45	7	1.7	276	2 G01564	proteasome chain L
46	7	1.7	276	2 C44324	proteasome endopep
47	7	1.7	291	2 D82491	hypothetical prote
48	7	1.7	296	2 JC6050	homoserine kinase
49	7	1.7	302	2 S61836	cher protein - Rhi
50	7	1.7	302	2 C64311	Na+/Ca2+-exchangin
51	7	1.7	306	1 CEECDL	D-alanine-D-alanin
52	7	1.7	306	2 H90640	D-alanine-D-alanin
53	7	1.7	306	2 H85491	D-alanine-D-alanin
54	7	1.7	306	2 AG0518	D-alanine,D-alanin
55	7	1.7	319	2 AH3527	D-xylose-binding p
56	7	1.7	320	2 C81972	probable 3-oxoacyl
57	7	1.7	320	2 C81029	3-oxoacyl-(acyl-ca
58	7	1.7	320	2 A40660	outer membrane pro
59	7	1.7	325	2 H96032	probable thiamine
60	7	1.7	326	2 J00855	hypothetical 36.8K
61	7	1.7	327	2 F95889	probable dehydroge
62	7	1.7	331	2 A83534	probable C4-dicarb
63	7	1.7	333	2 AH0268	anthranilate phosp
64	7	1.7	334	2 JC4870	pepsin A (EC 3.4.2
65	7	1.7	336	2 T49112	aspartic proteinas
66	7	1.7	337	2 F70071	hypothetical prote
67	7	1.7	345	2 AG3186	hypothetical prote
68	7	1.7	345	2 AI0926	probable capsid po
69	7	1.7	345	2 B75274	conserved hypothet
70	7	1.7	346	2 E86715	transcription regu
71	7	1.7	347	2 AG1817	rod shape-determin
72	7	1.7	354	2 C71368	probable UDP-N-ace
73	7	1.7	354	2 S60967	VGPI protein precu
74	7	1.7	365	2 T49733	probable homoserin
75	7	1.7	368	2 B97623	cpaA protein (AJ00
76	7	1.7	368	2 AB2846	Ca2+/H+ antiporter
77	7	1.7	373	2 T45747	GDP-D-mannose-4,6-
78	7	1.7	379	2 B71331	conserved hypothet
79	7	1.7	380	2 S03433	candidapepsin (EC
80	7	1.7	381	2 JC7247	prochymosin - comm
81	7	1.7	382	1 PECH	pepsin A (EC 3.4.2
82	7	1.7	383	2 JC7573	pepsinogen C - Afr
83	7	1.7	384	2 A39314	gastricsin (EC 3.4
84	7	1.7	386	1 PEPG	pepsin A (EC 3.4.2
85	7	1.7	387	2 D38302	pepsin (EC 3.4.23.
86	7	1.7	387	2 C38302	pepsin (EC 3.4.23.
87	7	1.7	387	2 B38302	pepsin (EC 3.4.23.
88	7	1.7	387	2 E38302	pepsin (EC 3.4.23.
89	7	1.7	387	2 I46617	pregnancy-associat
90	7	1.7	387	2 JC7245	pepsinogen A - com
91	7	1.7	388	1 PEMU	pepsin A (EC 3.4.2
92	7	1.7	388	1 PEMQAR	pepsin A (EC 3.4.2
93	7	1.7	388	1 S19684	pepsin A (EC 3.4.2
94	7	1.7	388	1 S19684	pepsin A (EC 3.4.2
95	7	1.7	388	1 S19684	pepsin A (EC 3.4.2
96	7	1.7	388	1 A30142	pepsin A (EC 3.4.2
97	7	1.7	388	2 B30142	pepsin A (EC 3.4.2
98	7	1.7	398	2 I51185	pepsin A (EC 3.4.2
99	7	1.7	398	2 B75475	cathepsin D (EC 3.
100	7	1.7	416	2 AG0125	glucose-fructose o
101	7	1.7	428	2 S47096	N-acetylmuramoyl-L
102	7	1.7	428	2 B90636	cynarase (EC 3.4.2
					survival protein [

probable pseudouri
ribosomal large ch
probable pseudouri
ribosomal large ch
asparagine transpo
protein R119.3 [im
hypothetical prote
conserved hypothet
exodeoxyribonuclea
exodeoxyribonuclea
probable transcrip
exodeoxyribonuclea
exonuclease III [i
exonuclease III [i
hypothetical prote
proteasome chain L
proteasome endopep
hypothetical prote
homoserine kinase
cher protein - Rhi
Na+/Ca2+-exchangin
D-alanine-D-alanin
D-alanine-D-alanin
D-alanine-D-alanin
D-xylose-binding p
probable 3-oxoacyl
3-oxoacyl-(acyl-ca
outer membrane pro
probable thiamine
hypothetical 36.8K
probable dehydroge
probable C4-dicarb
anthranilate phosp
pepsin A (EC 3.4.2
aspartic proteinas
hypothetical prote
hypothetical prote
probable capsid po
conserved hypothet
transcription regu
rod shape-determin
probable UDP-N-ace
VGPI protein precu
probable homoserin
cpaA protein (AJ00
Ca2+/H+ antiporter
GDP-D-mannose-4,6-
conserved hypothet
candidapepsin (EC
prochymosin - comm
pepsin A (EC 3.4.2
pepsinogen C - Afr
gastricsin (EC 3.4
pepsin A (EC 3.4.2
pepsin (EC 3.4.23.
pepsin (EC 3.4.23.
pepsin (EC 3.4.23.
pepsin (EC 3.4.23.
pregnancy-associat
pepsinogen A - com
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
cathepsin D (EC 3.
glucose-fructose o
N-acetylmuramoyl-L
cynarase (EC 3.4.2
survival protein [

103	7	1.7	428	2	B85487	survival protein l	176	6	1.5	71	2	S22905	lysis protein S -
104	7	1.7	428	2	E64726	probable peptidylp	177	6	1.5	72	2	S21799	pepsin (EC 3.4.23.
105	7	1.7	433	2	E96649	hypothetical prote	178	6	1.5	73	1	F2NT0P	photosystem II pho
106	7	1.7	434	2	AD0061	peptidylprolyl iso	179	6	1.5	73	2	S21754	gastricsin (EC 3.4
107	7	1.7	436	2	G96009	probable cell-surf	180	6	1.5	73	2	A87686	hypothetical prote
108	7	1.7	452	2	S41717	aspartic hemoglobi	181	6	1.5	79	2	S03266	aspartic proteinas
109	7	1.7	460	2	T43224	hypothetical prote	182	6	1.5	79	2	D64596	hypothetical prote
110	7	1.7	462	2	G70544	probable heml prot	183	6	1.5	81	2	H82515	hypothetical prote
111	7	1.7	474	2	T12049	cyprosin (EC 3.4.2	184	6	1.5	87	2	JQ1135	hypothetical prote
112	7	1.7	491	2	C98275	polyketide synthas	185	6	1.5	88	2	A28056	levitide precursor
113	7	1.7	491	2	AC3009	polyketide synthas	186	6	1.5	88	2	D64562	hypothetical prote
114	7	1.7	491	2	H84379	4-hydroxybutyrate	187	6	1.5	89	2	F86706	hypothetical prote
115	7	1.7	496	2	JS0732	aspartic proteinas	188	6	1.5	91	1	S00060	phospholipid trans
116	7	1.7	506	2	T07915	probable aspartic	189	6	1.5	91	2	T42907	hypothetical prote
117	7	1.7	506	2	S71591	aspartic proteinas	190	6	1.5	92	2	S06034	hypothetical prote
118	7	1.7	506	2	F86253	hypothetical prote	191	6	1.5	92	2	S06033	hypothetical prote
119	7	1.7	508	2	D85056	probable aspartic	192	6	1.5	94	2	S03380	hypothetical prote
120	7	1.7	509	2	D85056	aspartic proteinas	193	6	1.5	96	2	A87110	major fecal allerg
121	7	1.7	510	2	DC9796	hypothetical prote	194	6	1.5	98	2	PQ0496	conserved hypothet
122	7	1.7	513	2	T09739	aspartic endopepti	195	6	1.5	99	2	B95393	hypothetical prote
123	7	1.7	555	2	F86487	unknown protein li	196	6	1.5	99	2	A11907	protein limported
124	7	1.7	558	2	E70756	hypothetical glyci	197	6	1.5	101	2	G72450	hypothetical prote
125	7	1.7	569	2	S64957	aspargillopepsin I	198	6	1.5	102	2	D90915	hypothetical prote
126	7	1.7	596	2	S57971	aspartic proteinas	199	6	1.5	102	2	A85764	hypothetical prote
127	7	1.7	626	2	H82147	methyl-accepting c	200	6	1.5	102	2	AI2693	hypothetical prote
128	7	1.7	646	2	T38171	probable serine/th	201	6	1.5	105	2	S62844	conserved hypothet
129	7	1.7	682	2	AE0033	secretion system a	202	6	1.5	105	2	B69857	H+-transporting tw
130	7	1.7	690	2	B82409	alpha-amylase VCA0	203	6	1.5	105	2	T49332	chaperonin homolog
131	7	1.7	707	2	F86925	probable acyl-CoA	204	6	1.5	105	2	AD3365	hypothetical prote
132	7	1.7	709	2	T29692	hypothetical prote	205	6	1.5	107	2	JQ2035	hypothetical prote
133	7	1.7	722	2	T46560	swi2 protein - fis	206	6	1.5	107	2	T25670	hypothetical prote
134	7	1.7	754	2	S62512	probable cysteinyl	207	6	1.5	110	1	PEBO	pepsin A (EC 3.4.2
135	7	1.7	773	1	JH0609	protein-tyrosine-p	208	6	1.5	110	2	E69607	protein secretion
136	7	1.7	775	2	S55345	protein-tyrosine-p	209	6	1.5	112	2	T48324	DNAJ protein-like
137	7	1.7	784	2	AC1091	5'-nucleotidase, p	210	6	1.5	112	2	AB0687	probable membrane
138	7	1.7	802	2	D85035	ent-kaurene synthe	211	6	1.5	113	2	A70553	hypothetical prote
139	7	1.7	831	2	A48489	nitrate reductase	212	6	1.5	113	2	T42985	hypothetical prote
140	7	1.7	843	2	T16906	hypothetical prote	213	6	1.5	113	2	C83893	hypothetical prote
141	7	1.7	887	2	T20866	hypothetical prote	214	6	1.5	114	2	E72724	hypothetical prote
142	7	1.7	899	2	S62428	probable coiled co	215	6	1.5	115	2	D64914	hypothetical prote
143	7	1.7	933	1	BVECC	sensor protein rcs	216	6	1.5	117	2	T09155	lipid transfer pro
144	7	1.7	933	2	C91017	sensor for ctr cap	217	6	1.5	119	2	S24294	chorion protein -
145	7	1.7	933	2	E85861	hypothetical prote	218	6	1.5	119	2	S24291	early chorion prot
146	7	1.7	939	2	AE2275	hypothetical prote	219	6	1.5	119	2	B45937	chorion class CA p
147	7	1.7	967	2	S58360	lantibiotic Peps b	220	6	1.5	121	2	S24293	hypothetical 13K p
148	7	1.7	1015	2	T39697	beta-galactosidase	221	6	1.5	122	2	JQ0150	hypothetical prote
149	7	1.7	1015	2	A42915	type II cAMP-depen	222	6	1.5	123	2	NR4383	pancreatic ribonuc
150	7	1.7	1039	2	G83748	alpha-mannosidase	223	6	1.5	124	1	NRCB	glucagon 1 precurs
151	7	1.7	1073	2	S56220	probable membrane	224	6	1.5	124	1	GCAF	hypothetical prote
152	7	1.7	1131	2	AD2166	two-component sens	225	6	1.5	125	2	B97470	Na+/H+ antiporter
153	7	1.7	1142	2	C97080	levanase/invertase	226	6	1.5	125	2	AG2688	hypothetical prote
154	7	1.7	1236	2	T50904	Mg protoporphyrin	227	6	1.5	126	2	H86347	hypothetical prote
155	7	1.7	1269	2	T14476	psIA protein - sli	228	6	1.5	128	2	T30714	hypothetical prote
156	7	1.7	1379	2	T13718	pollux gene protei	229	6	1.5	129	2	E90535	hypothetical prote
157	7	1.7	1433	2	A46053	bullous pemphigoid	230	6	1.5	129	2	AB3459	transcriptional re
158	7	1.7	1533	2	A46221	abdominal segment	231	6	1.5	131	2	S24285	RNA-directed RNA p
159	7	1.7	1632	2	C70752	probable ctpi prot	232	6	1.5	131	2	D90419	hypothetical prote
160	7	1.7	2014	2	T21560	hypothetical prote	233	6	1.5	132	2	T35141	ATP synthase chain
161	7	1.7	2025	2	D86201	protein F12K11.6 l	234	6	1.5	132	2	AB1767	ATP synthase chain
162	7	1.7	2894	2	C64474	hypothetical prote	235	6	1.5	132	2	AH1391	hypothetical prote
163	6	1.5	9	2	PT0326	ig heavy chain CRD	236	6	1.5	133	2	D87690	hypothetical prote
164	6	1.5	16	2	A44352	candidapepsin (EC	237	6	1.5	134	2	F72802	gp24 protein - Myc
165	6	1.5	39	2	S35325	protein kinase sgg	238	6	1.5	134	2	F97475	id894 (AF322013) l
166	6	1.5	40	2	D96733	hypothetical prote	239	6	1.5	134	2	AC3234	conserved hypothet
167	6	1.5	48	2	JV0019	hypothetical prote	240	6	1.5	135	2	D71228	hypothetical prote
168	6	1.5	49	2	S55324	endo-beta-1,6-gluc	241	6	1.5	137	2	S53025	photosystem II pro
169	6	1.5	52	1	S07502	gene 5.9 protein -	242	6	1.5	137	2	G65096	hypothetical prote
170	6	1.5	52	1	S42315	gene 5.9 protein -	243	6	1.5	138	2	D91124	hypothetical prote
171	6	1.5	52	2	A34657	cathepsin E (EC 3.	244	6	1.5	138	2	C85969	hypothetical prote
172	6	1.5	59	2	B87614	pilus subunit prot	245	6	1.5	138	2	S20087	homeotic protein b
173	6	1.5	64	2	E98056	hypothetical prote	246	6	1.5	138	2	D72539	hypothetical prote
174	6	1.5	65	2	F81607	hypothetical prote	247	6	1.5	139	2	G69543	conserved hypothet
175	6	1.5	67	2	AB1771	hypothetical prote	248	6	1.5	141	2	A91249	probable transcrip

249	6	1.5	141	2	A90130	hypothetical prote	322	6	1.5	178	2	S03629	neurogenic gene co
250	6	1.5	141	2	AC3590	3-oxoadipate CoA-t	323	6	1.5	178	2	T08444	hypothetical prote
251	6	1.5	142	2	T40837	DNA-directed RNA p	324	6	1.5	178	2	E88637	protein W09G12.6 l
252	6	1.5	142	2	AC3345	LSU ribosomal prot	325	6	1.5	179	2	C75469	hypothetical prote
253	6	1.5	143	2	T13214	minor capsid prote	326	6	1.5	180	2	T16445	hypothetical prote
254	6	1.5	143	2	T41630	very hypothetical	327	6	1.5	182	2	S70689	adenine phosphorib
255	6	1.5	145	2	D83424	hypothetical prote	328	6	1.5	183	2	A72657	vp529-like phospho
256	6	1.5	146	2	A72115	conserved hypothet	329	6	1.5	185	2	B70072	conserved hypothet
257	6	1.5	146	2	D86508	hypothetical prote	330	6	1.5	186	2	AB2408	hypothetical prote
258	6	1.5	146	2	G90337	hypothetical prote	331	6	1.5	186	2	AF2556	hypothetical prote
259	6	1.5	147	2	A26697	echinoidln - sea u	332	6	1.5	187	2	S69315	hypothetical prote
260	6	1.5	147	2	S05320	transthyretin prec	333	6	1.5	188	2	F83855	GTP cyclohydrolase
261	6	1.5	148	2	C72422	hypothetical prote	334	6	1.5	188	2	T02781	probable conjugal
262	6	1.5	148	2	H95849	hypothetical prote	335	6	1.5	188	2	B84719	hypothetical prote
263	6	1.5	149	2	D98196	hypothetical prote	336	6	1.5	189	2	A71569	hypothetical prote
264	6	1.5	149	2	AF3090	conserved hypothet	337	6	1.5	189	2	JC7262	receptor activity
265	6	1.5	151	2	A86705	transcrtional re	338	6	1.5	189	2	T18480	hypothetical prote
266	6	1.5	151	2	G84165	hypothetical prote	339	6	1.5	190	2	T10740	carbonate dehydrat
267	6	1.5	151	2	T18478	hypothetical prote	340	6	1.5	191	2	I45716	GTP-binding protei
268	6	1.5	152	2	B75042	aspartate carbamoy	341	6	1.5	191	2	E75132	mllybdopterin-guan
269	6	1.5	152	2	B72754	hypothetical prote	342	6	1.5	192	2	G71089	hypothetical prote
270	6	1.5	153	2	S12206	hypothetical prote	343	6	1.5	195	2	G70211	hypothetical prote
271	6	1.5	153	2	D83012	hypothetical prote	344	6	1.5	195	2	A96998	CDP-dilyceride sy
272	6	1.5	155	2	AB3512	nodulation protein	345	6	1.5	196	2	F88382	protein W06B1.2 l
273	6	1.5	155	2	E72661	hypothetical prote	346	6	1.5	196	2	D81696	hypothetical prote
274	6	1.5	157	2	H83082	probable transcrip	347	6	1.5	197	2	S25106	capsid protein - b
275	6	1.5	157	2	C82121	phosphohistidine p	348	6	1.5	198	2	T29135	hypothetical prote
276	6	1.5	157	2	H72673	hypothetical prote	349	6	1.5	199	2	E95211	N-(5'-phosphoribos
277	6	1.5	159	2	G70841	hypothetical prote	350	6	1.5	199	2	S41316	coat protein - cuc
278	6	1.5	159	2	H86997	conserved hypothet	351	6	1.5	199	2	F18479	hypothetical prote
279	6	1.5	159	2	T35623	probable protein p	352	6	1.5	200	2	T18479	coat protein - bee
280	6	1.5	159	2	B71423	hypothetical prote	353	6	1.5	201	1	VCVOGB	probable lpqc prot
281	6	1.5	160	2	B70718	hypothetical prote	354	6	1.5	201	2	D70519	coat protein - bee
282	6	1.5	161	2	VCTMSH	coat protein - cuc	355	6	1.5	202	1	VCVOFL	probable heme expo
283	6	1.5	161	2	S54434	phosphoribosylamin	356	6	1.5	202	2	C72701	hypothetical prote
284	6	1.5	161	2	S27127	tropomyosin homolo	357	6	1.5	202	2	AC2875	guanylate kinase (
285	6	1.5	163	2	H72759	probable dCTP deam	358	6	1.5	205	2	C86862	heme exporter prote
286	6	1.5	164	1	RGECLR	leucine-responsive	359	6	1.5	205	2	PQ0272	D-alanine-D-alanin
287	6	1.5	164	2	G64132	phosphoribosylamin	360	6	1.5	205	2	G64989	heme exporter prot
288	6	1.5	164	2	S59991	transcription regu	361	6	1.5	205	2	B91015	ATP binding protei
289	6	1.5	164	2	S59992	transcription regu	362	6	1.5	205	2	D85859	heme exporter prot
290	6	1.5	164	2	S59992	transcription regu	363	6	1.5	205	2	AC0960	heme exporter prot
291	6	1.5	164	2	B82142	leucine-responsive	364	6	1.5	205	2	AD0768	heme exporter prot
292	6	1.5	164	2	A10167	leucine-responsive	365	6	1.5	206	2	JC4268	fibroblast growth
293	6	1.5	164	2	F90750	leucine-responsive	366	6	1.5	206	2	AE0891	probable membrane
294	6	1.5	164	2	D85614	leucine-responsive	367	6	1.5	206	2	T48149	hypothetical prote
295	6	1.5	164	2	AE0611	leucine-responsive	368	6	1.5	206	2	H89828	conserved hypothet
296	6	1.5	165	2	A12904	leucine-responsive	369	6	1.5	207	2	B86498	superoxide dismuta
297	6	1.5	165	2	S61602	hypothetical prote	370	6	1.5	207	2	B72124	superoxide dismuta
298	6	1.5	166	2	D69695	probable membrane	371	6	1.5	207	2	B84151	hypothetical prote
299	6	1.5	168	2	D75259	ribosomal protein	372	6	1.5	207	2	T36937	probable transcrip
300	6	1.5	169	2	A89912	hypothetical prote	373	6	1.5	208	2	T09901	hypothetical prote
301	6	1.5	169	2	D90857	hypothetical prote	374	6	1.5	209	1	S53657	hydrogenase matura
302	6	1.5	169	2	B75490	hypothetical prote	375	6	1.5	209	2	G98075	phosphoribosylanth
303	6	1.5	169	2	F85762	hypothetical prote	376	6	1.5	209	2	G72528	hypothetical prote
304	6	1.5	170	2	B90214	NADH dehydrogenase	377	6	1.5	210	2	F69510	fibrillarln (fib)
305	6	1.5	171	2	C87418	hypothetical prote	378	6	1.5	211	2	D69888	micrococcal nuclea
306	6	1.5	171	2	G84421	probable auxin-ind	379	6	1.5	211	2	A69619	deoxyribose-phosph
307	6	1.5	171	2	A84561	probable bZIP tran	380	6	1.5	211	2	A81700	conserved hypothet
308	6	1.5	172	2	A91070	hypothetical prote	381	6	1.5	212	1	R5HSLH	ribosomal protein
309	6	1.5	172	2	D85914	hypothetical prote	382	6	1.5	212	2	H84266	50S ribosomal prot
310	6	1.5	172	2	T02229	protein BYJ15 - co	383	6	1.5	212	2	T05721	germin-like protei
311	6	1.5	172	2	B86439	protein T19E23.11	384	6	1.5	212	2	T44970	gas-vesicle operon
312	6	1.5	173	2	AF3293	crossover junction	385	6	1.5	213	2	B87694	cytidylate kinase
313	6	1.5	173	2	F45392	orf6 protein - por	386	6	1.5	213	2	T27841	hypothetical prote
314	6	1.5	173	2	A44281	envelope protein -	387	6	1.5	214	2	B87424	outer membrane pro
315	6	1.5	173	2	D83464	conserved hypothet	388	6	1.5	215	2	B35534	hypothetical 23K p
316	6	1.5	174	2	A47113	glucuronosyltransf	389	6	1.5	215	2	F97825	50S ribosomal prot
317	6	1.5	174	2	E65046	hypothetical prote	390	6	1.5	215	2	C72635	triose-phosphate i
318	6	1.5	174	2	B72712	hypothetical prote	391	6	1.5	215	2	AH3389	transporter BME11
319	6	1.5	174	2	S73052	hypothetical prote	392	6	1.5	216	2	A71672	ribosomal protein
320	6	1.5	176	2	I48752	gene RXRbeta1 prot	393	6	1.5	216	2	S09500	outer membrane pro
321	6	1.5	178	2	I40124	outer surface prot	394	6	1.5	216	2	S40720	hypothetical prote

395	6	1.5	217	2	D82407	outer membrane pro
396	6	1.5	217	2	F83502	hypothetical prote
397	6	1.5	218	2	T50070	superoxide dismuta
398	6	1.5	218	2	S75100	ABC transport prote
399	6	1.5	218	2	S73675	hypothetical prote
400	6	1.5	218	2	C72747	probable endonucle
401	6	1.5	219	1	A35617	HDEL receptor ERD2
402	6	1.5	219	2	S75541	hypothetical prote
403	6	1.5	219	2	B71511	probable sugar nuc
404	6	1.5	219	2	T20732	hypothetical prote
405	6	1.5	219	2	C70855	hypothetical prote
406	6	1.5	219	2	A99194	iron (III) ABC tra
407	6	1.5	219	2	G87708	hypothetical prote
408	6	1.5	219	2	H81824	hypothetical perip
409	6	1.5	221	1	HLMSA1	H-2 class II histo
410	6	1.5	223	2	AG3263	propanediol dehydr
411	6	1.5	223	2	A86057	hypothetical prote
412	6	1.5	223	2	F91210	hypothetical prote
413	6	1.5	224	2	T32655	hypothetical prote
414	6	1.5	225	1	WZVZG2	G2R protein - Amsa
415	6	1.5	225	2	AC0587	KDP operon transcr
416	6	1.5	225	2	T29632	hypothetical prote
417	6	1.5	225	2	F72642	probable shikimate
418	6	1.5	226	1	TVWVSS	PDGF-related trans
419	6	1.5	226	2	AG0388	probable short-cha
420	6	1.5	226	2	S75665	ABC-type transport
421	6	1.5	226	2	G75342	hypothetical prote
422	6	1.5	226	2	H84213	hypothetical prote
423	6	1.5	227	2	B84696	probable glutathio
424	6	1.5	227	2	AG1314	hypothetical prote
425	6	1.5	227	2	AG1686	hypothetical prote
426	6	1.5	227	2	T45388	hypothetical prote
427	6	1.5	229	2	S33182	probable transport
428	6	1.5	229	2	T34277	hypothetical prote
429	6	1.5	229	2	F75482	transcription regu
430	6	1.5	230	2	F71122	hypothetical prote
431	6	1.5	230	2	H72244	conserved hypothet
432	6	1.5	230	2	E87578	hypothetical prote
433	6	1.5	231	2	G69403	conserved hypothet
434	6	1.5	231	2	S48966	hypothetical prote
435	6	1.5	232	2	T12740	hypothetical prote
436	6	1.5	232	2	G87629	hypothetical prote
437	6	1.5	232	2	AG1452	hypothetical prote
438	6	1.5	232	2	A87504	6-phospho-glucono-
439	6	1.5	232	2	G84382	cobalt transport A
440	6	1.5	232	2	D70537	hypothetical prote
441	6	1.5	233	2	I79358	IA-alpha polyprote
442	6	1.5	233	2	I79357	IA-alpha polyprote
443	6	1.5	233	2	AF0110	probable hemolysin
444	6	1.5	234	1	QOBE43	membrane antigen g
445	6	1.5	234	2	AC0431	conserved hypothet
446	6	1.5	234	2	E64331	hypothetical prote
447	6	1.5	235	2	C98204	hypothetical prote
448	6	1.5	235	2	AE3082	probable permease
449	6	1.5	235	2	F97391	hypothetical prote
450	6	1.5	235	2	AG2609	probable transcrip
451	6	1.5	236	2	D72729	transcription regu
452	6	1.5	237	2	E82674	hypothetical prote
453	6	1.5	237	2	A36149	3'-phosphoadenosin
454	6	1.5	237	2	D70463	spiralin - Spiropl
455	6	1.5	237	2	G87286	hypothetical prote
456	6	1.5	237	2	AG3573	conserved hypothet
457	6	1.5	238	2	T10771	6-phosphogluconola
458	6	1.5	238	2	S67594	NADPH-ferrihemopro
459	6	1.5	238	2	H87578	RAD59 protein - ye
460	6	1.5	238	2	B97634	transcription regu
461	6	1.5	238	2	AD2857	probable transcrip
462	6	1.5	239	1	S34193	transcription regu
463	6	1.5	239	2	AF0261	phosphoadenyl-su
464	6	1.5	240	2	JL0143	fatty acid metabol
465	6	1.5	241	1	D71233	antigen BCM1 precu
466	6	1.5	241	2	A75200	probable 3-isoprop
467	6	1.5	242	2	S30888	hypothetical prote
						PRP38 protein - ye
468	6	1.5	243	1	WMVZP2	F2 protein - fowlp
469	6	1.5	244	2	C83953	ribosomal protein
470	6	1.5	244	2	A39365	cyanamide hydratase
471	6	1.5	244	2	B83630	hypothetical prote
472	6	1.5	245	2	T47501	do6 zinc finger p
473	6	1.5	245	2	AG2203	glucose inhibited
474	6	1.5	246	2	E75481	RNA methyltransfer
475	6	1.5	247	2	C98340	2-deoxy-D-gluconat
476	6	1.5	247	2	AG2942	2-deoxy-D-gluconat
477	6	1.5	247	2	H70432	ABC transporter -
478	6	1.5	247	2	B64147	hypothetical prote
479	6	1.5	247	2	D69453	hypothetical prote
480	6	1.5	248	2	H70511	probable prca prot
481	6	1.5	249	1	B70693	probable echA6 pr
482	6	1.5	249	2	E75181	ribonuclease ph (r
483	6	1.5	249	2	E71032	hypothetical prote
484	6	1.5	249	2	S32609	phycocerythrin-asso
485	6	1.5	249	2	T10441	conserved hypothet
486	6	1.5	250	2	T43153	probable aldehyde
487	6	1.5	250	2	A82125	heme exporter prot
488	6	1.5	250	2	D69180	ABC transporter -
489	6	1.5	250	2	S28474	rfbi protein - Vib
490	6	1.5	250	2	H72704	probable iron (III
491	6	1.5	250	2	A95261	response regulator
492	6	1.5	250	2	F98126	response regulator
493	6	1.5	251	1	C36044	indole-3-glycerol-
494	6	1.5	251	1	WMADF4	early E1A 27K prot
495	6	1.5	251	2	F84958	probable hydroxyac
496	6	1.5	251	2	D71950	hypothetical prote
497	6	1.5	252	2	A82146	3-deoxy-manno-octu
498	6	1.5	252	2	H90476	hypothetical prote
499	6	1.5	253	2	H75083	hypothetical prote
500	6	1.5	253	2	T47757	hypothetical prote
501	6	1.5	253	2	T27279	hypothetical prote
502	6	1.5	253	2	AI0613	probable lipoprote
503	6	1.5	254	2	S11649	class II histocomp
504	6	1.5	254	2	S75814	hypothetical prote
505	6	1.5	255	2	S74930	hypothetical prote
506	6	1.5	255	2	C84071	hypothetical prote
507	6	1.5	255	2	T19747	hypothetical prote
508	6	1.5	256	1	HLMSA2	H-2 class II histo
509	6	1.5	256	2	H97649	probable gluconate
510	6	1.5	256	2	AG2873	dehydrogenase Atu2
511	6	1.5	256	2	T03371	glycine-rich prote
512	6	1.5	256	2	G83232	probable permease
513	6	1.5	256	2	C72261	spermidine/putresc
514	6	1.5	256	2	B71264	hypothetical prote
515	6	1.5	257	2	B83169	probable methyltra
516	6	1.5	258	2	JC2567	UDP-N-acetylmuramo
517	6	1.5	258	2	T19755	hypothetical prote
518	6	1.5	259	2	A83750	transcription regu
519	6	1.5	259	2	S76205	hypothetical prote
520	6	1.5	259	2	AB0565	probable membrane
521	6	1.5	259	2	E84886	probable beta-expa
522	6	1.5	259	2	D64362	hypothetical prote
523	6	1.5	259	2	B64697	UDP-N-acetylenolpy
524	6	1.5	259	2	B71823	udp-n-acetylenolpy
525	6	1.5	260	2	E71045	probable ABC trans
526	6	1.5	261	2	I48645	cell adhesion mole
527	6	1.5	263	2	G70583	probable dehydroge
528	6	1.5	263	2	S76548	hypothetical prote
529	6	1.5	264	2	C84028	septum site-determ
530	6	1.5	265	2	T46733	citr protein [limpo
531	6	1.5	265	2	T07800	inositol-1(or 4)-m
532	6	1.5	265	2	C70332	hypothetical prote
533	6	1.5	265	2	E87074	proteasome [alpha]
534	6	1.5	265	2	S72865	hypothetical prote
535	6	1.5	266	2	A90436	enoyl CoA hydratase
536	6	1.5	266	2	AB1630	cell division inhi
537	6	1.5	266	2	AH1267	cell division inhi
538	6	1.5	266	2	F70595	hypothetical prote
539	6	1.5	266	2	G97483	hypothetical prote
540	6	1.5	266	2	AF2701	aldolase Atu1014 [

541	6	1.5	266	2	B72108	conserved hypothet	614	6	1.5	294	2	G01606	hypothetical prote
542	6	1.5	266	2	C86514	methyase [importe	615	6	1.5	295	2	A64514	hypothetical prote
543	6	1.5	266	2	T31217	transcription regu	616	6	1.5	295	2	G71707	hypothetical prote
544	6	1.5	267	2	B87578	hypothetical prote	617	6	1.5	295	2	AF2610	conserved hypothet
545	6	1.5	267	2	B82068	ABC transporter, A	618	6	1.5	295	2	D97392	hypothetical prote
546	6	1.5	268	1	G45239	cell division inhi	619	6	1.5	295	2	AD0306	probable membrane
547	6	1.5	268	2	AC0710	exodeoxyribonuclea	620	6	1.5	296	2	E83049	conserved hypothet
548	6	1.5	268	2	S25311	chitinase (EC 3.2.	621	6	1.5	296	2	G97799	hypothetical prote
549	6	1.5	268	2	AE2363	inositol monophosp	622	6	1.5	297	2	H82500	conserved hypothet
550	6	1.5	268	2	A64361	hypothetical prote	623	6	1.5	297	2	G70185	mevalonate kinase
551	6	1.5	268	2	B83020	lipopolysaccharide	624	6	1.5	297	2	H69391	hypothetical prote
552	6	1.5	269	2	G75558	hypothetical prote	625	6	1.5	297	2	AC2380	hypothetical prote
553	6	1.5	269	2	D83090	probable ATP-bindi	626	6	1.5	298	2	S76437	dihydridipicolinat
554	6	1.5	269	2	E65110	hypothetical prote	627	6	1.5	299	2	T35844	cytochrome-c oxida
555	6	1.5	269	2	B91138	hypothetical prote	628	6	1.5	300	2	S69052	CDP-abequose synth
556	6	1.5	269	2	E85983	hypothetical prote	629	6	1.5	300	2	AF1286	hypothetical prote
557	6	1.5	270	2	F64057	energy transducer	630	6	1.5	300	2	AG2055	phosphoprotein pho
558	6	1.5	270	2	T35721	hypothetical prote	631	6	1.5	302	1	PAFF1A	phosphoprotein pho
559	6	1.5	270	2	AH0904	probable ABC-trans	632	6	1.5	302	2	S29396	phosphoprotein pho
560	6	1.5	270	2	D69127	hypothetical prote	633	6	1.5	302	2	H95075	hypothetical prote
561	6	1.5	270	2	D72334	sugar kinase, pfkB	634	6	1.5	302	2	T50784	hypothetical prote
562	6	1.5	271	2	A11102	dihydropteroate sy	635	6	1.5	303	2	E70848	probable oxidoredu
563	6	1.5	271	2	A11464	dihydropteroate sy	636	6	1.5	303	2	B70875	hypothetical prote
564	6	1.5	271	2	A25669	PDGF-related trans	637	6	1.5	303	2	T11206	spaO protein - Sal
565	6	1.5	271	2	G72380	conserved hypothet	638	6	1.5	303	2	S37307	spaO protein - Sal
566	6	1.5	271	2	F82346	lipopolysaccharide	639	6	1.5	303	2	AG0851	surface presentati
567	6	1.5	271	2	D70591	hypothetical prote	640	6	1.5	305	2	H95359	probable ABC trans
568	6	1.5	272	2	A44324	proteasome endopep	641	6	1.5	306	2	T08504	trbG protein - Ent
569	6	1.5	272	2	AH0434	probable ABC trans	642	6	1.5	306	2	G83152	hypothetical prote
570	6	1.5	273	2	T11585	hypothetical prote	643	6	1.5	307	2	PC2050	legumin type A alp
571	6	1.5	273	2	B70550	probable c1te prot	644	6	1.5	307	2	T03502	conserved hypothet
572	6	1.5	273	2	B37281	replication factor	645	6	1.5	308	2	H87095	conserved hypothet
573	6	1.5	273	2	A99963	conserved hypothet	646	6	1.5	309	2	E87559	peptidase M20/M25/
574	6	1.5	274	2	AG2312	5'-methylthioadeno	647	6	1.5	310	2	F82979	probable transcrip
575	6	1.5	274	2	T02797	thymidylate kinase	648	6	1.5	311	2	AB3322	transporter BME105
576	6	1.5	276	2	A41377	moxJ protein precu	649	6	1.5	312	2	S71207	serine O-acetyltra
577	6	1.5	277	2	AF1312	ketopantoate hydro	650	6	1.5	312	2	C70901	probable fnt prote
578	6	1.5	278	2	B98296	sulfate ABC transp	651	6	1.5	312	2	G75514	hypothetical prote
579	6	1.5	278	2	T04504	hypothetical prote	652	6	1.5	312	2	T11951	lipid A biosynthes
580	6	1.5	278	2	S36101	CAMP response elem	653	6	1.5	312	2	D97552	lipid A biosynthes
581	6	1.5	279	2	F87577	serine acetyltrans	654	6	1.5	312	2	AF2772	L-lactate dehydrog
582	6	1.5	279	2	AC2559	hypothetical prote	655	6	1.5	313	2	E96932	carbamate kinase (
583	6	1.5	279	2	E75573	transcription regu	656	6	1.5	314	2	A86879	ABC transporter, A
584	6	1.5	279	2	T52454	ATP-dependent Clp	657	6	1.5	314	2	A99446	conserved hypothet
585	6	1.5	280	2	A98159	lactose transport	658	6	1.5	314	2	A87528	hypothetical prote
586	6	1.5	280	2	AH3128	hypothetical prote	659	6	1.5	314	2	B86760	probable transcrip
587	6	1.5	280	2	T22524	hypothetical prote	660	6	1.5	314	2	AB0402	probable transcrip
588	6	1.5	281	2	A30471	hypothetical prote	661	6	1.5	315	2	H82512	probable 3-hydroxy
589	6	1.5	281	2	T16813	hypothetical prote	662	6	1.5	315	2	H86836	carbamate kinase (
590	6	1.5	281	2	B86244	hypothetical prote	663	6	1.5	315	2	S27784	phenylethanolamine
591	6	1.5	281	2	S41854	phosphoprotein pho	664	6	1.5	316	2	F69978	sugar-phosphate de
592	6	1.5	282	2	D97280	fumarate hydratase	665	6	1.5	317	2	AF0582	probable permease
593	6	1.5	282	2	A97214	uncharacterized co	666	6	1.5	317	2	I59379	metaxin - mouse
594	6	1.5	283	2	F75195	agmatinase (speb)	667	6	1.5	318	2	G72310	conserved hypothet
595	6	1.5	283	2	AF2531	hypothetical prote	668	6	1.5	318	2	A11203	transketolase homo
596	6	1.5	284	2	AH0442	probable glutathio	669	6	1.5	319	2	S73159	hypothetical prote
597	6	1.5	285	2	G72415	sensor histidine k	670	6	1.5	320	2	B75457	polyprenyl synthas
598	6	1.5	286	2	S44561	hypothetical prote	671	6	1.5	320	2	T45034	hypothetical prote
599	6	1.5	287	2	AE2067	nicotinate-nucleot	672	6	1.5	321	2	T06845	hypothetical prote
600	6	1.5	287	2	C82965	hypothetical prote	673	6	1.5	322	1	A26370	arginase (EC 3.5.3
601	6	1.5	287	2	T01758	hypothetical prote	674	6	1.5	322	2	T45567	flavonol synthase-
602	6	1.5	287	2	A12609	regulator protein	675	6	1.5	322	2	B87419	3-oxoacyl-(acyl-ca
603	6	1.5	287	2	H97391	probable regulator	676	6	1.5	322	2	D81962	probable inner mem
604	6	1.5	288	2	AE0056	probable right ori	677	6	1.5	322	2	AF0709	succinylglutamate
605	6	1.5	288	2	JS0659	homeotic protein H	678	6	1.5	322	2	AC2023	hypothetical prote
606	6	1.5	289	2	A83011	hypothetical prote	679	6	1.5	323	2	T04826	hypothetical prote
607	6	1.5	289	2	S48664	distal-less 3 prote	680	6	1.5	323	2	G84325	hypothetical prote
608	6	1.5	289	2	I53082	homeoprotein - rat	681	6	1.5	323	2	AC2479	hypothetical prote
609	6	1.5	290	2	T30215	monosaccharide tra	682	6	1.5	323	2	A89779	hypothetical prote
610	6	1.5	291	2	H97959	hypothetical prote	683	6	1.5	323	2	AF3630	nosxl protein [imp
611	6	1.5	292	1	E64226	hypothetical prote	684	6	1.5	324	2	T07832	probable steroid s
612	6	1.5	293	2	T38779	hypothetical RNA b	685	6	1.5	324	2	C72520	probable immunogen
613	6	1.5	294	2	A57478	serine O-acetyltra	686	6	1.5	324	2	F70531	hypothetical prote

687	6	1.5	324	2	T18818	hypothetical prote	760	6	1.5	342	2	S76463	hypothetical prote
688	6	1.5	325	2	S01698	alkanal monooxygen	761	6	1.5	342	2	S63404	hypothetical prote
689	6	1.5	326	2	C72483	probable formate d	762	6	1.5	342	2	E71101	probable geranylge
690	6	1.5	326	2	AF0220	flagellar hook-ass	763	6	1.5	342	2	D86022	probable heme/hemo
691	6	1.5	326	2	S76441	hypothetical prote	764	6	1.5	342	2	C91176	probable heme/hemo
692	6	1.5	326	2	T52030	gamma-glutamyl hyd	765	6	1.5	342	2	T16735	hypothetical prote
693	6	1.5	327	2	F96815	hypothetical prote	766	6	1.5	343	2	AH0328	probable 3',5'-cyc
694	6	1.5	327	2	AC2607	conserved hypothet	767	6	1.5	343	2	S70549	spsd protein - Sal
695	6	1.5	327	2	B97389	hypothetical prote	768	6	1.5	343	2	D84390	sulfate transport
696	6	1.5	328	2	JN0882	gonadotropin-relea	769	6	1.5	344	1	KHPGD	cathepsin D (EC 3.
697	6	1.5	328	2	T02046	prolamin box bindi	770	6	1.5	344	2	AE2144	pyruvate dehydroge
698	6	1.5	328	2	A13541	NADH2 dehydrogenas	771	6	1.5	344	2	C82835	anthranilate phosp
699	6	1.5	329	2	E82644	sugar-phosphate de	772	6	1.5	344	2	JC5601	cAMP response elem
700	6	1.5	329	2	F69849	probable heme A fa	773	6	1.5	344	2	JC5602	cAMP response elem
701	6	1.5	329	2	G71091	hypothetical prote	774	6	1.5	344	2	T46928	hypothetical prote
702	6	1.5	330	2	T36194	probable acyl carr	775	6	1.5	345	2	C90509	sorbitol dehydroge
703	6	1.5	330	2	AG1405	phosphotriesterase	776	6	1.5	345	2	AF0670	probable NADP-depe
704	6	1.5	330	2	AG1781	phosphotriesterase	777	6	1.5	345	2	B83371	conserved hypothet
705	6	1.5	331	2	AB1737	conserved hypothet	778	6	1.5	345	2	F83084	rod shape-determin
706	6	1.5	331	2	AI1367	conserved hypothet	779	6	1.5	345	2	A97956	rod shape-determin
707	6	1.5	331	2	F86835	hypothetical prote	780	6	1.5	345	2	D88108	DNA polymerase III
708	6	1.5	331	2	C89469	protein F07G6.1 [i	781	6	1.5	345	2	S72833	periplasmic bindin
709	6	1.5	332	2	S63660	NADH2 dehydrogenas	782	6	1.5	345	2	T38043	probable golgi per
710	6	1.5	332	2	T34174	hypothetical prote	783	6	1.5	346	2	F70666	probable alcohol d
711	6	1.5	332	2	C72485	probable high-affi	784	6	1.5	346	2	C98098	catabolite control
712	6	1.5	332	2	H69360	ABC transporter AF	785	6	1.5	346	2	D71637	rod shape-determin
713	6	1.5	332	2	C84061	ferrichrome ABC tr	786	6	1.5	346	2	G84028	cell-shape determin
714	6	1.5	333	2	D95968	probable amino aci	787	6	1.5	346	2	F97849	rod shape-determin
715	6	1.5	333	2	H98282	hypothetical prote	788	6	1.5	347	2	T09140	rod shape-determin
716	6	1.5	334	1	DGBEX2	uracil-DNA glycosy	789	6	1.5	347	2	E71826	rod shape-determin
717	6	1.5	334	2	T20728	hypothetical prote	790	6	1.5	347	2	E64691	rod shape-determin
718	6	1.5	334	2	G69028	conserved hypothet	791	6	1.5	347	2	AC0446	rod shape-determin
719	6	1.5	334	2	D95942	conserved hypothet	792	6	1.5	347	2	AC0912	rod shape-determin
720	6	1.5	334	2	A89835	probable deoxyribo	793	6	1.5	347	2	G72684	hypothetical prote
721	6	1.5	335	2	C97053	ferrichrome transp	794	6	1.5	347	2	B87500	conserved hypothet
722	6	1.5	335	2	F86586	mreB [imported] -	795	6	1.5	347	2	S53348	nuclear fusion pro
723	6	1.5	335	2	C72038	oxidoreductase [im	796	6	1.5	347	2	A95403	probable sulfate/t
724	6	1.5	335	2	T39033	conserved hypothet	797	6	1.5	348	2	AI1037	probable capsid po
725	6	1.5	335	2	T32294	hypothetical prote	798	6	1.5	348	2	AI2475	hypothetical prote
726	6	1.5	335	2	T52249	probable basic hel	799	6	1.5	349	2	H72715	hypothetical prote
727	6	1.5	335	2	B87328	transcription regu	800	6	1.5	349	2	T31934	hypothetical prote
728	6	1.5	336	2	F86923	probable oxidizedu	801	6	1.5	349	2	G83605	probable ATP-bindi
729	6	1.5	336	2	S22619	hypothetical prote	802	6	1.5	349	2	G98273	hypothetical prote
730	6	1.5	336	2	A95234	catabolite control	803	6	1.5	349	2	AG3010	hypothetical prote
731	6	1.5	336	2	T37159	hypothetical prote	804	6	1.5	350	1	S52153	alcohol dehydrogen
732	6	1.5	336	2	T36970	probable methyl est	805	6	1.5	350	2	G90199	acyl carrier prote
733	6	1.5	337	2	AD1268	cell-shape determi	806	6	1.5	350	2	E90075	intercellular adhe
734	6	1.5	337	2	AF1630	cell-shape determi	807	6	1.5	351	2	AE1923	c-type cytochrome
735	6	1.5	337	2	A89047	protein C10G8.1 [i	808	6	1.5	351	2	E97459	sulfate ABC transp
736	6	1.5	337	2	S31131	hypothetical prote	809	6	1.5	351	2	AG2677	hypothetical prote
737	6	1.5	338	2	A69278	branched-chain ami	810	6	1.5	353	2	G82232	anthranilate phosp
738	6	1.5	338	2	AB3453	prolyl aminopeptid	811	6	1.5	353	2	H83482	hypothetical prote
739	6	1.5	338	2	T40495	homoserine kinase	812	6	1.5	353	2	T25390	hypothetical prote
740	6	1.5	338	2	B69439	signal-transducin	813	6	1.5	353	2	E81680	conserved hypothet
741	6	1.5	338	2	C75338	conserved hypothet	814	6	1.5	353	2	AF0676	hydrogenase-1 oper
742	6	1.5	339	2	G87511	ketol-acid reducto	815	6	1.5	355	1	H71363	conserved hypothet
743	6	1.5	339	2	B69436	LSU ribosomal prot	816	6	1.5	355	2	G84651	biotin holocarboxy
744	6	1.5	339	2	S70218	sipd protein - Sal	817	6	1.5	356	2	G82938	hemin transport sy
745	6	1.5	339	2	B86277	hypothetical prote	818	6	1.5	356	2	T47313	hypothetical prote
746	6	1.5	340	2	A99193	transcription repr	819	6	1.5	356	2	AG3612	glycerol kinase (E
747	6	1.5	340	2	AI3093	transcription repr	820	6	1.5	357	2	T17470	hydroxyphenyl pyru
748	6	1.5	340	2	AG0850	pathogenicity isla	821	6	1.5	357	2	AF1346	hypothetical prote
749	6	1.5	340	2	F88545	protein F59B2.11 [822	6	1.5	357	2	AI1716	hypothetical prote
750	6	1.5	340	2	B83177	probable aminotran	823	6	1.5	358	2	C75375	branched-chain ami
751	6	1.5	340	2	F85724	hypothetical prote	824	6	1.5	358	2	E84467	hypothetical prote
752	6	1.5	341	1	JS0340	anthranilate phosp	825	6	1.5	359	2	F91219	hypothetical prote
753	6	1.5	341	2	AF1319	ferrichrome ABC tr	826	6	1.5	359	2	A86804	hypothetical prote
754	6	1.5	341	2	AF1691	ferrichrome ABC tr	827	6	1.5	359	2	H86065	hypothetical prote
755	6	1.5	341	2	B70373	rod shape determin	828	6	1.5	359	2	D97651	hypothetical prote
756	6	1.5	341	2	B86269	F21F23.4 protein -	829	6	1.5	359	2	AF3470	transcription regu
757	6	1.5	341	2	A48422	ecdysone-inducible	830	6	1.5	360	2	T04535	hypothetical prote
758	6	1.5	341	2	S20827	CAMP response elem	831	6	1.5	361	2	C83350	hypothetical prote
759	6	1.5	341	2	S26686	CAMP response elem	832	6	1.5	361	2	G83879	hypothetical prote

833	6	1.5	361	2	B83327	probable transcrip
834	6	1.5	362	2	D82644	sugar-phosphate de
835	6	1.5	362	2	T29053	branched-chain-ami
836	6	1.5	363	2	A84032	3-isopropylmalate
837	6	1.5	363	2	F96992	polyA polymerase r
838	6	1.5	364	2	T04994	hypothetical prote
839	6	1.5	364	2	T35353	hypothetical prote
840	6	1.5	365	2	S66466	hypothetical prote
841	6	1.5	366	2	S03770	cathepsin E (EC 3.
842	6	1.5	366	2	S03770	pectinesterase (EC
843	6	1.5	367	1	BVECEB	rod shape-determin
844	6	1.5	367	2	C91144	regulator of ftsI
845	6	1.5	367	2	F85989	hypothetical prote
846	6	1.5	367	2	E90890	oxygen sensing pro
847	6	1.5	367	2	H85360	hypothetical prote
848	6	1.5	367	2	E95930	probable sulfate u
849	6	1.5	367	2	D85727	oxygen sensing pro
850	6	1.5	367	2	H97686	hypothetical prote
851	6	1.5	368	2	AE2912	dehydrogenase Atu2
852	6	1.5	368	2	C70786	probable live prot
853	6	1.5	368	2	A53439	RP protein - human
854	6	1.5	371	1	I80811	histone H2A.1 - ra
855	6	1.5	371	1	DEBSPA	pyruvate dehydroge
856	6	1.5	371	2	WMBEYO	dUTP diphosphatase
857	6	1.5	371	2	S75555	hypothetical prote
858	6	1.5	371	2	C87446	queuine tRNA ribos
859	6	1.5	371	2	F83487	hypothetical prote
860	6	1.5	373	1	T29605	hypothetical prote
861	6	1.5	374	2	WMBET6	Utl6 protein - hum
862	6	1.5	376	2	T09111	probable magnesium
863	6	1.5	376	2	D64897	probable NADPH2:qu
864	6	1.5	376	2	B85733	probable oxidoredu
865	6	1.5	376	2	E90885	probable oxidoredu
866	6	1.5	376	2	I45856	aspartic proteinas
867	6	1.5	376	2	A75381	peptide ABC transp
868	6	1.5	377	1	PEMQCJ	gastricsin (EC 3.4
869	6	1.5	377	2	T10222	glibberellin 20-oxi
870	6	1.5	377	2	G75095	lps biosynthesis r
871	6	1.5	379	1	ZPBPMU	gene P protein - p
872	6	1.5	379	2	C86821	hypothetical prote
873	6	1.5	380	2	A45443	tubulin-tyrosine 1
874	6	1.5	380	2	B41545	pregnancy-specific
875	6	1.5	380	2	I47176	chymosin (EC 3.4.2
876	6	1.5	380	2	D72641	probable chorismat
877	6	1.5	381	2	A12185	hypothetical prote
878	6	1.5	381	2	S64089	probable membrane
879	6	1.5	382	1	SYECCS	carbamoyl-phosphat
880	6	1.5	382	2	S01319	carbamoyl-phosphat
881	6	1.5	382	2	B85484	carbamoyl-phosphat
882	6	1.5	382	2	C90633	carbamoyl-phosphat
883	6	1.5	382	2	AD0510	carbamoyl-phosphat
884	6	1.5	382	2	S78285	conserved hypothet
885	6	1.5	382	2	G75294	probable transamin
886	6	1.5	383	2	T52391	hypothetical prote
887	6	1.5	383	2	A41545	pregnancy-specific
888	6	1.5	383	2	A41443	pepsin (EC 3.4.23.
889	6	1.5	383	2	I53870	Edg-1 orphan recep
890	6	1.5	384	2	F86411	pnrotein FIK23.16
891	6	1.5	384	2	JC7574	pepsinogen A - Afr
892	6	1.5	384	2	B64515	hypothetical prote
893	6	1.5	384	2	E70036	capsular polysacch
894	6	1.5	385	2	C64752	yaGA protein - Esc
895	6	1.5	385	2	JC7575	pepsinogen A - bul
896	6	1.5	386	2	S48074	nuclear receptor T
897	6	1.5	387	2	A82036	protein B0238.8 [i
898	6	1.5	387	2	A45117	fatty oxidation co
899	6	1.5	387	2	D75594	aspartic proteinas
900	6	1.5	387	2	B98187	sulfate adenylyltr
901	6	1.5	387	2	JT0461	probable lacI-famI
902	6	1.5	387	2	H65132	sarcosine oxidase
903	6	1.5	388	2	A29937	hypothetical 44.3
904	6	1.5	388	2	JC7246	gastricsin (EC 3.4
905	6	1.5	388	2	B83228	pepsinogen C - com
						probable MFS trans
906	6	1.5	388	2	B86193	hypothetical prote
907	6	1.5	388	2	F89773	hypothetical prote
908	6	1.5	388	2	AF1907	hypothetical prote
909	6	1.5	389	2	JE0371	pepsin C (EC 3.4.2
910	6	1.5	389	2	A38302	pepsin (EC 3.4.23.
911	6	1.5	389	2	I46616	pregnancy-associat
912	6	1.5	389	2	T29410	hypothetical prote
913	6	1.5	389	2	T28954	hypothetical prote
914	6	1.5	389	2	T32516	hypothetical prote
915	6	1.5	389	2	C96603	hypothetical prote
916	6	1.5	389	2	E95422	probable transmemb
917	6	1.5	390	2	JT0334	acid proteinase (E
918	6	1.5	390	2	AG2549	hypothetical prote
919	6	1.5	390	2	AG2549	hypothetical prote
920	6	1.5	390	2	D70834	hypothetical prote
921	6	1.5	390	2	C95954	hypothetical prote
922	6	1.5	391	2	D97201	aICAR transformyla
923	6	1.5	391	2	C70677	probable fadA5 pro
924	6	1.5	391	2	A43356	cathepsin E (EC 3.
925	6	1.5	391	2	AG3243	conjugal transfer
926	6	1.5	391	2	F96729	gastricsin (EC 3.4
927	6	1.5	392	1	A24608	probable allinase
928	6	1.5	392	2	H84679	hypothetical prote
929	6	1.5	393	2	A70958	probable pks18 pro
930	6	1.5	393	2	T29412	hypothetical prote
931	6	1.5	393	2	S57671	hypothetical prote
932	6	1.5	393	2	F84381	hypothetical prote
933	6	1.5	394	2	T44867	hypothetical prote
934	6	1.5	394	2	B43356	gastricsin (EC 3.4
935	6	1.5	394	2	T32964	hypothetical prote
936	6	1.5	394	2	C90387	hypothetical prote
937	6	1.5	395	1	LIRTT	triacylglycerol 11
938	6	1.5	395	2	T29411	hypothetical prote
939	6	1.5	395	2	A47701	aspartic proteinas
940	6	1.5	396	1	DCBYDM	adenosylmethionine
941	6	1.5	396	2	A34401	cathepsin E (EC 3.
942	6	1.5	396	2	T47207	aspartic proteinas
943	6	1.5	396	2	T45033	hypothetical prote
944	6	1.5	396	2	T35254	conserved hypothet
945	6	1.5	396	2	F84679	hypothetical prote
946	6	1.5	397	2	H71116	hypothetical prote
947	6	1.5	397	2	H72668	hypothetical prote
948	6	1.5	397	2	A96681	hypothetical prote
949	6	1.5	397	2	AH3170	conserved hypothet
950	6	1.5	398	2	S66465	cathepsin E (EC 3.
951	6	1.5	398	2	T33383	hypothetical prote
952	6	1.5	398	2	A45280	candidapepsin (EC
953	6	1.5	398	2	I59399	oncogene P1-1 - h
954	6	1.5	398	2	A64982	hypothetical 43.3
955	6	1.5	398	2	B85851	probable outer mem
956	6	1.5	398	2	S17428	interleukin-1 rece
957	6	1.5	399	2	D96717	hypothetical prote
958	6	1.5	400	1	S22539	transcription fact
959	6	1.5	400	2	E96029	probable beta-keto
960	6	1.5	400	2	I47099	renin (EC 3.4.23.1
961	6	1.5	400	2	T51953	H-protein promoter
962	6	1.5	400	2	AH2303	hypothetical prote
963	6	1.5	401	1	REMS	renin (EC 3.4.23.1
964	6	1.5	401	2	H70658	probable arof prot
965	6	1.5	401	2	H75554	Nifs-related prote
966	6	1.5	401	2	D91082	probable transport
967	6	1.5	401	2	E85927	partial proteable t
968	6	1.5	402	1	REMSK	renin (EC 3.4.23.1
969	6	1.5	402	2	B47701	aspartic proteinas
970	6	1.5	402	2	AE1354	transport system p
971	6	1.5	402	2	AF1724	transport system p
972	6	1.5	402	2	A70559	hypothetical prote
973	6	1.5	403	2	D89786	hypothetical prote
974	6	1.5	403	2	D86687	conserved hypothet
975	6	1.5	403	2	A82423	3-oxoacyl-(acyl-ca
976	6	1.5	404	2	T34875	hypothetical prote
977	6	1.5	404	2	B41317	O-antigen ligase c
978	6	1.5	404	2	AE0973	O-antigen ligase f

979	6	1.5	404	2	AH3481	sulfate transport
980	6	1.5	405	2	A25379	saccharopepsin (EC
981	6	1.5	405	2	I50608	bone morphogenetic
982	6	1.5	405	2	H71692	hypothetical prote
983	6	1.5	405	2	S33601	cell adhesion mole
984	6	1.5	406	1	REHUK	renin (EC 3.4.23.1
985	6	1.5	406	2	A87107	hypothetical prote
986	6	1.5	406	2	B96982	probable membrane
987	6	1.5	407	1	KHRTD	cathepsin D (EC 3.
988	6	1.5	407	2	G71414	hydroxymandelonitr
989	6	1.5	407	2	D71862	probable zinc-met
990	6	1.5	407	2	F64567	zinc metalloprotei
991	6	1.5	408	1	BMHIV	bone morphogenetic
992	6	1.5	408	2	JH0801	bone morphogenetic
993	6	1.5	408	2	S38343	bone morphogenetic
994	6	1.5	408	2	S58791	bone morphogenetic
995	6	1.5	409	1	F69814	fosmidmycin resist
996	6	1.5	409	2	A70932	probable PPE prote
997	6	1.5	409	2	A95944	probable periplasm
998	6	1.5	410	1	KHMSD	cathepsin D (EC 3.
999	6	1.5	410	1	ZEBPAL	Ea47 protein - pha
1000	6	1.5	410	2	T04372	protein EA41 - bar

ALIGNMENTS

RESULT 1

AS59090

Aspartic proteinase (EC 3.4.23.-) BACE precursor - human
N;Alternate names: beta-secretase; beta-site APP cleaving enzyme
C;Species: Homo sapiens (man)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000
C;Accession: A59090

R;Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teplow, M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Roger Science 286, 735-741, 1999

A;Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transme
A;Reference number: A59090; MUID:20002972; PMID:10531052

A;Note: submitted to GenBank, September 1999
A;Accession: A59090

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-501 <VAS>

A;Cross-references: GB:AF190725; NID:g6118538; PIDN:AAFO4142.1; PID:g6118539

C;Genetics:

A;Gene: BACE

C;Superfamily: beta-secretase

C;Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; pr

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-45/Domain: propeptide #status predicted <PRO>

F;46-501/Product: acid proteinase BACE #status predicted <MAT>

F;461-477/Domain: transmembrane #status predicted <TRN>

F;93,289/Active site: Asp #status predicted

F;153,172,223,354/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;330-380/Disulfide bonds: #status predicted

Query Match 3.0%; Score 12; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.0009;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
|||||

Db 90 ILVDTGSSNFAV 101

transcription regulator H1596, leucine-responsive - Haemophilus influenzae (strain Rd K
H64131

N;Alternate names: leucine-responsive regulatory protein
C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C;Accession: H64131

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64131
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-166 <TIGR>
A;Cross-references: GB:U32833; GB:L42023; NID:g1574432; PIDN:AAAC23241.1; PID:g1574439; "C;Function:
A;Description: activates a number of operons in response to the presence of exogenous
C;Superfamily: regulatory protein asnc
C;Keywords: DNA binding; transcription regulation
F;34-60/Region: helix-turn-helix motif

Query Match 2.0%; Score 8; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 GTTLRLRP 250
|||||

Db 136 GTTLRLRP 143

RESULT 3

JQ0729

60K inner-membrane protein - Proteus mirabilis (fragment)
C;Species: Proteus mirabilis
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999

C;Accession: JQ0729
R;Skovgaard, O.
Gene 93, 27-34, 1990

A;Title: Nucleotide sequence of a Proteus mirabilis DNA fragment homologous to the 60K-

A;Reference number: JQ0729; MUID:91033012; PMID:2172087

A;Accession: JQ0729

A;Molecule type: DNA

A;Residues: 1-237 <SKO>

A;Cross-references: GB:M58352; GB:M31295; NID:g150873; PIDN:AAA83954.1; PID:g150874

A;Experimental source: strain LM1509

C;Keywords: DNA replication; membrane protein

Query Match 2.0%; Score 8; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 DTGSSNFA 55
|||||

Db 206 DTGSSNFA 213

RESULT 4

G96659

protein F2K1.24 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C;Accession: G96659

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G96659

A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-287 <STO>
A;Cross-references: GB:AE005173; NID:g6633844; PIDN:AAF19703.1; GSPDB:GN00141
C;Genetics:
A;Gene: F2K1.24
A;Map position: 1
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 2.0%; Score 8; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 239 IVDSGTTL 246
|||
Db 269 IVDSGTTL 276

RESULT 5
H75528
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: H75528
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <WHI>
A;Cross-references: GB:AE001896; GB:AE000513; NID:g6458032; PIDN:AAF09938.1; PID:g645803
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0358
A;Map position: 1

Query Match 2.0%; Score 8; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 184 GGSVLGG 191
|||
Db 137 GGSVLGG 144

RESULT 6
AG0742
high-affinity zinc uptake system periplasmic binding protein [imported] - Salmonella ent
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG0742
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0742
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05642.1; PID:g16503138; GSPDB:GN00176
C;Genetics:
A;Gene: STY2099
C;Superfamily: hypothetical protein HI0119

Query Match 2.0%; Score 8; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 256 AVEAVAR 263
|||
Db 271 AVEAVAR 278

RESULT 7
PRLJHD
proteinase (EC 3.4.23.-) - squirrel monkey retrovirus SMRV-H
C;Species: squirrel monkey retrovirus SMRV-H
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Feb-1997
C;Accession: B31827
R;Oda, T.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Akiyama, K.; Mitsuobu, F.
Virology 167, 468-476, 1988
A;Title: Molecular cloning, complete nucleotide sequence, and gene structure of the pro
A;Reference number: A31827; MUID:89073750; PMID:3201749
A;Accession: B31827
A;Molecule type: DNA
A;Residues: 1-323 <ODA>
C;Genetics:
A;Gene: prt
C;Complex: homodimer
C;Superfamily: retroviral proteinase
C;Keywords: aspartic proteinase; homodimer; hydrolase
F;193/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 2.0%; Score 8; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 99 DLVTIPKG 106
|||
Db 126 DLVTIPKG 133

RESULT 8
T42999
ethanolamine-phosphate cytidyltransferase homolog - fission yeast (Schizosaccharomyce
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42999
R;Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T42999
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-327 <YOS>
A;Cross-references: EMBL:DB9199; NID:g1749605; PIDN:BAA13860.1; PID:g1749606
A;Experimental source: strain PR745

Query Match 2.0%; Score 8; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 SGTTLRL 249
|||
Db 153 SGTTLRL 160

RESULT 9
PEIKL
polyporopepsin (EC 3.4.23.29) - Irpex lacteus
C;Species: Irpex lacteus
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993
C;Accession: JU0057
R;Kobayashi, H.; Sekibata, S.; Shibuya, H.; Yoshida, S.; Kusakabe, I.; Murakami, K.
Agric. Biol. Chem. 53, 1927-1933, 1989
A;Title: Cloning and sequence analysis of cDNA for Irpex lacteus aspartic proteinase.
A;Reference number: JU0057
A;Accession: JU0057
A;Molecule type: mRNA

A;Residues: 1-340 <KOB>
A;Note: the amino-terminal 24 residues were sequenced on the isolated proteinase
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; glycoprotein; hydrolase
F;32,212/Active site: Asp #status predicted
F;192,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.0%; Score 8; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LVDTGSSN 53
Db 30 LVDTGSSN 37

RESULT 10
C72748
probable sun protein APE0514 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: C72748

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: C72748

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-352 <KAW>

A;Cross-references: DDBJ:AP000059; NID:G5103911; PIDN:BAA79479.1; PID:G5104163

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE0514

C;Superfamily: hypothetical protein HI0624

Query Match 2.0%; Score 8; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 VEAVARAS 265
Db 11 VEAVARAS 18

RESULT 11

T37720
ethanolamine-phosphate cytidyltransferase (BC 2.7.7.14) - fission yeast (Schizosacchar

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T37720

R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Lyne, M.H.

submitted to the EMBL Data Library, August 1999

A;Reference number: Z21739

A;Accession: T37720

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-365 <MUR>

A;Cross-references: EMBL:AL109770; PIDN:CAB52424.1; GSPDB:GN00066; SPDB:SPAC15E1.05C

A;Experimental source: strain 972h-; cosmid c15E1

C;Genetics:

A;Gene: SPDB:SPAC15E1.05C

A;Map position: 1

A;Introns: 23/1

C;Keywords: nucleotidyltransferase

Query Match 2.0%; Score 8; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 SGTLLRL 249
|||||||

Db 191 SGTLLRL 198

RESULT 12

E96676

hypothetical protein T23K8.15 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: E96676

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E96676

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-449 <STO>

A;Cross-references: GB:AE005173; NID:G4646203; PIDN:AAD26876.1; GSPDB:GN00141

C;Genetics:

A;Gene: T23K8.15

A;Map position: 1

Query Match 2.0%; Score 8; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 IVDSGTTL 246
Db 301 IVDSGTTL 308

RESULT 13

JC7626

amino acid transport system N transporter, SN2 - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7626

R;Nakanishi, T.; Sugawara, M.; Huang, W.; Martindale, R.G.; Leibach, F.H.; Ganapathy, M

Biochem. Biophys. Res. Commun. 281, 1343-1348, 2001

A;Title: Structure, function, and tissue expression pattern of human SN2, a subtype of

A;Reference number: JC7626; MUID:21139776; PMID:11243884

A;Contents: Liver cell line HepG2

A;Accession: JC7626

A;Molecule type: mRNA

A;Residues: 1-472 <NAK>

A;Cross-references: GB:AF276889; GB:AF196972

C;Comment: This SN2, an amino acid transporter, mediates Na+-coupled transport of syste

ine, and glycine. The transport function of SN2 is pH-dependent and Li+-tolerant.

C;Genetics:

A;Gene: sn2

A;Map position: X p11.23

C;Keywords: amino acid transport; transport system

Query Match 2.0%; Score 8; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 GILGLAYA 140
Db 65 GILGLAYA 72

RESULT 14

B65173

probable 60K inner membrane protein - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C/Accession: B65173
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of *Escherichia coli* K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: B65173
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-548 <BLAT>
A/Cross-references: GB:AE000447; GB:U00096; NID:g2367266; PIDN:AAC76728.1; PID:g1790140;
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Gene: yldC
C/Superfamily: probable 60K inner membrane protein; stage III sporulation protein homolo
C/Keywords: inner membrane; transmembrane protein
F/335-531/Domain: stage III sporulation protein homology <SPOR>

Query Match 2.0%; Score 8; DB 1; Length 548;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 DTGSSNFA 55
|||||
Db 207 DTGSSNFA 214

RESULT 15

H91208
60 KD inner-membrane protein [imported] - *Escherichia coli* (strain O157:H7, substrain RI
C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C/Accession: H91208
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: H91208
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-548 <HAY>
A/Cross-references: GB:BA000007; PIDN:BAB38063.1; PID:g13364115; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RMD 0509952
C/Genetics:
A/Gene: ECs4640
C/Superfamily: probable 60K inner membrane protein; stage III sporulation protein homolo

Query Match 2.0%; Score 8; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 DTGSSNFA 55
|||||
Db 207 DTGSSNFA 214

Search completed: April 1, 2003, 11:53:51
Job time : 36 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:47:10 ; Search time 14 Seconds
(without alignments)
1202.814 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
Perfect score: 406
Sequence: 1 ALEPALASPAGANFLAMVD.....STEDVASNCVPAQSLSEPTL 406

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	406	100.0	518	1 BAE2_HUMAN	Q9Y5Z0 homo sapien
2	12	3.0	501	1 BACE_HUMAN	P56817 homo sapien
3	12	3.0	501	1 BACE_MOUSE	P56818 mus musculu
4	12	3.0	501	1 BACE_RAT	P56819 rattus norv
5	8	2.0	166	1 LRP_HAIEIN	P45265 haemophilus
6	8	2.0	237	1 60IM_PROMI	P22833 proteus mir
7	8	2.0	323	1 VPRT_SMRVH	P21407 squirlrel mo
8	8	2.0	340	1 CARP_POLTU	P17576 polyporus t
9	8	2.0	365	1 ECT1_SCHPO	Q9uti6 schizosacch
10	8	2.0	548	1 60IM_ECOLI	P25714 escherichia
11	8	2.0	1620	1 DNMI_MOUSE	P13864 mus musculu
12	8	2.0	1622	1 DNMI_RAT	Q9z330 rattus norv
13	7	1.7	126	1 G8_HUMAN	Q9ubaf homo sapien
14	7	1.7	267	1 EX3_HAIEIN	P44318 haemophilus
15	7	1.7	268	1 EX3_ECOLI	P09030 escherichia
16	7	1.7	276	1 PSB8_HUMAN	P28062 homo sapien
17	7	1.7	296	1 KHSE_LACLC	P52991 lactococcus
18	7	1.7	302	1 Y091_METJA	Q57556 methanococc
19	7	1.7	305	1 DDLB_ECO57	Q8x9y6 escherichia
20	7	1.7	305	1 DDLB_ECOLI	P07862 escherichia
21	7	1.7	305	1 DDLB_SALTI	Q8z9g7 salmonella
22	7	1.7	324	1 PEP1_GADMO	Q8zru1 salmonella
23	7	1.7	326	1 YR75_ECOLI	P56272 gadus morhu
24	7	1.7	337	1 YXAG_BACSU	P21314 escherichia
25	7	1.7	354	1 MURB_TREPA	P42106 bacillus su
26	7	1.7	354	1 YGPI_YEAST	O83128 treponema p
27	7	1.7	367	1 PEP4_CHICK	P38616 saccharomyc
28	7	1.7	379	1 MRAW_TREPA	P00793 gallus gall
29	7	1.7	381	1 CHYM_CALJA	O83399 treponema p
30	7	1.7	386	1 PEP1_PIG	Q9n2d2 callithrix
31	7	1.7	387	1 PEP1_RABIT	P00791 sus scrofa
32	7	1.7	387	1 PEP2_RABIT	P28712 oryctolagus
33	7	1.7	387	1 PEP2_RABIT	P27821 oryctolagus

34	7	1.7	387	1 PEP3_RABIT	P27822 oryctolagus
35	7	1.7	387	1 PEP4_RABIT	P28713 oryctolagus
36	7	1.7	387	1 PEP4_CALJA	Q9n2d4 callithrix
37	7	1.7	388	1 PEP1_MACFU	P03954 macaca fusc
38	7	1.7	388	1 PEP2_MACFU	P27677 macaca fusc
39	7	1.7	388	1 PEP4_MACFU	P27678 macaca fusc
40	7	1.7	388	1 PEP4_HUMAN	P00790 homo sapien
41	7	1.7	388	1 PEP4_MACMU	P11489 macaca mula
42	7	1.7	398	1 CATD_CHICK	Q05744 gallus gall
43	7	1.7	419	1 CARV_CANAL	P10977 candida alb
44	7	1.7	420	1 PAG2_PIG	Q29079 sus scrofa
45	7	1.7	428	1 SURA_ECOLI	P21202 escherichia
46	7	1.7	452	1 PLM1_PLAFA	P39898 plasmodium
47	7	1.7	460	1 VATB_THEVO	Q97cp9 thermoplasm
48	7	1.7	462	1 GSA_MYCTU	O06390 mycobacteri
49	7	1.7	473	1 CYP1_CYNCA	P40782 cynara card
50	7	1.7	496	1 ASPR_ORYSA	P42211 oryza sativ
51	7	1.7	513	1 ASPR_CUCPE	O04057 cucurbita p
52	7	1.7	558	1 YJ83_MYCTU	Q10873 mycobacteri
53	7	1.7	569	1 YAP3_YEAST	P32329 saccharomyc
54	7	1.7	596	1 MKC7_YEAST	P53379 saccharomyc
55	7	1.7	602	1 VEI_MNPV	O84356 mastomys na
56	7	1.7	646	1 KDBE_SCHPO	Q10364 schizosacch
57	7	1.7	754	1 YAF6_SCHPO	Q09860 schizosacch
58	7	1.7	775	1 PTNC_MOUSE	P35831 mus musculu
59	7	1.7	831	1 NAPA_ALCEU	P39185 alcaligenes
60	7	1.7	841	1 RELA_STRAT	O85709 streptomyce
61	7	1.7	863	1 AD17_DROME	Q9vac5 drosophila
62	7	1.7	899	1 VA8D_SCHPO	Q09778 schizosacch
63	7	1.7	949	1 RCSC_ECOLI	P14376 escherichia
64	7	1.7	1009	1 WS14_CAEEL	P14846 caenorhabdi
65	7	1.7	1015	1 BGAL_ARTSP	Q59140 arthrobacte
66	7	1.7	1073	1 YPD4_YEAST	P43564 saccharomyc
67	7	1.7	1343	1 VGR2_RAT	O08775 rattus norv
68	7	1.7	1533	1 PUM_DROME	P25822 drosophila
69	7	1.7	1625	1 CTP1_MYCTU	Q10900 mycobacteri
70	6	1.5	52	1 V59_BPT3	P20405 bacterioph
71	6	1.5	52	1 V59_BPT7	P20406 bacterioph
72	6	1.5	58	1 Y06H_BPT4	P13315 bacterioph
73	6	1.5	71	1 VLXS_BPP21	P27360 bacterioph
74	6	1.5	72	1 PEP2_THUTO	P20140 thunnus thy
75	6	1.5	72	1 PSBH_TOBAC	P06415 nicotiana t
76	6	1.5	73	1 PEP3_PIG	P30879 sus scrofa
77	6	1.5	80	1 Y6A9_YEREN	O85269 yersinia en
78	6	1.5	80	1 Y6A9_YERPE	Q9zgw3 yersinia pe
79	6	1.5	87	1 YI23_BURCE	P24538 burkholderi
80	6	1.5	88	1 LEVI_XENLA	P13684 xenopus lae
81	6	1.5	96	1 YS98_MYCLE	Q13024 mycobacteri
82	6	1.5	100	1 PINL_HUMAN	O15428 homo sapien
83	6	1.5	105	1 ATP1_MYCPN	Q59550 mycoplasma
84	6	1.5	105	1 YKXD_BACSU	P49857 bacillus su
85	6	1.5	108	1 RSBW_BACLI	O50230 bacillus li
86	6	1.5	110	1 CSAA_BACSU	P37584 bacillus su
87	6	1.5	110	1 PEP4_BOVIN	P01278 bos taurus
88	6	1.5	115	1 YNFD_ECOLI	P76172 escherichia
89	6	1.5	117	1 NLTI_PRUDU	Q43017 prunus dulc
90	6	1.5	117	1 NLTP_PRUAV	Q9m5x8 prunus aviu
91	6	1.5	117	1 NLTP_SPTOL	P10976 spinacia ol
92	6	1.5	119	1 CHC1_BOOMO	P13531 bombyx mori
93	6	1.5	119	1 CHC2_BOOMO	Q17212 bombyx mori
94	6	1.5	119	1 CHC5_BOOMO	Q17214 bombyx mori
95	6	1.5	121	1 CHC4_BOOMO	P08829 bombyx mori
96	6	1.5	124	1 GLUT_LOPAM	P01823 lophius ame
97	6	1.5	124	1 HIS3_ZYMOO	Q9x3w1 zymomonas m
98	6	1.5	124	1 RNP_CHIBR	P00675 chinchilla
99	6	1.5	128	1 CYB_CROVV	Q95776 croctalus vi
100	6	1.5	131	1 RRPB_CVPR8	Q04158 porcine res
101	6	1.5	134	1 CC42_ANOGA	Q17031 anophelis g
102	6	1.5	134	1 VG24_BPMD2	O64218 mycobacteri
103	6	1.5	137	1 PSBW_SPTOL	Q41387 spinacia ol
104	6	1.5	138	1 YGJM_ECOLI	P42594 escherichia
105	6	1.5	141	1 TNG1_HUMAN	P56846 homo sapien
106	6	1.5	142	1 RPB6_SCHPO	P36595 schizosacch

107	6	1.5	146	1	RBFA_RHILO	Q98bi7	rhizobium 1	180	6	1.5	231	1	YHS2_YEAST	P38829	saccharomyc
108	6	1.5	147	1	LEGE_ANTCR	P06027	anthocidari	181	6	1.5	232	1	6PGL_CAVCR	Q9a6n1	caulobacter
109	6	1.5	147	1	TTHV_SHEEP	P12303	ovis aries	182	6	1.5	233	1	HA2F_MOUSE	P14435	mus musculus
110	6	1.5	152	1	PYRI_PYRAB	P77919	pyrococcus	183	6	1.5	233	1	HA2R_MOUSE	P14436	mus musculus
111	6	1.5	153	1	YEH3_PSEAE	Q9hub0	pseudomonas	184	6	1.5	233	1	HA2S_MOUSE	P14437	mus musculus
112	6	1.5	160	1	COAT_CGMVS	P19521	cucumber gr	185	6	1.5	234	1	VGPR_EBV	P03224	epstein-bar
113	6	1.5	160	1	Y964_MYCTU	P71546	mycobacteri	186	6	1.5	237	1	CYSH_XYLFA	Q9p8d2	xylella fas
114	6	1.5	161	1	TPM_SCHPO	Q02088	schizosacch	187	6	1.5	237	1	YI94_AQUAE	O67734	aquifex aeo
115	6	1.5	163	1	LRP_ECOLI	P19494	escherichia	188	6	1.5	239	1	CYSH_THIRO	P52672	thiocapsa r
116	6	1.5	163	1	LRP_KLEPN	P37424	klebsiella	189	6	1.5	240	1	CD48_MOUSE	P18181	mus musculus
117	6	1.5	163	1	LRP_SALTY	P37403	salmonella	190	6	1.5	240	1	TPMT_MOUSE	O55060	mus musculus
118	6	1.5	163	1	LRP_SERMA	P37425	seetratia ma	191	6	1.5	241	1	TPMT_MUSSP	Q9qk22	mus spretus
119	6	1.5	164	1	PUR6_HAEIN	P43849	haemophilus	192	6	1.5	242	1	SPIR_SPIME	P21625	spiroplasma
120	6	1.5	165	1	RLI0_BACSU	P42923	bacillus su	193	6	1.5	242	1	PR38_YEAST	Q00723	saccharomyc
121	6	1.5	165	1	YGZD_YEAST	P53057	saccharomyc	194	6	1.5	243	1	VL28_FOWPV	P15910	fowlpox vir
122	6	1.5	169	1	MSAI_STAAM	Q99qd5	staphylococ	195	6	1.5	244	1	CYAH_MYRVE	P22143	myrothecium
123	6	1.5	170	1	HPAC_KLEPN	Q48441	klebsiella	196	6	1.5	244	1	NGN1_MOUSE	P70660	mus musculus
124	6	1.5	173	1	RUTC_BRUME	Q8yiv7	brucella me	197	6	1.5	244	1	NGN1_RAT	P70595	rattus norv
125	6	1.5	173	1	VENV_LELV	Q04565	lelystad vi	198	6	1.5	244	1	RS2_BACHD	Q9ka63	bacillus ha
126	6	1.5	174	1	YGAP_ECOLI	P55734	escherichia	199	6	1.5	245	1	GIDB_ANASP	Q4ysa7	anaabaena sp
127	6	1.5	178	1	ESMS_DROME	P13096	drosophila	200	6	1.5	246	1	YOR4_ANATH	Q44408	anaerocellu
128	6	1.5	180	1	CFPR_CAVPO	Q00552	cavia porce	201	6	1.5	247	1	SLT1_CAEEL	Q9u3n5	caenorhabdi
129	6	1.5	182	1	APT_STRCO	P52561	streptomyc	202	6	1.5	247	1	YFBB_HAEIN	P44611	haemophilus
130	6	1.5	185	1	YXAK_BACSU	P42110	bacillus su	203	6	1.5	247	1	YG29_ARCFU	O28644	archaeoglob
131	6	1.5	188	1	GCHI_BACHD	Q9kcc7	bacillus ha	204	6	1.5	249	1	HMX1_CHICK	P28361	gallus gall
132	6	1.5	188	1	TRAF_RHISN	P55417	rhizobium s	205	6	1.5	251	1	PYR2_FREDI	P18543	fremyella d
133	6	1.5	189	1	PUR2_CHRVI	Q46482	chromatium	206	6	1.5	251	1	E1A_ADE41	P10542	human adeno
134	6	1.5	189	1	Y006_CHLTR	O84009	chlamydia t	207	6	1.5	251	1	GLO2_BUCAI	P57736	buchnera ap
135	6	1.5	190	1	CAH2_FLALI	P46513	flaveria li	208	6	1.5	252	1	TRPC_HALVO	P18304	halobacteri
136	6	1.5	191	1	CC42_DROME	P40793	drosophila	209	6	1.5	252	1	KDSB_VIBCH	Q9kqx2	vibrio chol
137	6	1.5	191	1	MOBA_PYRAB	Q9v0d0	pyrococcus	210	6	1.5	254	1	HA2J_MOUSE	P23150	mus musculus
138	6	1.5	192	1	MOBA_PYRHO	O58708	pyrococcus	211	6	1.5	254	1	ST19_MOUSE	Q9jhn8	mus musculus
139	6	1.5	198	1	RLI9_CAEEL	O02639	caenorhabdi	212	6	1.5	256	1	HA2D_MOUSE	P04228	mus musculus
140	6	1.5	202	1	COAT_BWYVF	P09508	beet wester	213	6	1.5	256	1	MYF5_NOTVI	Q91154	notophthalm
141	6	1.5	202	1	COAT_BWYVG	P09509	beet wester	214	6	1.5	256	1	Y929_TREPA	O83899	treponema p
142	6	1.5	205	1	DDL_ANACE	P35660	anaplasma c	215	6	1.5	259	1	MURB_HELPJ	Q9shd1	arabidopsis
143	6	1.5	205	1	KGU4_LACTIA	Q9cee3	lactococcus	216	6	1.5	259	1	MURB_HELPJ	Q9zjja	helicobacte
144	6	1.5	205	1	YJ11_MYCTU	O07722	mycobacteri	217	6	1.5	259	1	MURB_HELPJ	O25963	helicobacte
145	6	1.5	206	1	FGF4_BOVIN	P48803	bos taurus	218	6	1.5	259	1	Y500_METJA	O57923	methanococc
146	6	1.5	207	1	CCMA_ECOLI	P33931	escherichia	219	6	1.5	259	1	Y500_METJA	P74369	synechocyst
147	6	1.5	207	1	SODM_CHLPN	Q9z9c4	chlamydia p	220	6	1.5	260	1	PSA1_CHICK	O42265	gallus gall
148	6	1.5	209	1	HUPM_AZOC	Q43954	azotobacter	221	6	1.5	263	1	SUMT_SYNY3	Q55749	synechocyst
149	6	1.5	210	1	FGFL_MOUSE	Q9ijn1	mus musculu	222	6	1.5	264	1	VAL1_WDV	P06847	wheat dwarf
150	6	1.5	210	1	FLPA_ARCFU	O28192	archaeoglob	223	6	1.5	265	1	MYO2_LYCES	P54927	lycopersico
151	6	1.5	211	1	DEOC_BACSU	P39121	bacillus su	224	6	1.5	268	1	CH14_BRANA	Q06209	brassica na
152	6	1.5	211	1	RLI_HALCU	P05966	halobacteri	225	6	1.5	268	1	EX3_SALTY	O9z612	salmonella
153	6	1.5	211	1	RLI_HALNI	P13575	halobacteri	226	6	1.5	268	1	MIND_BACSU	Q01464	bacillus su
154	6	1.5	213	1	PYRF_METJA	Q57700	methanococc	227	6	1.5	268	1	Y489_METJA	O57913	methanococc
155	6	1.5	214	1	CYB_AGRKO	P92845	agkistrodon	228	6	1.5	269	1	YRBF_ECOLI	P45393	escherichia
156	6	1.5	214	1	CYB_AGRKA	P92852	agkistrodon	229	6	1.5	270	1	TONB_HAEIN	P42872	haemophilus
157	6	1.5	214	1	CYB_BOTAT	P92846	bothrops at	230	6	1.5	271	1	CRK_DROME	Q9xym0	drosophila
158	6	1.5	214	1	CYB_BOTBI	P92847	bothriopsis	231	6	1.5	271	1	YW34_MYCTU	O05879	mycobacteri
159	6	1.5	214	1	CYB_BOTSC	P92849	bothriechis	232	6	1.5	271	1	Y233_AQUAE	O06414	aquifex aeo
160	6	1.5	214	1	CYB_CERCE	P87419	cerastes ce	233	6	1.5	273	1	Y233_AQUAE	P26754	saccharomyc
161	6	1.5	214	1	CYB_CROAT	P92850	crotalus at	234	6	1.5	273	1	YDF5_SCHPO	Q10477	schizosacch
162	6	1.5	214	1	CYB_LACMU	P92853	lachesis mu	235	6	1.5	276	1	YKA2_CAEEL	P34254	caenorhabdi
163	6	1.5	215	1	YFGS_TRIST	P92857	trimeresuru	236	6	1.5	276	1	MOXJ_PARDE	P29900	paracoccus
164	6	1.5	215	1	YFGS_LACCA	P35924	lactobacill	237	6	1.5	278	1	CEMA_CVACA	O9tm16	cyanidium c
165	6	1.5	216	1	RL3_RICPR	P48952	rickettsia	238	6	1.5	281	1	P2C1_YEAST	P35182	saccharomyc
166	6	1.5	216	1	YLM3_CAEEL	P34357	caenorhabdi	239	6	1.5	286	1	RER2_YEAST	P35196	saccharomyc
167	6	1.5	217	1	OMPW_VIBCH	P17266	vibriol chol	240	6	1.5	287	1	SMN_BOVIN	O18870	bos taurus
168	6	1.5	218	1	SGAH_MYCPN	P75293	mycoplasma	241	6	1.5	287	1	SMN_CANFA	O02771	canis famill
169	6	1.5	218	1	SODM_SCHPO	Q9uxx0	schizosacch	242	6	1.5	288	1	HMXX_CHICK	P50223	gallus gall
170	6	1.5	219	1	ERD2_YEAST	P18414	saccharomyc	243	6	1.5	289	1	DLX5_MOUSE	P70396	mus musculus
171	6	1.5	219	1	ISPD_CHLTR	O84468	chlamydia t	244	6	1.5	289	1	DLX5_RAT	P50575	rattus norv
172	6	1.5	220	1	TRBF_RHISN	P55403	rhizobium s	245	6	1.5	292	1	Y240_MYCGE	O14782	mycoplasma
173	6	1.5	221	1	HA2Q_MOUSE	P04227	mus musculu	246	6	1.5	293	1	CMFL_SCHPO	O14161	schizosacch
174	6	1.5	223	1	TPIS_AERBE	Q9ybr1	aeropyrum p	247	6	1.5	295	1	Y005_RICPR	Q9zed7	rickettsia
175	6	1.5	225	1	GIDB_THETH	Q91cy2	thermus the	248	6	1.5	295	1	Y234_METJA	Q0258	methanococc
176	6	1.5	225	1	VG2R_AMEBP	P29818	amsacta moo	249	6	1.5	297	1	Y103_HUMAN	O15006	homo sapien
177	6	1.5	225	1	Y574_AERBE	Q9yek4	aeropyrum p	250	6	1.5	299	1	DAPA_STRCO	O86841	streptomyc
178	6	1.5	226	1	TSIS_SMSAV	P01128	simian sarc	251	6	1.5	300	1	COX2_YEAST	P19516	saccharomyc
179	6	1.5	229	1	YOEI_STRAT	Q53683	streptomyc	252	6	1.5	302	1	PF12_DROME	P12982	drosophila

253	6	1.5	302	1	PP13_DROME	Q05547	drosophila	326	6	1.5	370	1	ODPA_BACSU	P21881	bacillus su
254	6	1.5	303	1	SPAO_SALDU	Q53968	salmonella	327	6	1.5	371	1	CYB_BOACO	P92848	boa constri
255	6	1.5	303	1	SPAO_SALTI	Q56022	salmonella	328	6	1.5	371	1	CYB_CALKE	Q9mld7	calliophis
256	6	1.5	303	1	SPAO_SALTY	P40699	salmonella	329	6	1.5	371	1	CYB_CALMC	Q9mld6	calliophis
257	6	1.5	309	1	MTH3_HAEIN	P43871	haemophilus	330	6	1.5	371	1	CYB_CANAS	Q48023	candoia asp
258	6	1.5	312	1	FMT_MYCTU	P71674	mycobacteri	331	6	1.5	371	1	CYB_CANCA	Q48025	candoia car
259	6	1.5	312	1	YC39_CYACA	O19883	cyanidium c	332	6	1.5	371	1	CYB_CASDU	Q48027	casarea dus
260	6	1.5	313	1	LDH_CLOAB	Q97md1	clostridium	333	6	1.5	371	1	CYB_COLCO	Q9m110	coluber con
261	6	1.5	314	1	YC39_GUITH	Q78472	guillardia	334	6	1.5	371	1	CYB_EPIMO	Q48052	epicrates m
262	6	1.5	317	1	KDT2_SALTI	Q8z8h3	salmonella	335	6	1.5	371	1	CYB_ERYCC	Q48066	eryx colubr
263	6	1.5	317	1	KDT2_SALTY	Q8zqz4	salmonella	336	6	1.5	371	1	CYB_ERYCL	Q48067	eryx colubr
264	6	1.5	317	1	MTX1_HUMAN	Q13505	homo sapien	337	6	1.5	371	1	CYB_ERYEL	Q48073	eryx elegan
265	6	1.5	317	1	MTX1_HUMAN	P47802	mus musculu	338	6	1.5	371	1	CYB_ERYJA	Q48076	eryx jaculu
266	6	1.5	318	1	Y986_THEMEA	Q9x081	thermotoga	339	6	1.5	371	1	CYB_ERYMI	Q48079	eryx miliar
267	6	1.5	319	1	YC39_PORPU	P51238	porphyra pu	340	6	1.5	371	1	CYB_ERYMN	Q48080	eryx miliar
268	6	1.5	321	1	YC39_CYAPA	P48279	cyamophora	341	6	1.5	371	1	CYB_ERYTA	Q48085	eryx tatari
269	6	1.5	322	1	ARGI_HUMAN	P05089	homo sapien	342	6	1.5	371	1	CYB_MICEU	Q9m1k5	micruroides
270	6	1.5	323	1	VANH_ENTFA	Q47748	enterococcu	343	6	1.5	371	1	CYB_TOXPR	Q9m1k3	toxilocalam
271	6	1.5	325	1	LXB1_PHOLE	P09141	photobacter	344	6	1.5	371	1	DUT_HSV11	P10234	herpes simp
272	6	1.5	326	1	GGH_ARATH	O65355	arabidopsis	345	6	1.5	371	1	H2AY_HUMAN	O75367	homo sapien
273	6	1.5	327	1	XYNA_ASFAC	O59859	aspergillus	346	6	1.5	371	1	TGT_CAUCR	Q9a7y1	caulobacter
274	6	1.5	328	1	GRHR_BOVIN	P32236	bos taurus	347	6	1.5	371	1	Y816_SYNY3	P74041	synchocyst
275	6	1.5	328	1	GRHR_SHEEP	P32237	ovis aries	348	6	1.5	372	1	CYB_ACRDU	Q48010	acrantophis
276	6	1.5	329	1	CTAO_BACSU	O31652	bacillus su	349	6	1.5	372	1	CYB_ACRMA	Q48012	acrantophis
277	6	1.5	332	1	TRPD_VIBPA	P22096	vibriio para	350	6	1.5	372	1	CYB_ASPSC	Q9m1k0	aspidelaps
278	6	1.5	333	1	HK32_HUMAN	P78367	homo sapien	351	6	1.5	372	1	CYB_ELABA	Q9g250	elaphe bair
279	6	1.5	334	1	MRP1_CAEEL	Q93459	caenorhabdi	352	6	1.5	372	1	CYB_ELAVU	Q9g210	elaphe obso
280	6	1.5	334	1	UNG_HSV11	P10186	herpes simp	353	6	1.5	372	1	CYB_HETSI	Q9m1i8	heterodon s
281	6	1.5	334	1	YC11_METTH	O27279	methanobact	354	6	1.5	372	1	CYB_ELAVU	Q9m1j0	paranaja mu
282	6	1.5	335	1	YD59_SCHPO	Q10312	schizosacch	355	6	1.5	372	1	CYB_PARMU	Q48114	sanzinia ma
283	6	1.5	338	1	KHSE_SCHPO	O43056	schizosacch	356	6	1.5	372	1	CYB_SANME	Q9m1j0	walterinnes
284	6	1.5	339	1	ILVC_CAUCR	Q9a6h4	caulobacter	357	6	1.5	372	1	CYB_WALAE	P10200	herpes simp
285	6	1.5	339	1	RLA0_ARCFU	O28781	archaeoglob	358	6	1.5	373	1	UL16_HSV11	Q28057	bos taurus
286	6	1.5	340	1	YMAJ_CAEEL	P34486	caenorhabdi	359	6	1.5	376	1	PAG2_BOVIN	P03955	macaca fusc
287	6	1.5	341	1	CREM_MOUSE	P27699	mus musculu	360	6	1.5	377	1	PEPC_MACFU	P38584	bos taurus
288	6	1.5	341	1	CREM_MOUSE	Q03061	rattus norv	361	6	1.5	377	1	TTL_BOVIN	P38160	sus scrofa
289	6	1.5	341	1	TRPD_LACCA	P17170	lactobacill	362	6	1.5	379	1	TTL_PIG	P08558	bacterioph
290	6	1.5	342	1	YN9A_YEAST	P53757	saccharomyc	363	6	1.5	379	1	VVP_BPMU	Q9yell4	aeropyrum p
291	6	1.5	344	1	CREM_CANFA	P79145	canis famill	364	6	1.5	380	1	AROJ_AERPE	Q29432	bos taurus
292	6	1.5	345	1	CATD_PIG	P00795	sus scrofa	365	6	1.5	380	1	PAG1_BOVIN	Q90972	gallus gall
293	6	1.5	345	1	YAT2_SCHPO	Q10149	schizosacch	366	6	1.5	381	1	YG12_YEAST	P53155	saccharomyc
294	6	1.5	347	1	MREB_ECOLI	P13519	escherichia	367	6	1.5	381	1	CARA_ECOLI	P00907	escherichia
295	6	1.5	348	1	ADH1_PICST	O00097	pichia stip	368	6	1.5	382	1	CARA_ECOLI	Q8z918	salmonella
296	6	1.5	350	1	ADH1_CANAL	P43067	candida alb	369	6	1.5	382	1	CARA_SALTY	P14845	salmonella
297	6	1.5	351	1	COLF_ARATH	Q9fth8	arabidopsis	370	6	1.5	382	1	CARA_SALTY	O08530	mus musculu
298	6	1.5	351	1	KLIF2_RAT	Q9et58	rattus norv	371	6	1.5	382	1	EDG1_MOUSE	Q28755	ovis aries
299	6	1.5	353	1	Y634_CHLMU	Q9pk39	chlamydia m	372	6	1.5	382	1	PAG1_SHEEP	O06000	bacillus ce
300	6	1.5	353	1	YNCB_ECOLI	P76113	escherichia	373	6	1.5	382	1	RS1H_BACCE	Q80951	human papil
301	6	1.5	354	1	KLIF2_MOUSE	Q60843	mus musculu	374	6	1.5	382	1	VE2_HPV61	P49539	odontella s
302	6	1.5	355	1	KLIF2_HUMAN	Q9y5w3	homo sapien	375	6	1.5	383	1	YC44_ODOSI	P48303	rattus norv
303	6	1.5	355	1	Y121_TREPA	O83158	treponema p	376	6	1.5	383	1	EDG1_RAT	P16476	gallus gall
304	6	1.5	358	1	VCOM_ADE40	P48753	human adeno	377	6	1.5	384	1	PEPE_CHICK	P37007	escherichia
305	6	1.5	358	1	Y4BE_RHISN	P55428	rhizobium s	378	6	1.5	384	1	Y243_METUA	Q60298	methanococc
306	6	1.5	359	1	WECF_ECOS7	Q8xaq8	escherichia	379	6	1.5	385	1	NR21_CHICK	Q91379	gallus gall
307	6	1.5	359	1	WECF_ECOLI	P56258	escherichia	380	6	1.5	385	1	CMG2_HUMAN	P58335	homo sapien
308	6	1.5	362	1	ILVE_STRCO	O86505	streptomyce	381	6	1.5	386	1	ASBP_AEDAE	Q03168	aedes aegyp
309	6	1.5	365	1	CATD_SHEEP	Q9mzs8	ovis aries	382	6	1.5	387	1	GLGC_BACST	O08326	bacillus bt
310	6	1.5	366	1	PMEA_ERWCH	P07863	erwinia chr	383	6	1.5	387	1	MSOX_BACSN	P23342	bacillus sp
311	6	1.5	366	1	YGH0_ECOLI	Q46840	escherichia	384	6	1.5	387	1	SAT_DEIRA	P56864	deinococcus
312	6	1.5	368	1	ILVE_MYCTU	Q10399	mycobacteri	385	6	1.5	387	1	YHFX_ECOLI	P45550	escherichia
313	6	1.5	368	1	ST19_HUMAN	P49842	homo sapien	386	6	1.5	387	1	PEPC_CALUA	Q9n2d3	callithrix
314	6	1.5	370	1	CYB_COREN	O48039	corallus en	387	6	1.5	388	1	PEPC_HUMAN	P20142	homo sapien
315	6	1.5	370	1	CYB_EPIAN	O48041	epicrates a	388	6	1.5	388	1	PEPC_HUMAN	P27823	oryctolagus
316	6	1.5	370	1	CYB_EPICE	O48043	epicrates c	389	6	1.5	388	1	PEPC_RABIT	Q29078	sus scrofa
317	6	1.5	370	1	CYB_EPIEX	O48047	epicrates e	390	6	1.5	389	1	PAG1_PIG	P22929	saccharomyc
318	6	1.5	370	1	CYB_EPIFO	O48049	epicrates f	391	6	1.5	390	1	CARP_SACFI	P80209	bos taurus
319	6	1.5	370	1	CYB_EPISF	O48060	epicrates s	392	6	1.5	391	1	CATD_BOVIN	P25796	cavia porce
320	6	1.5	370	1	CYB_EPISM	O48055	epicrates s	393	6	1.5	391	1	CATE_CAVPO	P04073	rattus norv
321	6	1.5	370	1	CYB_EPIS	O48057	epicrates s	394	6	1.5	392	1	PEPC_RAT	Q29612	cercopithec
322	6	1.5	370	1	CYB_EPIST	O48053	epicrates s	395	6	1.5	393	1	ILIS_CERAE	Q64411	cavia porce
323	6	1.5	370	1	CYB_EPISU	O48062	epicrates s	396	6	1.5	394	1	PEPC_CAVPO	Q9ky56	streptomyce
324	6	1.5	370	1	CYB_EUNNO	O48065	eunectes no	397	6	1.5	394	1	SUC1_STRCO		
325	6	1.5	370	1	H2AY_RAT	Q02874	rattus norv	398	6	1.5	394	1	SUC1_STRCO		

399	6	1.5	395	1	LIPG_RAT	P04634	rattus norv	472	6	1.5	433	1	RHO_CHRVI	P52152	chromatium
400	6	1.5	396	1	CARP_NEUCR	Q01294	neurospora	473	6	1.5	435	1	FIXC_BRAJA	P10331	bradyrhizob
401	6	1.5	396	1	CATE_HUMAN	P14091	homo sapien	474	6	1.5	435	1	YOD7_CAEEL	Q09267	caenorhabdi
402	6	1.5	396	1	DCAM_YEAST	P21182	saccharomyc	475	6	1.5	436	1	COAT_CHVP1	P30328	paramecium
403	6	1.5	397	1	CATE_MOUSE	P70269	mus musculu	476	6	1.5	436	1	EPE2_RALSO	Q45411	ralstonia s
404	6	1.5	398	1	APLI_HUMAN	O14791	homo sapien	477	6	1.5	436	1	MNTH_DEIRA	Q9rt88	deinococcus
405	6	1.5	398	1	ASP3_CAEEL	P55956	caenorhabdi	478	6	1.5	437	1	GLA2_RHILQ	Q98a81	rhizobium 1
406	6	1.5	398	1	CAR2_CANAL	P28871	candida alb	479	6	1.5	437	1	NEOR_STRCY	P14501	streptomyc
407	6	1.5	398	1	CATE_RAT	P16228	rattus norv	480	6	1.5	437	1	YOEZ_BACSU	P54465	bacillus su
408	6	1.5	398	1	ILIS_HUMAN	P27930	homo sapien	481	6	1.5	438	1	SYS_HELAN	O81983	helianthus
409	6	1.5	400	1	PRTZ_HUMAN	P22891	homo sapien	482	6	1.5	438	1	Y16R_MYCIO	Q49573	mycoplasma
410	6	1.5	400	1	RENI_SHEEP	P52115	ovis aries	483	6	1.5	439	1	IDNT_ECOLI	P39344	escherichia
411	6	1.5	401	1	AROC_MYCTU	P95013	mycobacteri	484	6	1.5	440	1	BIK1_YEAST	P11709	saccharomyc
412	6	1.5	401	1	RENS_MOUSE	P00796	mus musculu	485	6	1.5	440	1	HIPA_ECOLI	P23874	escherichia
413	6	1.5	402	1	CAR1_CANPA	P32951	candida par	486	6	1.5	441	1	FLID_AQUAE	O67805	aquifex aeo
414	6	1.5	402	1	RENI_MOUSE	P06281	mus musculu	487	6	1.5	441	1	HISX_STRCO	P16245	streptomyc
415	6	1.5	404	1	RFAL_CHICK	P26471	salmonella	488	6	1.5	443	1	FTSA_AGRTS	O30991	agrobacteri
416	6	1.5	405	1	BMP4_CHICK	O90752	gallus gall	489	6	1.5	444	1	XK_HUMAN	P51811	homo sapien
417	6	1.5	405	1	CAR8_CANAL	O42778	candida alb	490	6	1.5	445	1	YGC5_ECOLI	Q46909	escherichia
418	6	1.5	405	1	CARP_YEAST	P07267	saccharomyc	491	6	1.5	450	1	MOO_HELPJ	Q92my5	helicobacte
419	6	1.5	406	1	DXR_MYCLE	O9cbu3	mycobacteri	492	6	1.5	450	1	MOO_HELPJ	O24913	helicobacte
420	6	1.5	406	1	RENI_HUMAN	P00797	homo sapien	493	6	1.5	451	1	SYS_ARATH	O39230	arabidopsis
421	6	1.5	407	1	CATD_RAT	P24268	rattus norv	494	6	1.5	453	1	PLM2_PLAFA	P46925	plasmodium
422	6	1.5	408	1	BMP4_DAMDA	Q29607	dama dama	495	6	1.5	453	1	VG_DROME	Q26366	drosofila
423	6	1.5	408	1	BMP4_HUMAN	P12644	homo sapien	496	6	1.5	454	1	MNTH_RHILQ	Q98199	rhizobium 1
424	6	1.5	408	1	BMP4_MOUSE	P21275	mus musculu	497	6	1.5	454	1	YGBN_ECOLI	Q46892	escherichia
425	6	1.5	408	1	BMP4_MOUSE	Q06826	rattus norv	498	6	1.5	455	1	MNTH_BRUME	Q9yi76	bruceella me
426	6	1.5	409	1	BMP4_RABIT	O46576	oryctolagus	499	6	1.5	459	1	EX7L_PSEAE	Q9hx18	pseudomonas
427	6	1.5	410	1	CATD_MOUSE	P18242	mus musculu	500	6	1.5	461	1	EF1A_ORYLA	Q9yic0	pseudomonas
428	6	1.5	410	1	EFTU_CODER	P50372	codium frag	501	6	1.5	462	1	EF10_XENLA	P13549	xenopus lae
429	6	1.5	410	1	VE47_LAMBD	P03752	bacterioph	502	6	1.5	462	1	EF11_CRIGR	P20001	cricetus
430	6	1.5	411	1	AATC_CHICK	P00504	gallus gall	503	6	1.5	462	1	EF11_HUMAN	P04720	homo sapien
431	6	1.5	411	1	BCAT_RAT	P54690	rattus norv	504	6	1.5	462	1	EF11_MOUSE	P10126	mus musculu
432	6	1.5	412	1	CAR2_CANPA	P32950	candida par	505	6	1.5	462	1	EF1A_BRARE	Q92005	brachydanio
433	6	1.5	412	1	CATD_HUMAN	P07339	homo sapien	506	6	1.5	462	1	OCT2_MOUSE	Q90835	gallus gall
434	6	1.5	412	1	PUR2_LACLA	O9zf44	lactococcus	507	6	1.5	462	1	COAT_FRG3V	Q00196	mus musculu
435	6	1.5	413	1	DXR_MYCTU	Q10798	mycobacteri	508	6	1.5	463	1	COAT_FRG3V	Q67473	frog virus
436	6	1.5	414	1	GLTF_BACSU	P39817	bacillus su	509	6	1.5	463	1	MURD_RHIME	Q91q28	rana tigrin
437	6	1.5	414	1	MTR_ECOLI	P22306	escherichia	510	6	1.5	463	1	COAT_RTRV	Q52953	rhizobium m
438	6	1.5	414	1	P2C3_SCHPO	Q09173	schizosacch	511	6	1.5	464	1	CASB_KLEOX	Q48409	klebsiella
439	6	1.5	416	1	DAD2_PSEAE	Q9hu99	pseudomonas	512	6	1.5	466	1	DLDH_ZYMMO	P50970	zymomonas m
440	6	1.5	416	1	PGK2_RAT	P16617	rattus norv	513	6	1.5	467	1	EUTA_SALTY	Q9zfy2	salmonella
441	6	1.5	416	1	PGK_CRIGR	P50310	cricetus	514	6	1.5	468	1	SYFA_SULSO	P95561	sulfolobus
442	6	1.5	416	1	PGK_HORSE	P00559	equus cabal	515	6	1.5	471	1	YEGB_ECOLI	P36554	escherichia
443	6	1.5	417	1	CAR4_CANAL	P43093	candida alb	516	6	1.5	474	1	CREG_ECOLI	P08401	escherichia
444	6	1.5	418	1	CAR5_CANAL	P43094	candida alb	517	6	1.5	474	1	DLDH_ALCEU	P52992	alcaligenes
445	6	1.5	418	1	CAR6_CANAL	P43095	candida alb	518	6	1.5	475	1	MOTD_RHIME	Q52964	rhizobium m
446	6	1.5	418	1	LEU2_THETN	Q8rdk2	thermoanaer	519	6	1.5	477	1	BAIG_EUBSP	P32369	eubacterium
447	6	1.5	418	1	RHAA_BACHD	Q9kcl9	bacillus ha	520	6	1.5	477	1	FIBB_PETMA	P02678	petromyzon
448	6	1.5	419	1	GSC_DROME	P54366	drosophila	521	6	1.5	477	1	NOMI_PSEAE	Q913y3	pseudomonas
449	6	1.5	419	1	KDAF_MOUSE	O09043	mus musculu	522	6	1.5	478	1	ALDA_ECOLI	P25553	escherichia
450	6	1.5	419	1	NOEB_RHISN	P55472	rhizobium s	523	6	1.5	478	1	EGR4_RAT	Q00911	rattus norv
451	6	1.5	419	1	NOEB_RHISN	P55472	rhizobium s	524	6	1.5	478	1	OCT2_HUMAN	P09086	homo sapien
452	6	1.5	420	1	NAPI_HUMAN	O96009	homo sapien	525	6	1.5	478	1	PUO_MICRU	P40974	micrococcus
453	6	1.5	420	1	PGK_TETTH	P50313	tetrahymena	526	6	1.5	478	1	YOHG_ECOLI	P33369	escherichia
454	6	1.5	420	1	RHO_HAEIN	P44619	haemophilus	527	6	1.5	479	1	6PGD_TRYBB	P31072	trypanosoma
455	6	1.5	420	1	VIT3_DROME	P06607	drosophila	528	6	1.5	482	1	MANC_ECO57	O85342	escherichia
456	6	1.5	421	1	TRAB_AGRTS	Q44351	agrobacteri	529	6	1.5	484	1	HEMZ_HORVU	P42045	hordeum vul
457	6	1.5	426	1	MNTH_MYCLE	O50103	mycobacteri	530	6	1.5	487	1	SYE2_THEMA	Q9x2i8	thermotoga
458	6	1.5	426	1	S6AA_HUMAN	P53796	homo sapien	531	6	1.5	489	1	FLIF_AQUAE	O67241	aquifex aeo
459	6	1.5	426	1	VA20_VACCC	P20095	vaccinia vi	532	6	1.5	490	1	TIGR_THEMA	Q9wy79	thermotoga
460	6	1.5	426	1	VA20_VARIV	P33843	variola vir	533	6	1.5	492	1	MURE_RHILQ	Q981e8	rhizobium 1
461	6	1.5	427	1	DSL1_CHICK	P34822	gallus gall	534	6	1.5	495	1	NUSA_ECOLI	P03003	escherichia
462	6	1.5	427	1	RHO_BACSU	Q03222	bacillus su	535	6	1.5	496	1	NUSA_BUCAI	P57459	buchnera ap
463	6	1.5	428	1	GLYA_AQUAE	O66776	aquifex aeo	536	6	1.5	498	1	NMT2_HUMAN	O60551	homo sapien
464	6	1.5	428	1	ZF26_MOUSE	P10076	mus musculu	537	6	1.5	499	1	C1W5_HUMAN	O95279	homo sapien
465	6	1.5	429	1	PUR2_ECOLI	P15640	escherichia	538	6	1.5	500	1	NUSA_SALTY	P37430	salmonella
466	6	1.5	429	1	PUR2_SALTI	O8z334	salmonella	539	6	1.5	503	1	HSF1_MOUSE	P38532	mus musculu
467	6	1.5	429	1	PUR2_SALTY	P26977	salmonella	540	6	1.5	504	1	AMPX_VIBPR	Q01693	vibrio prot
468	6	1.5	430	1	GLGC_ECOLI	P00584	escherichia	541	6	1.5	504	1	PGI1_YEAST	P27705	saccharomyc
469	6	1.5	431	1	NOOE_THETH	Q56229	thermus the	542	6	1.5	506	1	PALL_PHAVU	P07218	phaseolus v
470	6	1.5	432	1	YALI_RHISN	P55495	rhizobium s	543	6	1.5	507	1	CP3S_BOVIN	P79102	bos taurus
471	6	1.5	433	1	ENO_CAEEL	Q27527	caenorhabdi	544	6	1.5	507	1	FUMH_MOUSE	P97807	mus musculu

545	6	1.5	508	1	ASPR_HORVU	P42210	hordeum vul	618	6	1.5	602	1	2A5D_HUMAN	Q14738	h serine/th
546	6	1.5	508	1	YL12_YEAST	Q12303	saccharomyc	619	6	1.5	602	1	PEHX_ERWCH	P15922	erwinia chr
547	6	1.5	509	1	APR1_ORYSA	Q42456	oryza sativ	620	6	1.5	602	1	TX15_MOUSE	O70306	mus musculu
548	6	1.5	509	1	NUOM_ECOLI	P31978	escherichia	621	6	1.5	604	1	HEMA_CDVO	P24306	canine dist
549	6	1.5	512	1	HUTH_STRCO	Q9eww1	streptomyce	622	6	1.5	607	1	DNAX_STRPN	P95829	streptococc
550	6	1.5	512	1	K2C5_XENLA	P16878	xenopus lae	623	6	1.5	607	1	DNAX_STRPY	P95831	streptococc
551	6	1.5	513	1	EX7L_BRUME	O8ycx1	bruceella me	624	6	1.5	607	1	HEMA_CDV44	Q66001	canine dist
552	6	1.5	514	1	SAD1_SCHPO	Q09825	schizosacch	625	6	1.5	607	1	HEMA_CDV46	Q66000	canine dist
553	6	1.5	515	1	RHO_BORBU	P33561	borrelia bu	626	6	1.5	607	1	HEMA_PHODV	P28882	phocine dis
554	6	1.5	515	1	SIR2_CANAL	O59923	candida alb	627	6	1.5	608	1	DEXT_PENMI	P48845	penicillium
555	6	1.5	516	1	T2D5_YEAST	P53040	saccharomyc	628	6	1.5	608	1	YD6C_SCHPO	Q10324	schizosacch
556	6	1.5	520	1	SCOT_PIG	Q29551	sus scrofa	629	6	1.5	609	1	DNAX_STRAG	P95693	streptococc
557	6	1.5	520	1	YEAE_SCHPO	O14079	schizosacch	630	6	1.5	609	1	GLPO_LACLA	Q9cgg5	lactococcu
558	6	1.5	521	1	EX7L_RHILO	Q987v3	rhizobium l	631	6	1.5	609	1	PRXC_CURIN	P49053	curvularia
559	6	1.5	521	1	FD33_MYCTU	Q11015	mycobacteri	632	6	1.5	611	1	CALG_MOUSE	P52194	mus musculu
560	6	1.5	521	1	PHLB_MYCTU	P95246	mycobacteri	633	6	1.5	614	1	CYSN_MOUSE	Q10600	m cyn/cysc
561	6	1.5	522	1	NIFK_AZOVI	P07329	azotobacter	634	6	1.5	614	1	TU11_SCHPO	Q09715	schizosacch
562	6	1.5	522	1	NU62_HUMAN	P37198	homo sapien	635	6	1.5	616	1	MUTA_STRCM	Q05064	streptomyce
563	6	1.5	522	1	UAP1_HUMAN	Q16222	h udp-n-ace	636	6	1.5	617	1	VG31_BPMD2	O64225	mycobacteri
564	6	1.5	523	1	TRXB_CAEEL	Q17745	caenorhabdi	637	6	1.5	626	1	GPBA_HUMAN	P07359	homo sapien
565	6	1.5	523	1	UL21_PRVN3	Q00703	pseudorabie	638	6	1.5	626	1	NR43_HUMAN	Q92570	homo sapien
566	6	1.5	525	1	SERA_METHN	O27051	methanobact	639	6	1.5	628	1	NR43_RAT	P51179	rattus norv
567	6	1.5	525	1	VMT1_HUMAN	P54219	homo sapien	640	6	1.5	629	1	ASM_HUMAN	P17405	homo sapien
568	6	1.5	526	1	BGI_ARATH	P02896	trypanosoma	641	6	1.5	629	1	MUTL_HAEIN	P44494	haemophilus
569	6	1.5	528	1	PPBE_MOUSE	Q9ses0	arabidopsis	642	6	1.5	630	1	MLA3_HUMAN	Q9nr34	homo sapien
570	6	1.5	530	1	TRPG_ECOLI	P24823	mus musculu	643	6	1.5	630	1	PARE_ECOLI	P20083	escherichia
571	6	1.5	530	1	TRPG_SALTY	P00904	escherichia	644	6	1.5	631	1	PTBA_ERWCH	P26207	erwinia chr
572	6	1.5	530	1	KPYK_EIMTE	P00905	salmonella	645	6	1.5	632	1	AFUB_HAEIN	Q57341	haemophilus
573	6	1.5	531	1	PPBI_BOVIN	O44006	eimeria ten	646	6	1.5	632	1	RCAC_FREDI	Q01473	fremyella d
574	6	1.5	533	1	RRPB_CVPSN	P19111	bos taurus	647	6	1.5	634	1	GHR_BOVIN	P79108	bos taurus
575	6	1.5	533	1	YD19_MYCTU	P18457	porcine tra	648	6	1.5	635	1	S6A8_BOVIN	O18875	bos taurus
576	6	1.5	535	1	SR54_YARLI	Q10632	mycobacteri	649	6	1.5	635	1	S6A8_HUMAN	P48029	homo sapien
577	6	1.5	536	1	ZF94_RAT	Q99150	yarrowia li	650	6	1.5	635	1	S6A8_RABIT	P31661	oryctolagus
578	6	1.5	536	1	YIV9_YEAST	Q9z2K3	rattus norv	651	6	1.5	635	1	S6A8_RAT	P28570	rattus norv
579	6	1.5	537	1	YA94_HUMAN	P40583	saccharomyc	652	6	1.5	641	1	LIP_STAHY	P04635	staphylococ
580	6	1.5	538	1	CGT_HUMAN	Q9upg8	homo sapien	653	6	1.5	641	1	TETS_LISMO	Q48791	listeria mo
581	6	1.5	541	1	CGT_MOUSE	Q16880	homo sapien	654	6	1.5	643	1	VE1_HP27	P36723	human papil
582	6	1.5	541	1	CBPY_RAT	Q64676	mus musculu	655	6	1.5	645	1	HRC2_XANCV	P80150	xanthomonas
583	6	1.5	542	1	DSK1_SCHPO	Q09426	rattus norv	656	6	1.5	646	1	TETS_LACLA	Q48712	lactococcu
584	6	1.5	544	1	EX7L_ZYMO	P36616	schizosacch	657	6	1.5	650	1	RAB1_RAT	P37727	rattus norv
585	6	1.5	544	1	ILVD_SULSO	Q9fd14	zymomonas m	658	6	1.5	654	1	SPH2_HUMAN	Q9nra0	homo sapien
586	6	1.5	548	1	SRG8_HUMAN	Q05240	mycobacteri	659	6	1.5	658	1	GSPD_PSEAE	P35818	pseudomonas
587	6	1.5	550	1	GPT1_CANAL	Q14247	homo sapien	660	6	1.5	659	1	POL_CERV	P05400	carnation e
588	6	1.5	551	1	TNSC_ECOLI	P22034	synechocyst	661	6	1.5	668	1	PBS2_YEAST	P08018	saccharomyc
589	6	1.5	553	1	ILVD_SULSO	O74248	candida alb	662	6	1.5	672	1	SL52_HUMAN	P31639	homo sapien
590	6	1.5	555	1	ZDS_ARATH	P05846	escherichia	663	6	1.5	672	1	COAT_PAVBO	P26430	oryctolagus
591	6	1.5	558	1	POTA_MYCGE	Q97ub2	sulfolobus	664	6	1.5	673	1	GSPD_AERHY	P07297	bovine parv
592	6	1.5	559	1	HEMA_IACKG	Q38893	arabidopsis	665	6	1.5	678	1	RSPD_AGR75	P31780	aeromonas h
593	6	1.5	561	1	HEMA_IAMIN	P47288	mycoplasma	666	6	1.5	678	1	GSPD_AGR75	P45778	aeromonas s
594	6	1.5	561	1	ESR3_MICUN	P12581	influenza a	667	6	1.5	684	1	RSPD_AGR75	P33452	agrobacteri
595	6	1.5	565	1	VNUC_INCCA	P57783	microgoni	668	6	1.5	690	1	FLHA_ECOLI	P35656	raistonia s
596	6	1.5	565	1	LAC3_THACU	P08028	influenza c	669	6	1.5	692	1	FLHA_TREPA	P81683	staphylococ
597	6	1.5	572	1	DPOL_MOUSE	Q02079	thanatephor	670	6	1.5	692	1	FLHA_TREPA	P40729	salmonella
598	6	1.5	573	1	ITRI_YEAST	Q9qxe2	mus musculu	671	6	1.5	694	1	LCF3_YEAST	P39002	saccharomyc
599	6	1.5	575	1	PSP2_YEAST	Q9ugp5	homo sapien	672	6	1.5	694	1	LCF4_YEAST	P47912	saccharomyc
600	6	1.5	575	1	YD49_MYCTU	P25248	brassica na	673	6	1.5	696	1	FLHA_PROMI	Q51910	proteus mir
601	6	1.5	578	1	FKBX_MOUSE	P50109	saccharomyc	674	6	1.5	697	1	CEAD_ECOLI	P17998	escherichia
602	6	1.5	579	1	HEMA_STRCO	Q11019	mycobacteri	675	6	1.5	700	1	BIB_DROME	P23645	drosophila
603	6	1.5	581	1	DNL1_PYRAE	O61576	mus musculu	676	6	1.5	702	1	UMOB_PROMI	O86988	proteus mir
604	6	1.5	581	1	ITRI_YEAST	Q9wx15	streptomyce	677	6	1.5	707	1	FLHA_TREPA	O56338	treponema p
605	6	1.5	584	1	PUR9_SCHPO	P30605	saccharomyc	678	6	1.5	707	1	ABBI_MOUSE	P52157	streptomyce
606	6	1.5	584	1	PUR9_YEAST	O74928	s bifunctio	679	6	1.5	708	1	ABBI_MOUSE	Q9ngq7	homo sapien
607	6	1.5	585	1	PUR9_YEAST	P54113	s bifunctio	680	6	1.5	710	1	ABBI_MOUSE	O00213	homo sapien
608	6	1.5	591	1	PUR9_YEAST	P31939	homo sapien	681	6	1.5	710	1	ABBI_MOUSE	P19143	phaseolus v
609	6	1.5	591	1	PUR9_YEAST	P38009	s bifunctio	682	6	1.5	710	1	ABBI_MOUSE	Q01992	rattus norv
610	6	1.5	592	1	PUR9_YEAST	Q9cwj9	mus musculu	683	6	1.5	713	1	PMIP_RAT	P27991	glycine max
611	6	1.5	592	1	PUR9_YEAST	P51689	homo sapien	684	6	1.5	713	1	PMIP_RAT	Q99797	homo sapien
612	6	1.5	592	1	PUR9_YEAST	Q08346	haemophilus	685	6	1.5	714	1	CDG1_PAEWA	P04830	paenibacill
613	6	1.5	593	1	PUR9_YEAST	P31335	gallus gall	686	6	1.5	714	1	NARB_SYNY3	P73448	synechocyst
614	6	1.5	593	1	PUR9_YEAST	Q05647	erysipeloth	687	6	1.5	714	1	NARB_SYNY3	Q05001	catharantlu
615	6	1.5	593	1	PUR9_YEAST			688	6	1.5	714	1	NARB_SYNY3		
616	6	1.5	593	1	PUR9_YEAST			689	6	1.5	716	1	KIF2_MOUSE		
617	6	1.5	600	1	DNAX_ERYRH			690	6	1.5	716	1	KIF2_MOUSE		

691	6	1.5	716	1	PEP DROME	P41073 drosophila	764	6	1.5	960	1	CSE1_YEAST	P33307 saccharomyc
692	6	1.5	722	1	AD2I_HUMAN	Q9ukj8 homo sapien	765	6	1.5	967	1	ATSI_RAT	Q9wuq1 rattus norv
693	6	1.5	726	1	BP1I_HUMAN	P50747 h biotin--p	766	6	1.5	968	1	SLA2_YEAST	P33338 saccharomyc
694	6	1.5	731	1	NGP1_HUMAN	Q13823 homo sapien	767	6	1.5	969	1	YEAC_SCHPO	Q14077 schizosacch
695	6	1.5	735	1	ADDA_MOUSE	Q9qyc0 mus musculu	768	6	1.5	993	1	YIS2_YEAST	P40562 saccharomyc
696	6	1.5	735	1	ADDA_RAT	Q63028 rattus norv	769	6	1.5	994	1	MERK_RAT	P57097 rattus norv
697	6	1.5	735	1	YDD7_SCHPO	Q10432 schizosacch	770	6	1.5	997	1	ATS7_HUMAN	Q9ukp4 homo sapien
698	6	1.5	737	1	ADDA_HUMAN	P35611 homo sapien	771	6	1.5	999	1	RLK5_ARATH	P47735 arabidopsis
699	6	1.5	738	1	AB10_HUMAN	Q9nrk6 homo sapien	772	6	1.5	1000	1	S155_YEAST	P43612 saccharomyc
700	6	1.5	739	1	CATA_MYCSM	Q59557 mycobacteri	773	6	1.5	1002	1	VGNM_CPSMV	P31630 cowpea seve
701	6	1.5	743	1	CUU2_CAEEL	Q17390 caenorhabdi	774	6	1.5	1014	1	ACA2_ARATH	O81108 arabidopsis
702	6	1.5	757	1	CIKF_HUMAN	Q14003 homo sapien	775	6	1.5	1015	1	ACA7_ARATH	O64806 arabidopsis
703	6	1.5	762	1	SLAP_ANCEKI	P22258 acetogenium	776	6	1.5	1015	1	HIRA_MOUSE	O61666 mus musculu
704	6	1.5	764	1	TGMH_TACTR	Q05187 tachypleus	777	6	1.5	1017	1	TRL3_HUMAN	Q9hcf6 homo sapien
705	6	1.5	770	1	NASB_BACSU	P42433 bacillus su	778	6	1.5	1030	1	STK9_HUMAN	O76039 homo sapien
706	6	1.5	771	1	CTPG_MYCTU	Q10866 mycobacteri	779	6	1.5	1041	1	DDI6_HUMAN	O60231 homo sapien
707	6	1.5	771	1	NTRY_AZOCA	Q04850 azorhizobiu	780	6	1.5	1047	1	RIR1_CHLMU	Q9p193 chlamydia m
708	6	1.5	775	1	SM3E_HUMAN	O15041 homo sapien	781	6	1.5	1047	1	RIR1_CHLTR	O84834 chlamydia t
709	6	1.5	775	1	SM3E_MOUSE	P70275 mus musculu	782	6	1.5	1054	1	IF2_STIAU	P55875 stigmatella
710	6	1.5	779	1	LEU2_YEAST	P07264 saccharomyc	783	6	1.5	1056	1	AMP1_PLAFQ	O96935 plasmodium
711	6	1.5	783	1	GCR_MOUSE	P06537 mus musculu	784	6	1.5	1070	1	Y355_HUMAN	O15063 homo sapien
712	6	1.5	790	1	RELA_MYCTU	Q50638 mycobacteri	785	6	1.5	1081	1	MSH3_ARATH	O65607 arabidopsis
713	6	1.5	791	1	POLG_DENIC	P27913 dengue viru	786	6	1.5	1082	1	A3B2_HUMAN	Q13367 homo sapien
714	6	1.5	792	1	POLG_DENIA	P27912 dengue viru	787	6	1.5	1082	1	RGR1_YEAST	P19263 saccharomyc
715	6	1.5	795	1	GCR_RAT	P06536 rattus norv	788	6	1.5	1083	1	T2D3_HUMAN	Q00268 homo sapien
716	6	1.5	799	1	YDDU_ECOLI	P76129 escherichia	789	6	1.5	1087	1	POM1_SCHPO	O09690 schizosacch
717	6	1.5	800	1	RR3_CHLEU	P46307 chlamydomon	790	6	1.5	1090	1	PULA_KLEPN	P07206 klebsiella
718	6	1.5	810	1	HTR4_HALN1	Q9hp84 halobacteri	791	6	1.5	1091	1	ATN1_YEAST	P13587 saccharomyc
719	6	1.5	810	1	HTR4_HALSA	Q48317 halobacteri	792	6	1.5	1091	1	ATN2_YEAST	Q01896 saccharomyc
720	6	1.5	815	1	AKH_HAEIN	P44505 haemophilus	793	6	1.5	1091	1	ATN5_YEAST	Q12691 saccharomyc
721	6	1.5	816	1	AKH_BUCAL	P57290 buchnera ap	794	6	1.5	1093	1	TME1_HUMAN	P82094 homo sapien
722	6	1.5	819	1	AHMI_ARATH	Q9m3h5 arabidopsis	795	6	1.5	1097	1	DPOL_MCMVS	P27172 murine cyto
723	6	1.5	819	1	AKIH_SERMA	P27725 serratia ma	796	6	1.5	1097	1	TOLL_DROME	P08953 drosophila
724	6	1.5	820	1	AKIH_ECOLI	P00561 escherichia	797	6	1.5	1103	1	PMAI_DUNAC	P54210 dunaliella
725	6	1.5	823	1	YNS2_CAEEL	P34586 caenorhabdi	798	6	1.5	1116	1	RPOB_HETCA	P36440 heterosigma
726	6	1.5	831	1	NAH3_RAT	P26433 rattus norv	799	6	1.5	1125	1	CYGS_STRPV	P16065 strongyloce
727	6	1.5	832	1	NAH3_RABIT	P26432 oryctolagus	800	6	1.5	1131	1	PMAI_DUNBI	P54211 dunaliella
728	6	1.5	834	1	NAH3_HUMAN	P48764 homo sapien	801	6	1.5	1132	1	NUU1_YEAST	P53114 saccharomyc
729	6	1.5	836	1	GLK1_MOUSE	Q60934 mus musculu	802	6	1.5	1137	1	MSB1_YEAST	P21339 saccharomyc
730	6	1.5	840	1	MUTS_LACLA	Q9cdk9 lactococcus	803	6	1.5	1146	1	YHC3_YEAST	P38742 saccharomyc
731	6	1.5	843	1	SECA_STAUV	O06446 staphylococ	804	6	1.5	1150	1	APMU_PIG	P12021 sus scrofa
732	6	1.5	844	1	SECA_STACA	P47994 staphylococ	805	6	1.5	1156	1	C9AA_BACTG	Q99031 bacillus th
733	6	1.5	849	1	AKA4_MOUSE	Q60662 mus musculu	806	6	1.5	1186	1	DNBI_HSVB2	P12639 bovine herp
734	6	1.5	856	1	POLG_FVYO	P22602 potato viru	807	6	1.5	1187	1	M10L_MOUSE	Q99mvs mus musculu
735	6	1.5	863	1	YS97_CAEEL	Q09966 caenorhabdi	808	6	1.5	1191	1	NKCI_SOUAC	P55013 squalus aca
736	6	1.5	865	1	LAC9_KLULA	P08657 kluvereromyc	809	6	1.5	1197	1	Y4CA_RHISN	P55383 rhizobium s
737	6	1.5	877	1	DPOI_STRPN	P13252 streptococc	810	6	1.5	1220	1	SLN1_YEAST	P39928 saccharomyc
738	6	1.5	881	1	GLND_VIBCH	Q9kpv0 vibrio chol	811	6	1.5	1225	1	KF4A_CHICK	Q90640 gallus gall
739	6	1.5	883	1	CHB_VIBHA	P13670 vibrio harv	812	6	1.5	1237	1	YG2L_YEAST	P53254 saccharomyc
740	6	1.5	885	1	UE3A_MOUSE	O08759 mus musculu	813	6	1.5	1238	1	BVGS_BORPE	P16575 bordetella
741	6	1.5	886	1	SYA_BARBA	P70865 bartonella	814	6	1.5	1253	1	SC25_YEAST	P14771 saccharomyc
742	6	1.5	887	1	GLND_KLEPN	P41393 klebsiella	815	6	1.5	1254	1	POLS_EEVB8	P05674 venezuelan
743	6	1.5	887	1	MCM2_DROME	P49735 drosophila	816	6	1.5	1254	1	POLS_EEVEE	P36330 venezuelan
744	6	1.5	889	1	CIKF_RAT	Q01956 rattus norv	817	6	1.5	1254	1	POLS_EEVT	P36331 venezuelan
745	6	1.5	896	1	NAH5_HUMAN	Q14940 homo sapien	818	6	1.5	1254	1	POLS_EEVM	P09592 venezuelan
746	6	1.5	897	1	RBB8_HUMAN	Q99708 homo sapien	819	6	1.5	1255	1	POLS_EEVT	P36329 venezuelan
747	6	1.5	901	1	VP3_BTIVA	P20608 bluetongue	820	6	1.5	1255	1	POLS_EEVP	P36332 venezuelan
748	6	1.5	903	1	AD12_MOUSE	Q61824 mus musculu	821	6	1.5	1265	1	METH_HUMAN	Q99707 homo sapien
749	6	1.5	908	1	PSD2_HUMAN	Q13200 homo sapien	822	6	1.5	1271	1	TRPS_XENLA	Q90z86 xenopus lae
750	6	1.5	918	1	GLK1_HUMAN	P39086 homo sapien	823	6	1.5	1273	1	WEB1_YEAST	P38968 saccharomyc
751	6	1.5	920	1	CO4_BOVIN	P01030 bos taurus	824	6	1.5	1275	1	COBN_PSEDE	P29929 pseudomonas
752	6	1.5	921	1	DPOI_RICHE	Q9rlb6 rickettsia	825	6	1.5	1284	1	NRX4_DROME	Q94887 drosophila
753	6	1.5	922	1	DPOI_RICFE	Q9raa9 rickettsia	826	6	1.5	1289	1	MCE_REOVD	P11079 reovirus (t
754	6	1.5	923	1	HEPA_HAEIN	P44781 haemophilus	827	6	1.5	1290	1	PIG1_HUMAN	P19174 homo sapien
755	6	1.5	928	1	PM11_CHLPN	O86164 chlamydia p	828	6	1.5	1291	1	PIG1_BOVIN	P08487 bos taurus
756	6	1.5	929	1	ART1_HUMAN	Q9nz08 h adipocyte	829	6	1.5	1333	1	RDPO_SCHPO	Q05654 schizosacch
757	6	1.5	929	1	DPOW_MAIZE	P10582 zea mays (m	830	6	1.5	1356	1	VGR2_HUMAN	P35918 homo sapien
758	6	1.5	933	1	ODOI_ECOLI	P07015 escherichia	831	6	1.5	1367	1	VGR2_MOUSE	P35918 mus musculu
759	6	1.5	935	1	IF38_MEDTR	Q9xhmi medicago tr	832	6	1.5	1375	1	RPOB_VIBCH	Q9kv30 vibrio chol
760	6	1.5	943	1	ODOI_AZOVI	P20707 azotobacter	833	6	1.5	1411	1	Y197_DROME	Q9vkj3 drosophila
761	6	1.5	946	1	RHG4_HUMAN	P98171 homo sapien	834	6	1.5	1455	1	FACA_HUMAN	O15360 homo sapien
762	6	1.5	948	1	CDAA_HUMAN	Q9y512 homo sapien	835	6	1.5	1476	1	AT7A_CRIGR	P49015 cricetus
763	6	1.5	949	1	GLK1_RAT	P22756 rattus norv	836	6	1.5	1483	1	UFD4_YEAST	P33202 saccharomyc

837	6	1.5	1538	1	PPSB_MYCTU	Q10978	mycobacteri	910	5	1.2	57	1	RBL_CAMSI	P31181	camellia si
838	6	1.5	1574	1	SVJ1_YEAT	Q62910	rattus norv	911	5	1.2	58	1	PEPI_THUTO	P20139	thunmus thy
839	6	1.5	1609	1	FIG2_YEAST	P25653	saccharomyc	912	5	1.2	58	1	RBL_EUOBU	P31185	euonymus bu
840	6	1.5	1675	1	POL_RTBVP	P27502	rice tungro	913	5	1.2	58	1	RBL_EUOMA	P31186	euonymus ma
841	6	1.5	1738	1	CO4_MOUSE	P01029	mus musculu	914	5	1.2	58	1	RBL_EUPCH	P31187	euphorbia c
842	6	1.5	1886	1	GP21_RAT	P11654	rattus norv	915	5	1.2	58	1	RBL_WEISY	P31203	weimannia
843	6	1.5	1980	1	MY9B_RAT	Q63358	rattus norv	916	5	1.2	58	1	Y354_METJA	Q57800	methanococc
844	6	1.5	2026	1	CYAA_YEAST	P08678	saccharomyc	917	5	1.2	59	1	AT18_YEAST	P81450	saccharomyc
845	6	1.5	2033	1	EVPL_HUMAN	Q92817	homo sapien	918	5	1.2	60	1	RCSB_KLEAE	P05339	klebsiella
846	6	1.5	2035	1	EVPL_MOUSE	Q9d952	mus musculu	919	5	1.2	61	1	ASSY_LACTC	Q59491	lactococcus
847	6	1.5	2038	1	FSH_DROME	P13709	drosophila	920	5	1.2	61	1	DNBI_BFDV	P13893	budgerigar
848	6	1.5	2114	1	MY9B_MOUSE	Q9qy06	mus musculu	921	5	1.2	61	1	RS14_BACST	P54798	bacillus st
849	6	1.5	2183	1	RRPL_MEASA	P35975	measles vir	922	5	1.2	61	1	SECE_PYRAB	Q9v2s1	pyrococcus
850	6	1.5	2183	1	RRPL_MEASE	P12576	measles vir	923	5	1.2	61	1	TEMG_RANTE	P79875	rana tempor
851	6	1.5	2324	1	COAC_CHICK	P11029	gallus gall	924	5	1.2	62	1	RL19_MAIZE	Q08066	zea mays (m
852	6	1.5	2345	1	COA1_RAT	P11497	rattus norv	925	5	1.2	62	1	YCF9_PINTH	P41642	pinus thunb
853	6	1.5	2346	1	COA1_BOVIN	Q9tfs3	bos taurus	926	5	1.2	63	1	GBAK_CRIGR	Q60397	cricetus
854	6	1.5	2346	1	COA1_HUMAN	Q13085	homo sapien	927	5	1.2	63	1	YCF9_CYAPA	P17159	cyanophora
855	6	1.5	2346	1	COA1_SHEEP	Q28559	ovis aries	928	5	1.2	66	1	Y2A8_PSEAE	Q51384	pseudomonas
856	6	1.5	2481	1	UN52_CAEEL	Q06561	caenorhabdi	929	5	1.2	67	1	YORR_TTV1	P19302	thermoprote
857	6	1.5	2483	1	COA2_HUMAN	O00763	homo sapien	930	5	1.2	68	1	LCNB_LACTC	P35518	lactococcus
858	6	1.5	2493	1	YBA4_YEAST	P35194	saccharomyc	931	5	1.2	70	1	RS21_HAEIN	P44386	haemophilus
859	6	1.5	3010	1	POLG_HCVBK	P26663	h genome po	932	5	1.2	71	1	BRIE_RANES	P32412	rana esculu
860	6	1.5	3010	1	POLG_HCVJA	P26662	h genome po	933	5	1.2	72	1	RL40_TOBAC	P19379	nicotiana t
861	6	1.5	3010	1	POLG_HCVTW	P29846	h genome po	934	5	1.2	72	1	VSMO_TRYBB	P07209	trypanosoma
862	6	1.5	3110	1	HD_RAT	P51111	rattus norv	935	5	1.2	73	1	H171_HUMAN	O43727	homo sapien
863	6	1.5	3381	1	PGCV_BOVIN	P81282	bos taurus	936	5	1.2	73	1	PUFQ_RHOSU	Q9wx87	rhodovulum
864	6	1.5	3390	1	POLG_DEN3	P27915	d genome po	937	5	1.2	73	1	RS27_METKA	Q8ty87	methanopyru
865	6	1.5	3396	1	PGCV_HUMAN	P13611	homo sapien	938	5	1.2	73	1	YUEG_BACSU	O32094	bacillus su
866	6	1.5	3396	1	POLG_DENIS	P33478	d genome po	939	5	1.2	74	1	ATP9_MAIZE	P00840	zea mays (m
867	6	1.5	3707	1	PGBM_MOUSE	O05793	mus musculu	940	5	1.2	74	1	ATP9_MARPO	P26855	marchantia
868	6	1.5	4196	1	DYHC_SCHPO	O13290	schizosacch	941	5	1.2	74	1	ATP9_PEA	P05717	pisum sativ
869	6	1.5	4451	1	GRSB_BACBR	P14688	b gramicidi	942	5	1.2	74	1	ATP9_WHEAT	P13547	tritium ae
870	5	1.5	5376	1	ZAN_MOUSE	O88799	mus musculu	943	5	1.2	74	1	DEF2_CAPAN	O65740	capsicum an
871	5	1.2	12	1	FREI_LITIN	P07496	megabombus	944	5	1.2	75	1	RS3_COXBU	O85388	coxiella bu
872	5	1.2	17	1	BOL5_MEGPE	P28524	hordeum vul	945	5	1.2	77	1	LAF4_LACTO	P24022	lactobacill
873	5	1.2	20	1	SODM_HORVU	P80400	rana rugosa	946	5	1.2	77	1	YLDH_ALCEU	P40289	alcaligenes
874	5	1.2	24	1	GAE6_RANRU	P80285	micrococcus	947	5	1.2	78	1	MT2_MUSAC	O22319	musa acumin
875	5	1.2	25	1	ATPD_MICLU	P14610	sus scrofa	948	5	1.2	79	1	DEF_TACTR	P80957	tachyples
876	5	1.2	26	1	THIL_PIG	P31479	euglena gra	949	5	1.2	79	1	RS16_BUCAI	P57474	buchnera ap
877	5	1.2	31	1	PSAM_EUGGR	Q28207	bos taurus	950	5	1.2	79	1	NSNP_HUMAN	P80697	homo sapien
878	5	1.2	32	1	IAPP_BOVIN	Q28605	ovis aries	951	5	1.2	79	1	YTX1_BORPE	Q45389	bordetella
879	5	1.2	32	1	IAPP_SHEEP	P04842	pichia past	952	5	1.2	80	1	YZ_SHEEP	P08105	ovis aries
880	5	1.2	33	1	ALOX_PICPA	P51421	zea mays (m	953	5	1.2	80	1	PERX_WHEAT	P15984	tritium ae
881	5	1.2	42	1	RL32_MAIZE	P33044	hordeum vul	954	5	1.2	80	1	PRGI_SALTY	P41784	salmonella
882	5	1.2	44	1	THHR_HORVU	P23834	acheta dome	955	5	1.2	80	1	PSAC_SKECO	O96804	skeletonema
883	5	1.2	46	1	DIUH_ACHDN	P42365	streptococc	956	5	1.2	81	1	DINI_ECOLI	Q47143	escherichia
884	5	1.2	49	1	TPX2_STRPN	Q57644	methanococc	957	5	1.2	81	1	PSAC_ODOSI	P49477	odontella s
885	5	1.2	49	1	Y185_METJA	P19326	lymphocytic	958	5	1.2	81	1	RS18_CHLMU	P24286	chlamydia m
886	5	1.2	51	1	ZNPF_LYCVF	P49633	acanthamoeb	959	5	1.2	81	1	YE47_ARCFU	O28825	archaeoglob
887	5	1.2	52	1	RL40_ACACA	P19232	arabidopsis	960	5	1.2	81	1	YFFM_ECOLI	P76544	escherichia
888	5	1.2	52	1	RL40_ARATH	P51423	brassica ra	961	5	1.2	81	1	YOGY_BACSU	P54502	bacillus su
889	5	1.2	52	1	RL40_BRARA	P49632	caenorhabdi	962	5	1.2	82	1	PER_CHRVI	P00208	chromatium
890	5	1.2	52	1	RL40_CABEL	P14695	chlamydomon	963	5	1.2	82	1	NUMM_MOUSE	P52503	mus musculu
891	5	1.2	52	1	RL40_CHLRE	P14794	dictyosteli	964	5	1.2	82	1	RS18_CHLPN	Q926v4	chlamydia p
892	5	1.2	52	1	RL40_DICDI	P18101	drosophila	965	5	1.2	82	1	V082_ASFB7	P18557	african swi
893	5	1.2	52	1	RL40_HUMAN	P14793	homo sapien	966	5	1.2	82	1	Y233_ARCFU	O30006	archaeoglob
894	5	1.2	52	1	RL40_DROME	P49636	nicotiana s	967	5	1.2	83	1	CYC5_AZOV1	P11732	azotobacter
895	5	1.2	52	1	RL40_NICSY	P14796	saccharomyc	968	5	1.2	83	1	Y098_RICPR	Q9ze49	rickettsia
896	5	1.2	52	1	RL40_YEAST	O83081	treponema p	969	5	1.2	84	1	DHSD_CHOCR	P54323	chondrus cr
897	5	1.2	52	1	RHG6_FUGRU	O57414	fugu rubrip	970	5	1.2	84	1	IAC2_HUMAN	P20155	homo sapien
898	5	1.2	53	1	RL40_CRYNE	P40909	cryptococcu	971	5	1.2	84	1	RS18_MYCLE	O82tj2	pyrobaculum
899	5	1.2	53	1	RL40_ORYSA	P46575	eimeria bov	972	5	1.2	84	1	RNS_GIRCA	Q29535	giraffa cam
900	5	1.2	53	1	ATPE_CABEL	P35296	oryza sativ	973	5	1.2	84	1	YB72_METTA	O53125	mycobacteri
901	5	1.2	54	1	CHYM_FELCA	P34539	caenorhabdi	974	5	1.2	84	1	YB72_METTA	Q44156	actinococc
902	5	1.2	54	1	YP14_VIBAL	P09873	felis silve	975	5	1.2	84	1	YB72_METTA	O48572	methanococc
903	5	1.2	54	1	YPI4_VIBAL	P52064	vibrio algi	976	5	1.2	84	1	YB72_METTA	P46146	escherichia
904	5	1.2	54	1	YPI4_VIBAL	P18018	clostridium	977	5	1.2	85	1	VPOL_METTH	O27372	methanobact
905	5	1.2	55	1	SCP2_MESMA	Q9njp7	mesobuthus	978	5	1.2	85	1	VG35_HAEIN	P44228	haemophilus
906	5	1.2	56	1	SCP2_MESMA	Q9ubd1	mesobuthus	979	5	1.2	85	1	YCF3_ECOLI	P75953	escherichia
907	5	1.2	56	1	VGK_BPPHX	P03653	bacterioph	980	5	1.2	85	1	Y173_BURCE	P24579	burkholderia
908	5	1.2	56	1	VGK_BPPHX	P31180	buxus sempe	981	5	1.2	85	1	Y173_BURCE	P24579	burkholderia
909	5	1.2	57	1	RBL_BUXSE	P31180	buxus sempe	982	5	1.2	85	1	YIDD_BUCAP	P29432	buchnera ap

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983 5 1.2 86 1 PAK1_SVNY3 P72712 synechocyst
984 5 1.2 86 1 REV_HV1Z3 P05867 human immun
985 5 1.2 86 1 RU3E_ARCFU O28389 archaoglob
986 5 1.2 86 1 YE86_CLOAB Q97j00 clostridium
987 5 1.2 87 1 FXY4_RAT Q63113 rattus norv
988 5 1.2 87 1 VAPL_BP186 P21681 bacterioph
989 5 1.2 87 1 VG07_BPMU Q38479 bacterioph
990 5 1.2 87 1 Y476_MYCLE Q9cb43 mycobacteri
991 5 1.2 88 1 MS2S_MOUSE O9z224 mus musculi
992 5 1.2 88 1 RS15_HAEIN P44389 haemophilus
993 5 1.2 88 1 S108_MOUSE O34274 yersinia en
994 5 1.2 88 1 YDFK_ECOLI P27005 mus musculi
995 5 1.2 88 1 YNAE_ECOLI P76154 escherichia
996 5 1.2 88 1 DRPH_ROMMI P76073 escherichia
997 5 1.2 89 1 DRPH_ROMMI P09929 romalea mic
998 5 1.2 89 1 RPOK_AERPE O9yjd9 aeropyrum p
999 5 1.2 89 1 RS15_TREPA O83857 treponema p
1000 5 1.2 89 1 YS22_BORBU P70844 borrelia bu
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ALIGNMENTS

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RESULT 1
BAE2_HUMAN STANDARD; PRT; 518 AA.
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ID O9Y5Z0; O9UJT6;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta secretase 2 precursor (EC 3.4.23.-) (Beta-site APP-cleaving
DE enzyme 2) (Aspartyl protease 1) (Asp 1) (ASPI) (Membrane-associated
DE aspartic protease 1) (Memapsin-1).
GN BACE2 OR ASP21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Torry M.C., Pauley A.M.,
RA Brashler J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Xin H., Stephens J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,
RA Giese K.;
RT "Identification of a novel aspartic-like protease differentially
RT expressed in human breast cancer cell lines.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;
RT "Cloning of a gene from chromosome 21 Down region encoding a potential
RT transmembrane aspartyl protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Solans A., Estivill X., de la Luna S.;
RT "Cloning of a novel mammalian aspartyl protease.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20120043; PubMed=10656250;
RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA Smith T.S., Simons D.L., Walsh F.S., Dingwall C., Christie G.;
RT "Identification of a novel aspartic proteinase (Asp 2) as
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RT beta-secretase.";
RL Mol. Cell. Neurosci. 14:419-427(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=2014060; PubMed=10677483;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
RT beta-amyloid precursor protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehmach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; AF200342; AAF17078.1; -.
DR EMBL; AF117892; AAD45240.1; -.
DR EMBL; AF050171; AAD45963.1; -.
DR EMBL; AF178532; AAF29494.1; -.
DR EMBL; AF204944; AAF26368.1; -.
DR EMBL; AF200192; AAF13714.1; -.
DR EMBL; AF163284; CAB90458.1; -.
DR EMBL; AL163285; CAB90554.1; -.
DR EMBL; BC014453; AAH14453.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR Genew; HGNC:934; BACE2.
DR MIM; 605668; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEP SIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 ? POTENTIAL.
FT CHAIN ? 518 BETA_SECRETASE 2.
FT DOMAIN 21 473 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 474 494 POTENTIAL.
FT DOMAIN 495 518 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 110 110 BY SIMILARITY.
FT ACT_SITE 303 303 BY SIMILARITY.
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 36 36 A -> T (IN REF. 6).
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SQ SEQUENCE 518 AA; 56180 MW; 2E903150823760D3 CRC64;
 Query Match 100.0%; Score 406; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPQKLQILVDTGSSNFAVAGTP 60
 DB 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPQKLQILVDTGSSNFAVAGTP 122
 QY 61 HSYIDTYFDTERSSSTYRSKGFVDVTKYTGSGSWTGFVEDLVTPKGFNTSFLVNIAITFE 120
 DB 123 HSYIDTYFDTERSSSTYRSKGFVDVTKYTGSGSWTGFVEDLVTPKGFNTSFLVNIAITFE 182
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 DB 183 SENFELPGIKWNGILGLAYATLAKPSSSLETFFDLSLVQANIPNVFSMQMGAGLPVAGS 242
 QY 181 GTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEIKLEIGQSINLDCREYNADKAIV 240
 DB 243 GTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEIKLEIGQSINLDCREYNADKAIV 302
 QY 241 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQLACWTNSETPWSYFPKISIVL 300
 DB 303 DSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQLACWTNSETPWSYFPKISIVL 362
 QY 301 RDENSSRSFRITILPOLYIQPMGAGLNEYCYRFGISPTNALVIGATWEGFYVIFDRA 360
 DB 363 RDENSSRSFRITILPOLYIQPMGAGLNEYCYRFGISPTNALVIGATWEGFYVIFDRA 422
 QY 361 QKRVGFAASPCAIEAGAVSEISGFSTEDVASCNCPAOSLSEPII 406
 DB 423 QKRVGFAASPCAIEAGAVSEISGFSTEDVASCNCPAOSLSEPII 468

RESULT 2
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 ID_BACE_HUMAN STANDARD; PRT; 501 AA.
 AC P56817; Q9UT5; Q9BYC1; Q9BYC0; Q9BYB9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
 DE protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
 DE (Memapsin-2).
 GN BACE OR BACE1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Brain;
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amaratne P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.;
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND
 RP CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20057171; PubMed=10591214;
 RA Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
 RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
 RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
 RA Tatsuno G., Tung J., Shenk D., Seubert P., Suomensaari S.M., Wang S.,
 RA Walker D., Zhao J., McConlogue L., Varghese J.;

RT "Purification and cloning of amyloid precursor protein beta-secretase
 RT from human brain.";
 RL Nature 402:537-540(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
 RA Bashier J.R., Stracman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 RT secretase activity.";
 RL Nature 402:533-537(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20120043; PubMed=10656250;
 RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
 RT secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC TISSUE=Brain, and Pancreas;
 RA Michel B., De Pietri Tonelli D., Zaccchetti D., Keller P.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
 RT human brain and pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Pancreas;
 RA Zaccchetti D., De Pietri Tonelli D., Schnurbus R.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
 RT human pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
 RC TISSUE=Brain;
 RX MEDLINE=21408467; PubMed=11516562;
 RA Tanahashi H., Tabira T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site
 RT amyloid precursor protein cleaving enzyme (BACE) and their effect on
 RL amyloid beta-peptide production.";
 RN Neurosci. Lett. 307:9-12(2001).
 RN [8]
 RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
 RX MEDLINE=20144060; PubMed=10677483;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=21950860; PubMed=11953458;
 RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
 RT "The disulphide bonds in the catalytic domain of BACE are critical but
 RT not essential for amyloid precursor protein processing activity.";
 RL J. Neurochem. 80:1079-1088(2002).
 CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
 CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
 CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
 CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; A/BACE-1A/BAC-501 (shown here),
 CC B/BACE-1B/BACE-I-476; C/BACE-1C/BACE-I-457 and D/BACE-1D/BACE-I-
 CC 432; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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CC -----
DR EMBL; AF190725; AAF04142.1; -
DR EMBL; AF201468; AAF18982.1; -
DR EMBL; AF200343; AAF17079.1; -
DR EMBL; AF204943; AAF26367.1; -
DR EMBL; AF338816; AAK38374.1; -
DR EMBL; AF338817; AAK38375.1; -
DR EMBL; AB050436; BAB40931.1; -
DR EMBL; AB050437; BAB40932.1; -
DR EMBL; AB050438; BAB40933.1; -
DR EMBL; AF200193; AAF13715.1; -
DR HSSP; P32329; 1YPS.
DR MEROPS; A01.004; -
DR Genew; HGNC:933; BACE.
DR MIM; 604252; -
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hydrolyase; Aspartyl protease; Zymogen; Transmembrane;
KW Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420
FT DISULFID 278 443
FT DISULFID 330 380
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 146 189 MISSING (IN ISOFORM C AND ISOFORM D).
FT VARSPLIC 190 214 MISSING (IN ISOFORM B AND ISOFORM D).
SQ SEQUENCE 501 AA; 55763 MW; 377CE4C824ACEF05 CRC64;

Query Match 3.0%; Score 12; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
| | | | | | | | | |
Db 90 ILVDTGSSNFAV 101

RESULT 3

BACE_MOUSE STANDARD; PRT; 501 AA.

AC P56818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
DE protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
DE (Memapsin-2).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
RN [2]
RP REVISIONS TO 6 AND 81-87.
RA Bennett B.D., Vassar R., Citron M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashler J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).
CC -!- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
CC FRAGMENT WHICH IS LATER RELEASE BY GAMMA-SECRETASE (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

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CC -----
DR EMBL; AF190726; AAF04143.2; -
DR EMBL; AF200346; AAF17082.1; -
DR HSSP; P56272; 1AMS.
DR MEROPS; A01.004; -
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hydrolyase; Aspartyl protease; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45 POTENTIAL.
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420 BY SIMILARITY.
FT DISULFID 278 443 BY SIMILARITY.
FT DISULFID 330 380 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 501 AA; 55747 MW; C085A013145E874E CRC64;

Query Match 3.0%; Score 12; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
 Db 90 ILVDTGSSNFAV 101

RESULT 4

BACE_RAT
 ID_BACE_RAT STANDARD; PRT; 501 AA.

AC P56819;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
 DE protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
 DE (Memapsin-2).
 GN BACE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loefloft R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.,
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE."
 RL Science 286:735-741(1999).
 CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
 CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
 CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
 CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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 CC -----
 DR EMBL; AF190727; AAF04144.1; -.
 DR HSSP; P32329; 1YPS.
 DR MEROPS; A01.004; -.
 DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 45 POTENTIAL.
 FT CHAIN 46 501 BETA-SECRETASE.
 FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 458 478 POTENTIAL.
 FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 93 93 BY SIMILARITY.
 FT ACT_SITE 289 289 BY SIMILARITY.
 FT DISULFID 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT DISULFID 330 380 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT

FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55806 MW; 24B445BC8BE87DE3 CRC64;

Query Match

Best Local Similarity 3.0%; Score 12; DB 1; Length 501;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
 Db 90 ILVDTGSSNFAV 101

RESULT 5

LRP_HAEIN
 ID_LRP_HAEIN STANDARD; PRT; 166 AA.

AC P45265;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Leucine-responsive regulatory protein.
 GN LRP OR H1596.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd."
 RL Science 269:496-512(1995).
 CC -1- FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE
 CC AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS; LRP
 CC MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC -----
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 CC -----
 DR EMBL; U32833; AAC23241.1; -.
 DR TIGR; H1596; -.
 DR InterPro; IPR000485; ASNC trans_reg.
 DR Pfam; PF01037; ASNC trans_reg; 1.
 DR PRINTS; PR00033; HTHASNC.
 DR SMART; SM00344; HTH_ASNC; 1.
 DR PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
 KW DNA-binding; Transcription_regulation; Activator; Complete proteome.
 FT DNA_BIND 35 54 H-T-H MOTIF (POTENTIAL).
 SQ SEQUENCE 166 AA; 18910 MW; 22C0F1B78B110CEB CRC64;

Query Match

Best Local Similarity 2.0%; Score 8; DB 1; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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CC  -----
DR  EMBL; D00589; BAA00467.1; -.
DR  PIR; J00057; PEIKL.
DR  HSSP; P32329; 1YPS.
DR  MEROPS; A01.019; -.
DR  InterPro; IPR001461; AspproteaseA1.
DR  InterPro; IPR001969; Aspprotease_site.
DR  Pfam; PF00026; asp; 1.
DR  PRINTS; PR00792; PEPsin.
DR  PROSITE; PS00141; ASP_PROTEASE; 2.
KW  Hydroxylase; Aspartyl protease; Glycoprotein.
FT  ACT_SITE      32      32
FT  ACT_SITE      212     212
FT  CARBOHYD      192     192      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD      238     238      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE      340 AA;  35050 MW;  9BAF837264D42FEF CRC64;

Query Match
Best Local Similarity  2.0%; Score 8; DB 1; Length 340;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  46  LVDTGSSN 53
    |||||
Db  30  LVDTGSSN 37

RESULT 9
ECT1_SCHPO
ID  ECT1 SCHPO      STANDARD;      PRT;      365 AA.
AC  Q9UT16;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Probable ethanolamine-phosphate cytidylyltransferase (EC 2.7.7.14)
DE  (Phosphorylethanolamine transferase) (CTP:phosphoethanolamine
DE  cytidylyltransferase).
GN  SPAC15E1.05C.
OS  Schizosaccharomyces pombe (Fission yeast).
OC  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC  Schizosaccharomycetales; Schizosaccharomycetaceae;
OC  Schizosaccharomyces.
OX  NCBI_TaxID=4896;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=972;
RX  MEDLINE=21848401; PubMed=11859360;
RA  Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA  Sgourcos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA  Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA  Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA  Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA  Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA  James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA  Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA  Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA  Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA  Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA  Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA  Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA  Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA  Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA  Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA  Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA  Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA  Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA  Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA  Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA  Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA  Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA  Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT  "The genome sequence of Schizosaccharomyces pombe.";
```

```
RL  Nature 415:871-880(2002).
CC  -1- CATALYTIC ACTIVITY: CTP + ethanolamine phosphate = diphosphate +
CC  CDP-ethanolamine.
CC  -1- PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CDP-ETHANOLAMINE SYNTHESIS;
CC  SECOND STEP.
CC  -1- SIMILARITY: BELONGS TO THE CYTIDYLYLTRANSFERASE FAMILY.
CC  -----
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CC  -----
DR  EMBL; AL109770; CAB52424.1; -.
DR  InterPro; IPR004821; Cyt tran rel.
DR  InterPro; IPR004820; Cytidylyltransf.
DR  Pfam; PF01467; Cytidylyltransf; 1.
DR  TIGRFAMs; TIGR00125; cyt tran rel; 2.
KW  Transferase; Nucleotidylyltransferase; Phospholipid biosynthesis.
FT  DOMAIN      1      182      CATALYTIC (POTENTIAL).
FT  SEQUENCE      365 AA;  41556 MW;  ACDB6A974ABB4734 CRC64;

Query Match
Best Local Similarity  2.0%; Score 8; DB 1; Length 365;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  242  SGTTLRL 249
    |||||
Db  191  SGTTLRL 198

RESULT 10
60IM_ECOLI
ID  60IM ECOLI      STANDARD;      PRT;      548 AA.
AC  P25714;
DT  01-MAY-1992 (Rel. 22, Created)
DT  01-JUL-1993 (Rel. 26, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  60 kDa inner-membrane protein.
GN  YIDC OR B3705.
OS  Escherichia coli.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=K12 / MG1655;
RX  MEDLINE=93315143; PubMed=7686882;
RA  Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT  "DNA sequence and analysis of 136 kilobases of the Escherichia coli
RT  genome: organizational symmetry around the origin of replication.";
RL  Genomics 16:551-561(1993).
RN  [2]
RP  SEQUENCE OF 1-2 FROM N.A.
RX  MEDLINE=86056995; PubMed=2415431;
RA  Hansen F.G., Hansen E.B., Atlung T.;
RT  "Physical mapping and nucleotide sequence of the rnpA gene that
RT  encodes the protein component of ribonuclease P in Escherichia
RT  coli.";
RL  Gene 38:85-93(1985).
RN  [3]
RP  TOPOLOGY.
RX  MEDLINE=99023968; PubMed=9804807;
RA  Saaef A., Monne M., de Gier J.W., von Heijne G.;
RT  "Membrane topology of the 60-kDa OxalP homologue from Escherichia
RT  coli.";
RL  J. Biol. Chem. 273:30415-30418(1998).
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC  (Probable).
CC  -1- SIMILARITY: BELONGS TO THE OXA1 / 60 KDA IMP FAMILY.
CC  -----
```


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CC -----
DR EMBL; L10328; AAA62056.1; -.
DR EMBL; AE000447; AAC76728.1; -.
DR EMBL; M11056; -; NOT ANNOTATED_CDS.
DR EcoGene; EG1197; Y1dC.
DR InterPro; IPR001708; 60kDa_innerneb.
DR Pfam; PF02096; 60KD_IMP; 1.
DR PRINTS; PR00701; 60KDINNERMP.
KW Transmembrane; Inner membrane; Complete proteome.
FT DOMAIN 1 5 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 6 23 PROBABLE.
FT DOMAIN 24 342 PERIPLASMIC (PROBABLE).
FT TRANSMEM 343 370 PROBABLE.
FT DOMAIN 371 416 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 417 446 PROBABLE.
FT DOMAIN 447 463 PERIPLASMIC (PROBABLE).
FT TRANSMEM 464 481 PROBABLE.
FT DOMAIN 482 493 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 494 509 PROBABLE.
FT DOMAIN 510 512 PERIPLASMIC (PROBABLE).
FT TRANSMEM 513 535 PROBABLE.
FT DOMAIN 536 548 CYTOPLASMIC (PROBABLE).
SQ SEQUENCE 548 AA; 61526 MW; 95EBC5DAB4F2FCFB CRC64;

Query Match 2.0%; Score 8; DB 1; Length 548;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 DTGSSNFA 55
| | | | | | | |
Db 207 DTGSSNFA 214

RESULT 11
DNM1_MOUSE STANDARD; PRT; 1620 AA.
ID DNM1_MOUSE
AC P13864; P97413; Q9QXX6; Q9CSC6;
DT 01-JAN-1990 (Rel. 13, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA
DE methyltransferase Mmui) (DNA Mase Mmui) (MCMT) (M.Mmui) (Met-1).
GN DNM1 OR DNMT OR UIM OR MET1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89094873; PubMed=3210246;
RA Bestor T.H., Laudano A., Mattaliano R., Ingram V.;
RT "Cloning and sequencing of a cDNA encoding DNA methyltransferase of
RT mouse cells. The carboxyl-terminal domain of the mammalian enzymes is
RT related to bacterial restriction methyltransferases.";
RL J. Mol. Biol. 203:971-983(1988).
RN [2]
RP REVISIONS TO N-TERMINUS.
RC TISSUE=Embryo;
RX MEDLINE=97094871; PubMed=8940105;
RA Yoder J.A., Yen R.-W.C., Vertino P.M., Bestor T.H., Baylin S.B.;
RT "New 5' regions of the murine and human genes for DNA (cytosine-5)-
RT methyltransferase.";
RL J. Biol. Chem. 271:31092-31097(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Skeletal muscle;

RX MEDLINE=20515133; PubMed=11063128;
RA Aguirre-Arteta A.M., Grunewald I., Cardoso M.C., Leonhardt H.;
RT "Expression of an alternative Dnmt1 isoform during muscle
RT differentiation.";
RL Cell Growth Differ. 11:551-559(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=C57BL/6;
RX MEDLINE=20181859; PubMed=10715201;
RA Margot J.B., Aguirre-Arteta A.M., Di Giacco B.V., Pradhan S.,
RA Roberts R.J., Cardoso M.C., Leonhardt H.;
RT "Structure and function of the mouse DNA methyltransferase gene: Dnmt1
RT shows a tripartite structure.";
RL J. Mol. Biol. 297:293-300(2000).

RN [5]
RP SEQUENCE OF 1-27 AND 119-1619 FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=98119799; PubMed=9449671;
RA Mertineit C., Yoder J.A., Takeito T., Laird D.W., Trasler J.M.,
RA Bestor T.H.;
RT "Sex-specific exons control DNA methyltransferase in mammalian germ
RT cells.";
RL Development 125:889-897(1998).

RN [6]
RP SEQUENCE OF 1-144 FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 3-6.
RX STRAIN=129/Sv, and BAB/c; TISSUE=Embryonic stem cells;
MEDLINE=99047652; PubMed=9830015;
RA Gaudet F., Talbot D., Leonhardt H., Jaenisch R.;
RT "A short DNA methyltransferase isoform restores methylation in vivo.";
RL J. Biol. Chem. 273:32725-32729(1998).

RN [7]
RP SEQUENCE OF 1-119 FROM N.A. (ISOFORM 1).
RC STRAIN=129/Sv; TISSUE=Embryonic stem cells, and Kidney;
RX MEDLINE=97075093; PubMed=8917520;
RA Tucker K.L., Talbot D., Lee M.A., Leonhardt H., Jaenisch R.;
RT "Complementation of methylation deficiency in embryonic stem cells by
RT a DNA methyltransferase minigene.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12920-12925(1996).

RL [8]
RP SEQUENCE OF 1-272 FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
RA Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [9]
RP PHOSPHORYLATION OF SER-515, AND MASS SPECTROMETRY.
RC TISSUE=Erythroleukemia;
RX MEDLINE=97362284; PubMed=9211941;
RA Glickman J.F., Pavlovich J.G., Reich N.O.;
RT "peptide mapping of the murine DNA methyltransferase reveals a major
RT phosphorylation site and the start of translation.";
RL J. Biol. Chem. 272:17851-17857(1997).

RN [10]
RP INTERACTION WITH HDAC1.
RX MEDLINE=20082816; PubMed=10615135;
RA Fuks F., Burgers W.A., Brehm A., Hughes-Davies L., Kouzarides T.;

RT "DNA methyltransferase Dnmt1 associates with histone deacetylase
RT activity.";
RL Nat. Genet. 24:88-91(2000).
RN [11]
RP INTERACTIONS WITH HDAC2 AND DNAP1.
RX MEDLINE=20347709; PubMed=10888872;
RA Rountree M.R., Bachman K.E., Baylin S.B.;
RT "DNMT1 binds HDAC2 and a new co-repressor, DNAP1, to form a complex at
RT replication foci.";
RL Nat. Genet. 25:269-277(2000).
RN [12]
RP FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=21185930; PubMed=11290321;
RA Howell C.Y., Bestor T.H., Ding F., Latham K.E., Mertineit C.,
RA Trasler J.M., Chaillet J.R.;
RT "Genomic imprinting disrupted by a maternal effect mutation in the
RT Dnmt1 gene.";
RL Cell 104:829-838(2001).
RN [13]
RP ALLOSTERIC ACTIVATION.
RX MEDLINE=21293215; PubMed=11399088;
RA Fatemi M., Hermann A., Pradhan S., Jeltsch A.;
RT "The activity of the murine DNA methyltransferase Dnmt1 is controlled
RT by interaction of the catalytic domain with the N-terminal part of
RT the enzyme leading to an allosteric activation of the enzyme after
RT binding to methylated DNA.";
RL J. Mol. Biol. 309:1189-1199(2001).
RN -1- FUNCTION: Methylates CpG residues. Preferentially methylates
RP hemimethylated DNA. It is responsible for maintaining methylation
CC patterns established in development. Isoform 2, in oocytes, may
CC provide maintenance methyltransferase activity specifically at
CC imprinted loci during the fourth embryonic S phase. Mediates
CC transcriptional repression by direct binding to HDAC2.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
CC homocysteine + DNA containing 5-methylcytosine.
CC -1- ENZYME REGULATION: Allosterically regulated. The binding of 5-
CC methylcytosine-containing DNA to the N-terminal parts of Dnmt1
CC causes an allosteric activation of the catalytic domain by a
CC direct interaction of its Zn-binding domain with the catalytic
CC domain.
CC -1- SUBUNIT: Interacts with HDAC1 and with PCNA. Forms a complex with
CC DNAP1 and HDAC2, with direct interaction.
CC -1- SUBCELLULAR LOCATION: Nuclear; it is nucleoplasmic through most of
CC the cell cycle and associates with replication foci during S-
CC phase. In germ cells: spermatogonia, preleptotene and leptotene
CC spermatocytes all express high levels of nuclear protein, while
CC the protein is not detected in pachytene spermatocytes, despite
CC the fact they expressed high levels of mRNA. In females, the
CC protein is not detected in non-growing oocytes, in contrast to the
CC growing oocytes. During the growing, the protein is no longer
CC detectable in nuclei but accumulates to very high levels first
CC throughout the cytoplasm. At the time of ovulation, all the
CC protein is cytoplasmic and is actively associated with the oocyte
CC cortex. After fecundation, in the preimplantation embryo, the
CC protein remains cytoplasmic and after implantation, it is
CC exclusively nuclear in all tissue types. Isoform 2 is sequestered
CC in the cytoplasm of maturing oocytes and of preimplantation
CC embryos, except for the 8-cell stage, while isoform 1 is
CC exclusively nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/long form (shown here) and
CC 2/short form; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in embryonic stem cells
CC and in somatic tissues. Isoform 2 is expressed in oocytes,
CC preimplantation embryos, testis and in skeletal muscle during
CC myogenesis.
CC -1- DEVELOPMENTAL STAGE: In germ cells, it is present at high levels
CC in spermatogonia and spermatocytes until the pachytene stage,
CC where it falls to undetectable levels. The transient drop at the
CC pachytene stage coincides with the disappearance of the 5.2 kb
CC mRNA and the accumulation of a larger 6.0 kb mRNA. Oocytes
CC accumulate very large amounts of Dnmt1 protein during the growth
CC phase.
CC -1- MISCELLANEOUS: There are three 5' exons, one specific to the

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CC oocyte (1c), one specific to the pachytene spermatocyte and also
CC found in skeletal muscle (1b) and one found in somatic cells (1a).
CC Three different mRNAs can be produced which give rise to two
CC different translation products: isoform 1 (mRNAs-1a) and isoform 2
CC (mRNA-1b or -1c).
CC -1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BAH DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGER.
CC -----
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CC
CC EMBL; X14805; CAA32910.1; -.
CC EMBL; AF175432; AAF97695.1; -.
CC EMBL; AF162282; AAF19352.1; -.
CC EMBL; AF175431; AAF60965.1; -.
CC EMBL; AF175412; AAF60965.1; JOINED.
CC EMBL; AF175413; AAF60965.1; JOINED.

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Query Match      2.0%; Score 8; DB 1; Length 1620;
Best Local Similarity 100.0%; Pred. No. 14;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	4	PALASPAG	11
Db	11	PALASPAG	18

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RESULT 12
ID      DNMI_RAT      STANDARD;      PRT; 1622 AA.
AC      Q9Z330; Q9WTX3; P70487; Q9WU57; Q9R252;
DT      15-JUN-2002 (Rel. 41, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnm1) (DNA
DN      methyltransferase I) (DNA MTase RnoIP) (MCMT) (M.RnoIP).
DE      DNM1.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 0).
RC      STRAIN=Sprague-Dawley; TISSUE=Brain, and Placenta;
RX      MEDLINE=99097263; PubMed=9878564;
RA      Kimura H., Takeda T., Tanaka S., Ogawa T., Shiota K.;
RT      "Expression of rat DNA (cytosine-5) methyltransferase (DNA MTase) in
RT      rodent trophoblast giant cells: molecular cloning and characterization
RT      of rat DNA MTase.";
RL      Biochem. Biophys. Res. Commun. 253:495-501(1998).
RN      [2]
RP      SEQUENCE OF 1-144 FROM N.A. (ISOFORMS 0 AND 8).
RC      TISSUE=Brain;
RA      Deng J., Szyf M.;
RT      "Multiple N-terminal isoforms of DNA (cytosine-5)-methyltransferase
RT      in vivo.";
RL      Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 17-356 FROM N.A., AND IN VITRO BINDING TO ANNEXIN V.
RC      STRAIN=Wistar; TISSUE=Brain;
RX      MEDLINE=96301899; PubMed=8667030;
RA      Ohsawa K., Imai Y., Ito D., Kohsaka S.;
RT      "Molecular cloning and characterization of annexin V-binding proteins
RT      with highly hydrophilic peptide structure.";
RL      J. Neurochem. 67:89-97(1996).
RN      [4]
RP      SEQUENCE OF 1169-1517 FROM N.A. (ISOFORMS 0: 1; 2: 3; 4: 5; 6 AND 7).

```

RX MEDLINE=98389705; PubMed=9722504;
RA Deng J.; Szyf M.;
RT "Multiple isoforms of DNA methyltransferase are encoded by the
RL J. Biol. Chem. 273:22869-22872(1998).
CC -!- FUNCTION: Methylates CpG residues. Preferentially methylates
CC hemimethylated DNA. It is responsible for maintaining methylation
CC patterns established in development (By similarity). Mediates
CC transcriptional repression by direct binding to HDAC2 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
CC homocysteine + DNA containing 5-methylcytosine.
CC -!- SUBUNIT: Binds annexin V (Potential).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS: At least 9 isoforms; 0 (shown here), 1/SF1,
CC 2/SF2, 3/SF3, 4/SF4, 5/SF5, 6/SF6, 7/SF7 and 8/short; are produced
CC by alternative splicing.
CC -!- TISSUE SPECIFICITY: Isoforms 0 and 8 are highly expressed in
CC placenta, brain, lung, spleen, kidney, heart, and at much lower
CC levels in liver. Isoform 1 is expressed in cerebellum, isoform
CC 2 in muscle and testis, isoform 3 in lung, isoform 4 in spleen and
CC brain, and isoform 5 in brain.
CC -!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
CC -!- SIMILARITY: CONTAINS 2 BAH DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL; AB012214; BAA37118.1; -.
DR EMBL; AF116344; AAD32541.1; -.
DR EMBL; AF116345; AAD32542.1; -.
DR EMBL; D64060; BAA20854.1; -.
DR EMBL; AF083043; AAD28102.1; -.
DR EMBL; AF083038; AAD28102.1; JOINED.
DR EMBL; AF083039; AAD28102.1; JOINED.
DR EMBL; AF083040; AAD28102.1; JOINED.
DR EMBL; AF083041; AAD28102.1; JOINED.
DR EMBL; AF083042; AAD28102.1; JOINED.
DR REBASE; 3019; M.RnoIP.
DR InterPro; IPR001025; BAH.
DR InterPro; IPR001525; C5_DNA_meth.
DR InterPro; IPR002857; ZnF_CXXC.
DR Pfam; PF00145; DNA_methylase; 1.
DR Pfam; PF01426; BAH; 2.
DR Pfam; PF02008; zf-CXXC; 1.
DR SMART; SMO0439; BAH; 2.
DR TIGRFAMs; TIGR00675; dcm; 1.
DR PROSITE; PS00094; C5_MTASE_1; 1.
DR PROSITE; PS00095; C5_MTASE_2; 1.
KW Transferase; Methyltransferase; Transcription regulation; Repressor;
KW DNA-binding; Zinc-finger; Zinc; Metal-binding; Nuclear protein;
KW Repeat; Phosphorylation; Alternative splicing.
FT DOMAIN 173 200 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 327 556 DNA REPLICATION FOCI-TARGETING SEQUENCE.
FT ZN_FING 649 695 CXXC-TYPE.
FT DOMAIN 759 884 BAH 1.
FT DOMAIN 935 1105 BAH 2.
FT DOMAIN 1114 1126 6.5 X 2 AA TANDEM REPEATS OF K-G.
FT DOMAIN 1144 1622 CATALYTIC.
FT DOMAIN 149 152 POLY-SER.
FT DOMAIN 269 274 POLY-ASP.
FT DOMAIN 729 729 POLY-LYS.
FT ACT_SITE 1231 1231 BY SIMILARITY.
FT MOD_RES 515 515 PHOSPHORYLATION (BY SIMILARITY).
FT VARSPPLIC 1 118 MISSING (IN ISOFORM 8).
FT VARSPPLIC 1218 1430 OKGDVEMLCGGPCCGFGSGMNRFSRTYSKFNLSVGFSL
YCDYRPRFFLLENVRNFVSFRSMVLKLTLRCLVRMGYQC

FT TFGVLQAGGYGVAQTRRAITLAAPEKTLPEPELVHFA
FT PRACOLSVVDDKKFVSNITRLSGPRTITMRDMSDLPE
FT IONGASAPETISYKWRATLVLPPEAARVALPAHPQGPYPQVH
FT ERAGGCRM -> VC (IN ISOFORM 4).
FT MISSING (IN ISOFORM 5).
FT MISSING (IN ISOFORM 7).
FT MISSING (IN ISOFORM 3).
FT MISSING (IN ISOFORM 2).
FT MISSING (IN ISOFORM 6).
FT MISSING (IN ISOFORM 1).
FT AGSLPDHVR -> RQARPRPCP (IN REF. 3).
FT A -> V (IN REF. 3).
FT F -> S (IN REF. 1).
FT T -> I (IN REF. 4).
FT M -> V (IN REF. 1).
FT KWRATLVPEAARVALPAHPQGPYPQVHERAGGC -> NG
FT EPQSWFQRLRGSHYQPILRDHICKDMSALVAA (IN
FT REF. 1).
SQ SEQUENCE 1622 AA; 182773 MW; FCFPA4AAA69E234BA CRC64;
Query Match 2.0%; Score 8; DB 1; Length 1622;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PALASPAGE 11
Db 11 PALASPAGE 18
RESULT 13
G8_HUMAN STANDARD; PRT; 126 AA.
ID G8_HUMAN
AC Q9UBA6; Q9UBA8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G8 protein.
GN G8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93206277; PubMed=8096093;
RA Partanen J., Milner C., Campbell R.D., Maki M., Lipsanen V.,
RA Koskimies S.;
RT "HLA-linked heat-shock protein 70 (HSP70-2) gene polymorphism and
RT celiac disease.";
RL Tissue Antigens 41:15-19(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Partanen J., Campbell R.D.;
RT "Characterization of the novel gene G8 located in the class III region
RT of the human major histocompatibility complex.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; G8 (SHOWN HERE) AND G8.1; MAY BE
CC PRODUCED BY ALTERNATIVE SPLICING.
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CC -----
DR EMBL; AJ249732; CAB56508.1; -.
DR EMBL; AJ249731; CAB56506.1; -.
DR MIM; 605447; -.
KW Alternative splicing.
FT VARSPPLIC 86 126
MNSGSPARDNAPSORFCTNLSEGLRFGISPSWREALYGCHA
-> SCKTFIAVLISLKE (IN ISOFORM G8.1).

SEQ SEQUENCE 126 AA; 13270 MW; 59610E786B9C4F60 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 333 RFGISPS 339
Db 110 RFGISPS 116

RESULT 14
EX3_HAEIN
ID EX3_HAEIN STANDARD; PRT; 267 AA.
AC P44318;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exodeoxyribonuclease III (EC 3.1.11.2) (Exonuclease III) (EXO III).
GN XTHA OR HI0041.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uteerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: MAJOR APURINIC-APYRIMIDINIC ENDONUCLEASE OF E. COLI. IT
CC REMOVES THE DAMAGED DNA AT CYTOSINES AND GUANINES BY CLEAVING ON
CC THE 3' SIDE OF THE AP SITE BY A BETA-ELIMINATION REACTION
CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Degradation of double-stranded DNA. It acts
CC progressively in a 3'-to 5'-direction, releasing nucleoside 5'-
CC phosphates.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AP/EXO A FAMILY OF DNA REPAIR ENZYMES.
CC -----
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CC -----
DR EMBL; U32689; AAC21719.1; -.
DR HSSP; P09030; IAKO.
DR TIGR; HI0041; -.
DR InterPro; IPR000097; Apendonclsel.
DR InterPro; IPR004442; ExoDNase III.
DR InterPro; IPR004808; ExoIII_xth.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR TIGRFAMs; TIGR00195; exoDNase_III; 1.
DR TIGRFAMs; TIGR00633; xth; 1.
DR PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
DR PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
DR PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
KW Hydrolyase; Nuclease; Exonuclease; DNA repair; Complete proteome.
FT METAL 34 34 MAGNESIUM OR MANGANESE (BY SIMILARITY).

FT ACT SITE 259 259 GENERAL BASE (BY SIMILARITY).
SEQ SEQUENCE 267 AA; 31025 MW; 6B3ADE465A1E347C CRC64;
Query Match 1.7%; Score 7; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 YRSKGF 82
Db 215 YRSKGF 221

RESULT 15
EX3_ECOLI
ID EX3_ECOLI STANDARD; PRT; 268 AA.
AC P09030;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exodeoxyribonuclease III (EC 3.1.11.2) (Exonuclease III) (EXO III) (AP
DE endonuclease VI).
GN XTHA OR XTH OR B1749.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=89008066; PubMed=3049539;
RA Saporito S.M., Smith-White B.J., Cunningham R.P.;
RT "Nucleotide sequence of the xth gene of Escherichia coli K-12.";
RL J. Bacteriol. 170:4542-4547(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Wurst H., Hoheisel J.D., Pohl F.M.;
RL Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubdaram S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=95191690; PubMed=7885481;
RA Mol C.D., Kuo C.-F., Thayer M.M., Cunningham R.P., Tainer J.A.;
RT "Structure and function of the multifunctional DNA-repair enzyme
RT exonuclease III.";
RL Nature 374:381-386(1995).
RN [6]
RP CHARACTERIZATION.
RX MEDLINE=97105903; PubMed=8948651;
RA Shida T., Noda M., Sekiguchi J.;

RT "Cleavage of single-and double-stranded DNAs containing an abasic
RL residue by Escherichia coli exonuclease III (Ap endonuclease VI).";
Nucleic Acids Res. 24:4572-4576(1996).
CC -!- FUNCTION: MAJOR APURINIC-APYRIMIDINIC ENDONUCLEASE OF E. COLI. IT
CC REMOVES THE DAMAGED DNA AT CYTOSINES AND GUANINES BY CLEAVING ON
CC THE 3' SIDE OF THE AP SITE BY A BETA-ELIMINATION REACTION. IT
CC EXHIBITS 3'-5'-EXONUCLEASE, 3'-PHOSPHOMONONESTERASE, 3'-REPAIR
CC DIESTERASE AND RIBONUCLEASE H ACTIVITIES.
CC -!- CATALYTIC ACTIVITY: Degradation of double-stranded DNA. It acts
CC progressively in a 3'-to 5'-direction, releasing nucleoside 5'-
CC phosphates.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE AP/EXO A FAMILY OF DNA REPAIR ENZYMES.
CC -----
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CC -----
DR EMBL; X13002; CA31424.1; -.
DR EMBL; M22592; AAA24767.1; -.
DR EMBL; AE000270; AAC74819.1; -.
DR EMBL; D90818; BAA15540.1; -.
DR EMBL; D90819; BAA15544.1; -.
DR PIR; A31839; NCECX3.
DR PIR; S03102; S03102.
DR PDB; 1AKO; 20-AUG-97.
DR SWISS-2DPAGE; P09030; COLI.
DR ECO2DBASE; G028.2; 6TH EDITION.
DR Ecogene; EG1073; xthA.
DR InterPro; IPR000097; Apendonclse1.
DR InterPro; IPR004442; ExoDNase_III.
DR InterPro; IPR004808; ExoIII_xth.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR TIGRFAMS; TIGR00195; exoDNase_III; 1.
DR TIGRFAMS; TIGR00633; xth; 1.
DR PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
DR PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
DR PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
KW Hydrolase; Nuclease; Exonuclease; DNA repair; Multifunctional enzyme;
KW 3D-structure; Complete proteome.
FT METAL 34 MAGNESIUM OR MANGANESE.
FT SITE 153 153 IMPORTANT FOR SUBSTRATE RECOGNITION.
FT ACT_SITE 259 259 GENERAL BASE.
FT CONFLICT 49 50 KL -> NV (IN REF. 1).
SQ SEQUENCE 268 AA; 30969 MW; 09E0E263DCFC38634 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 YRSKGFD 82
| | | | | | | |
Db 215 YRSKGFD 221

Search completed: April 1, 2003, 11:51:46
Job time : 28 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:49:45 ; Search time 88 Seconds
(without alignments)
950.626 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
Perfect score: 406
Sequence: 1 ALEPALASPAGANFLAMVD.....STEDVASNCVPAQSLSEPTL 406

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	95.8	439	4 Q9H2V8	Q9h2v8 homo sapien
2	316	77.8	396	4 Q9NZL1	Q9nzl1 homo sapien
3	266	65.5	468	4 Q9NZL2	Q9nzl2 homo sapien
4	59	14.5	514	11 Q9JL18	Q9jll8 mus musculu
5	38	9.4	255	11 Q9R1P7	Q9rlp7 mus musculu
6	12	3.0	432	4 Q9BYB9	Q9byb9 homo sapien
7	12	3.0	457	4 Q9BYC0	Q9byc0 homo sapien
8	12	3.0	476	4 Q9BYC1	Q9byc1 homo sapien
9	12	3.0	532	4 Q9ULS1	Q9uls1 homo sapien
10	9	2.2	213	4 Q9P0D2	Q9pod2 homo sapien
11	9	2.2	266	11 Q9CUT5	Q9cut5 mus musculu
12	8	2.0	96	10 Q9M8Y6	Q9m8y6 arabidopsis
13	8	2.0	159	16 Q9CPI4	Q9cpi4 pasteurilla
14	8	2.0	241	16 Q9L0R0	Q9l0r0 streptomyce
15	8	2.0	244	5 Q8WQY9	Q8wqy9 aphrocallis
16	8	2.0	254	16 Q983Z3	Q983z3 rhizobium 1

17	8	2.0	287	10 Q9SH24	Q9sh24 arabidopsis
18	8	2.0	303	16 Q9RXF5	Q9rxf5 deinococcus
19	8	2.0	319	16 Q8Z5W7	Q8z5w7 salmonella
20	8	2.0	327	3 P78849	P78849 schizosacch
21	8	2.0	333	16 Q8ZNV8	Q8znv8 salmonella
22	8	2.0	341	6 Q46495	Q46495 bos taurus
23	8	2.0	342	2 Q68868	Q68868 synechococc
24	8	2.0	352	17 Q9YER7	Q9yer7 aeropyrum p
25	8	2.0	386	10 Q8S1T9	Q8s1t9 oryza sativ
26	8	2.0	449	10 Q9S9K4	Q9s9k4 arabidopsis
27	8	2.0	451	10 Q9LGF1	Q9l9f1 oryza sativ
28	8	2.0	471	11 Q91XR7	Q91xr7 rattus norv
29	8	2.0	472	4 Q96PQ4	Q96pq4 homo sapien
30	8	2.0	472	4 Q8WUX1	Q8wux1 homo sapien
31	8	2.0	473	5 Q9VEE0	Q9vee0 drosophila
32	8	2.0	474	5 Q8SQZ9	Q8sqz9 encephalito
33	8	2.0	476	4 Q9UTU8	Q9uju8 homo sapien
34	8	2.0	482	2 Q8RMG9	Q8rmg9 acetobacter
35	8	2.0	504	4 Q99624	Q99624 homo sapien
36	8	2.0	504	11 Q9JHZ9	Q9jhz9 rattus norv
37	8	2.0	505	11 Q9DCP2	Q9dcp2 mus musculu
38	8	2.0	505	11 Q9JL18	Q9jll8 mus musculu
39	8	2.0	548	16 Q8Z2N7	Q8z2n7 salmonella
40	8	2.0	548	16 Q8XB42	Q8xb42 escherichia
41	8	2.0	548	16 Q8ZKY4	Q8zky4 salmonella
42	8	2.0	592	5 Q9VTS5	Q9vts5 drosophila
43	8	2.0	612	5 Q8T0E6	Q8t0e6 drosophila
44	8	2.0	637	10 Q82612	Q82612 arabidopsis
45	8	2.0	671	17 Q8TJA8	Q8tja8 methanosarc
46	8	2.0	682	16 Q8XVM2	Q8xvm2 ralstonia s
47	8	2.0	904	16 Q9HUM7	Q9hum7 pseudomonas
48	8	2.0	985	3 Q8X027	Q8x027 neurospora
49	7	1.7	32	16 Q98AB6	Q98ab6 rhizobium 1
50	7	1.7	84	17 Q8TWE3	Q8twe3 methanopyru
51	7	1.7	85	2 Q9AP00	Q9ap00 burkholderi
52	7	1.7	86	2 Q9WXF8	Q9wxf8 rhodococcus
53	7	1.7	86	8 Q95786	Q95786 diabtrotica
54	7	1.7	86	8 Q95778	Q95778 diabtrotica
55	7	1.7	86	8 Q95787	Q95787 diabtrotica
56	7	1.7	92	16 Q98JG3	Q98jg3 rhizobium 1
57	7	1.7	103	2 Q9ZEH7	Q9zeh7 enterococcu
58	7	1.7	107	3 Q8X1T7	Q8x1t7 pholiota na
59	7	1.7	112	5 Q9VLE8	Q9vle8 drosophila
60	7	1.7	115	2 P72321	P72321 rhodospiril
61	7	1.7	119	11 Q9OXI4	Q9oxi4 rattus norv
62	7	1.7	123	15 Q9YV02	Q9yv02 human immun
63	7	1.7	123	15 Q9YUZ5	Q9yuz5 human immun
64	7	1.7	131	16 Q98QNI	Q98qnl mycoplasma
65	7	1.7	141	16 Q9KCU3	Q9kcus bacillus ha
66	7	1.7	150	16 Q8XKV6	Q8xkv6 clostridium
67	7	1.7	160	16 Q98K01	Q98k01 rhizobium 1
68	7	1.7	180	16 P71704	P71704 mycobacteri
69	7	1.7	187	8 Q03012	Q03012 molitugo ver
70	7	1.7	197	2 Q9WM61	Q9wm61 streptococc
71	7	1.7	206	10 Q9LSK3	Q9lsk3 arabidopsis
72	7	1.7	206	10 Q9LSK2	Q9lsk2 arabidopsis
73	7	1.7	206	16 Q8UE19	Q8ue19 agrobacteri
74	7	1.7	210	2 Q9XCJ9	Q9xcj9 streptococc
75	7	1.7	218	2 Q9XCK5	Q9xck5 streptococc
76	7	1.7	235	2 Q9XCK9	Q9xck9 streptococc
77	7	1.7	235	16 Q9JRU0	Q9jru0 chlamydia p
78	7	1.7	235	16 Q9Z742	Q9z742 chlamydia p
79	7	1.7	240	11 Q9D1A3	Q9dia3 mus musculu
80	7	1.7	241	16 Q9PLK3	Q9plk3 chlamydia m
81	7	1.7	241	16 Q84728	Q84728 chlamydia t
82	7	1.7	244	16 Q8YJH0	Q8yjh0 brucella me
83	7	1.7	249	2 Q8VMT4	Q8vmj4 pseudomonas
84	7	1.7	253	2 Q9L4V7	Q9l4v7 streptomyc
85	7	1.7	253	5 Q61709	Q61709 caenorhabdi
86	7	1.7	254	16 Q9A3X5	Q9a3x5 caulobacter
87	7	1.7	255	10 Q43406	Q43406 brassica ol
88	7	1.7	257	2 Q69217	Q69217 azotobacter
89	7	1.7	264	2 Q9JRS5	Q9jrs5 actinobacil

90	7	1.7	267	2	005382	005382 actinobacil	163	7	1.7	387	6	Q9GMY8	Q9gmy8 sorex ungui
91	7	1.7	267	2	066261	066261 actinobacil	164	7	1.7	387	6	046496	046496 bos taurus
92	7	1.7	267	5	Q9VHH4	Q9vhh4 drosophila	165	7	1.7	388	6	046524	046524 felis silve
93	7	1.7	267	16	Q9HMB2	Q9hmb2 pseudomonas	166	7	1.7	389	3	Q9Y775	Q9y775 candida tro
94	7	1.7	267	16	Q9CMW2	Q9cmw2 pasteurella	167	7	1.7	389	6	Q9MYK3	Q9myk3 sus scrofa
95	7	1.7	268	16	Q8XDY5	Q8xdy5 escherichia	168	7	1.7	389	6	Q9MYK2	Q9myk2 sus scrofa
96	7	1.7	269	2	Q9RFW5	Q9rfw5 mycoplasma	169	7	1.7	390	6	Q9GK10	Q9gk10 camelus dro
97	7	1.7	269	4	Q9UKP1	Q9ukp1 homo sapien	170	7	1.7	396	13	Q93428	Q93428 chionodraco
98	7	1.7	270	16	P71638	P71638 mycobacteri	171	7	1.7	398	16	Q9RW70	Q9rw70 deinococcus
99	7	1.7	277	2	Q9F5Q9	Q9f5q9 vibrio chol	172	7	1.7	399	13	Q93458	Q93458 podarcis si
100	7	1.7	278	2	Q9RHL8	Q9rhl8 actinobacil	173	7	1.7	407	17	Q9HJF2	Q9hjf2 thermoplasm
101	7	1.7	281	2	Q93Q45	Q93q45 clostridium	174	7	1.7	413	3	Q14413	Q14413 pichia angu
102	7	1.7	289	11	Q8R296	Q8r296 mus musculu	175	7	1.7	413	16	Q8RG42	Q8rg42 fusobacteri
103	7	1.7	289	12	Q9QA18	Q9qa18 murid herpe	176	7	1.7	416	16	Q987L1	Q987l1 rhizobium 1
104	7	1.7	291	16	Q9KMY5	Q9kmy5 vibrio chol	177	7	1.7	416	16	Q987H5	Q987h5 yersinia pe
105	7	1.7	302	16	Q52882	Q52882 rhizobium m	178	7	1.7	419	10	Q94HM8	Q94hm8 oryza sativ
106	7	1.7	306	16	Q8ZRUI	Q8zrui salmonella	179	7	1.7	423	2	Q9EZF6	Q9ezf6 streptococc
107	7	1.7	306	16	Q8Z9G7	Q8z9g7 salmonella	180	7	1.7	434	16	Q8ZIK4	Q8zik4 yersinia pe
108	7	1.7	306	16	Q8X9Y6	Q8x9y6 escherichia	181	7	1.7	436	16	Q92U00	Q92u00 rhizobium m
109	7	1.7	319	5	Q9N3J6	Q9n3j6 caenorhabdi	182	7	1.7	437	2	Q9EZF7	Q9ezf7 streptococc
110	7	1.7	319	16	Q9CMU4	Q9cmu4 pasteurella	183	7	1.7	438	10	Q8W347	Q8w347 oryza sativ
111	7	1.7	319	16	Q8YDM9	Q8ydm9 brucella me	184	7	1.7	441	17	Q8TW66	Q8tw66 methanopyru
112	7	1.7	320	2	Q9KHS4	Q9khs4 leptospira	185	7	1.7	449	17	Q8TWG3	Q8twg3 methanopyru
113	7	1.7	320	2	Q9L586	Q9l586 leptospira	186	7	1.7	450	5	060989	060989 plasmodium
114	7	1.7	320	2	Q48546	Q48546 leptospira	187	7	1.7	450	5	076965	076965 plasmodium
115	7	1.7	320	16	Q9JXR6	Q9jxr6 neisseria m	188	7	1.7	451	16	Q8RHG6	Q8rhg6 fusobacteri
116	7	1.7	320	16	Q9JWS6	Q9jws6 neisseria m	189	7	1.7	452	10	Q9LI73	Q9li73 arabadopsis
117	7	1.7	322	5	Q9N3J7	Q9n3j7 caenorhabdi	190	7	1.7	460	4	Q9H8M0	Q9hm0 homo sapien
118	7	1.7	325	16	Q9ZTF8	Q9ztf8 rhizobium m	191	7	1.7	461	10	Q9FUL9	Q9ful9 zea mays (m
119	7	1.7	326	16	Q8YUJ4	Q8yuj4 ralstonia s	192	7	1.7	465	5	Q9VEK5	Q9vek5 drosophila
120	7	1.7	327	16	Q92WF7	Q92wf7 rhizobium m	193	7	1.7	470	11	Q99LK8	Q99lk8 mus musculu
121	7	1.7	331	16	Q9I561	Q9i561 pseudomonas	194	7	1.7	473	4	Q96A99	Q96a99 homo sapien
122	7	1.7	333	2	Q9XAT5	Q9xat5 rhizobium 1	195	7	1.7	484	2	Q9Z911	Q9z911 magnetospir
123	7	1.7	333	16	Q8ZEG7	Q8zeg7 yersinia pe	196	7	1.7	486	10	Q88934	Q88934 arabadopsis
124	7	1.7	335	5	Q965L5	Q965l5 caenorhabdi	197	7	1.7	486	13	Q8QGX2	Q8qgx2 brachydanio
125	7	1.7	336	10	Q65453	Q65453 arabadopsis	198	7	1.7	491	16	Q8U9P9	Q8u9p9 agrobacteri
126	7	1.7	339	16	Q8XXA2	Q8xxa2 ralstonia s	199	7	1.7	491	17	Q9HN17	Q9hn17 halobacteri
127	7	1.7	341	6	002728	002728 ovis aries	200	7	1.7	507	5	Q9GY92	Q9gy92 leishmania
128	7	1.7	345	5	Q96439	Q96439 leishmania	201	7	1.7	504	10	Q9XFX3	Q9xfx3 cynara card
129	7	1.7	345	16	Q9RRR0	Q9rrr0 deinococcus	202	7	1.7	505	10	Q9FRW6	Q9frw6 nepenthes a
130	7	1.7	345	16	Q8Z359	Q8z359 salmonella	203	7	1.7	506	10	Q39311	Q39311 brassica na
131	7	1.7	345	16	Q8UKA3	Q8uka3 agrobacteri	204	7	1.7	506	10	Q40140	Q40140 lycopersico
132	7	1.7	346	6	002729	002729 ovis aries	205	7	1.7	507	10	Q65390	Q65390 arabadopsis
133	7	1.7	346	16	Q9CHK6	Q9chk6 lactococcus	206	7	1.7	507	10	Q9FRW7	Q9frw7 nepenthes a
134	7	1.7	347	16	Q8Z0K4	Q8z0k4 anabaena sp	207	7	1.7	508	10	Q948P0	Q948p0 glycine max
135	7	1.7	353	2	P70901	P70901 borrelia he	208	7	1.7	508	10	Q9XEC4	Q9xec4 arabadopsis
136	7	1.7	354	5	Q9GYX7	Q9gyx7 boophilus m	209	7	1.7	509	10	Q9SSZ1	Q9ssz1 helianthus
137	7	1.7	358	2	P70899	P70899 borrelia he	210	7	1.7	510	16	Q99WR2	Q99wr2 staphylococ
138	7	1.7	358	10	Q9FRW5	Q9frw5 nepenthes a	211	7	1.7	512	10	Q04593	Q04593 arabadopsis
139	7	1.7	360	2	P70905	P70905 borrelia he	212	7	1.7	513	10	Q8VYL3	Q8vy13 arabadopsis
140	7	1.7	361	16	Q92S90	Q92s90 rhizobium m	213	7	1.7	514	10	Q9FRW9	Q9frw9 nepenthes a
141	7	1.7	366	2	P70900	P70900 borrelia he	214	7	1.7	525	16	Q99ZJ0	Q99zj0 streptococc
142	7	1.7	367	16	Q98UF1	Q98uf1 rhizobium 1	215	7	1.7	526	2	Q93N65	Q93n65 coxiella bu
143	7	1.7	368	16	Q8UDJ2	Q8udd2 agrobacteri	216	7	1.7	540	5	Q962J4	Q962j4 plasmodium
144	7	1.7	371	2	Q9EZH2	Q9ezh2 streptococc	217	7	1.7	541	4	Q8TBY2	Q8tby2 homo sapien
145	7	1.7	373	10	Q9SD30	Q9sd30 arabadopsis	218	7	1.7	544	12	Q41936	Q41936 murid herpe
146	7	1.7	373	10	P93031	P93031 arabadopsis	219	7	1.7	555	10	Q9C7N0	Q9c7n0 arabadopsis
147	7	1.7	374	6	Q9TTW0	Q9ttw0 bos taurus	220	7	1.7	559	10	Q9FKP2	Q9fkp2 arabadopsis
148	7	1.7	378	13	Q9PUR9	Q9pur9 pseudopleur	221	7	1.7	582	11	Q8VHU6	Q8vhu6 rattus norv
149	7	1.7	379	11	Q9UTX1	Q9ujxl rattus norv	222	7	1.7	583	16	Q8RCR3	Q8rcr3 thermoaer
150	7	1.7	380	6	Q46492	Q46492 bos taurus	223	7	1.7	600	5	Q9U2N6	Q9u2n6 caenorhabdi
151	7	1.7	380	6	Q9TTW5	Q9ttw5 capra hircu	224	7	1.7	609	10	Q9AUY9	Q9auy9 arabadopsis
152	7	1.7	380	6	Q9TTV4	Q9ttv4 bos taurus	225	7	1.7	615	13	Q42565	Q42565 xenopus lae
153	7	1.7	380	6	002723	002723 ovis aries	226	7	1.7	626	16	Q9KQX9	Q9kqx9 vibrio chol
154	7	1.7	381	6	Q9GK11	Q9gk11 camelus dro	227	7	1.7	633	16	Q98LR9	Q98lr9 rhizobium 1
155	7	1.7	382	13	Q9PRG9	Q9prg9 gallus gall	228	7	1.7	649	4	Q9H0T2	Q9hot2 homo sapien
156	7	1.7	383	13	Q9DEC3	Q9dec3 xenopus lae	229	7	1.7	659	12	Q66383	Q66383 dengue viru
157	7	1.7	384	13	Q91322	Q91322 rana catesb	230	7	1.7	666	10	Q94GB7	Q94gb7 oryza sativ
158	7	1.7	385	6	Q29080	Q29080 sus' scrofa	231	7	1.7	674	4	Q9H917	Q9h917 homo sapien
159	7	1.7	386	6	Q9GMY7	Q9gmy7 rhinolophus	232	7	1.7	682	16	Q8ZJ57	Q8zj57 yersinia pe
160	7	1.7	386	6	Q9GMY6	Q9gmy6 canis famli	233	7	1.7	690	16	Q9K186	Q9k186 vibrio chol
161	7	1.7	386	6	Q9TTW8	Q9ttw8 capra hircu	234	7	1.7	707	16	Q9CD82	Q9cd82 mycobacteri
162	7	1.7	387	6	Q9GMY9	Q9gmy9 suncus murti	235	7	1.7	709	5	Q22548	Q22548 caenorhabdi

236	7	1.7	711	5	Q24205	Q24205 drosophila	309	6	1.5	62	5	P82170	P82170 locusta mig
237	7	1.7	722	3	Q10668	Q10668 schizosacch	310	6	1.5	64	8	Q36146	Q36146 thamnophis
238	7	1.7	732	10	Q94HA5	Q94ha5 oryza sativ	311	6	1.5	65	16	Q9K2D5	Q9k2d5 chlamydia p
239	7	1.7	784	16	Q8YAJ5	Q8yaJ5 listeria mo	312	6	1.5	67	16	Q927S6	Q927s6 listeria in
240	7	1.7	802	10	Q38802	Q38802 arabidopsis	313	6	1.5	69	10	Q9AUF7	Q9auf7 brassica na
241	7	1.7	813	10	Q9LDT8	Q9ldt8 oryza sativ	314	6	1.5	70	10	Q9AUF6	Q9auf6 brassica na
242	7	1.7	854	5	Q9NDZ8	Q9ndz8 leishmania	315	6	1.5	70	10	Q9AUF5	Q9auf5 brassica ol
243	7	1.7	873	2	Q9S4K0	Q9s4k0 streptococc	316	6	1.5	70	10	Q9AUF4	Q9auf4 brassica ca
244	7	1.7	880	16	Q9A1M8	Q9a1m8 streptococc	317	6	1.5	71	2	Q9FCW3	Q9fcw3 escherichia
245	7	1.7	887	5	Q19428	Q19428 caenorhabdi	318	6	1.5	72	10	Q65618	Q65618 arabidopsis
246	7	1.7	893	10	Q8S615	Q8s615 oryza sativ	319	6	1.5	72	12	Q8VB96	Q8vb96 white spot
247	7	1.7	907	16	Q9L248	Q9l248 streptomyce	320	6	1.5	73	4	Q93067	Q93067 homo sapien
248	7	1.7	912	16	Q9K3Y2	Q9k3y2 streptomyce	321	6	1.5	73	8	Q9XOR3	Q9xqr3 pisum sativ
249	7	1.7	923	2	Q9S3T2	Q9s3t2 streptococc	322	6	1.5	73	8	Q35148	Q35148 nerodia ery
250	7	1.7	933	16	Q8XE39	Q8xe39 escherichia	323	6	1.5	73	16	Q9A2N3	Q9a2n3 caulobacter
251	7	1.7	934	11	Q924X9	Q924x9 mus musculu	324	6	1.5	74	16	Q8Y2X8	Q8y2x8 ralstonia s
252	7	1.7	939	16	Q8YOR3	Q8yqr3 anabaena sp	325	6	1.5	75	2	Q9EYZ7	Q9eyz7 photobacter
253	7	1.7	967	2	Q54123	Q54123 staphylococ	326	6	1.5	75	2	P94765	P94765 erwinia chr
254	7	1.7	968	2	Q9F848	Q9f848 streptomyce	327	6	1.5	76	8	Q48083	Q48083 eryx tatari
255	7	1.7	991	4	Q15043	Q15043 homo sapien	328	6	1.5	77	8	Q99364	Q99364 elaphe rufo
256	7	1.7	1015	2	Q93T50	Q93t50 streptococc	329	6	1.5	77	8	Q9ZXV7	Q9zxv7 elaphe rufo
257	7	1.7	1015	4	Q14572	Q14572 homo sapien	330	6	1.5	77	10	Q9XIX4	Q9xix4 oryza sativ
258	7	1.7	1027	2	Q93T51	Q93t51 streptococc	331	6	1.5	78	8	Q36087	Q36087 thamnophis
259	7	1.7	1039	16	Q9KEQ8	Q9keq8 bacillus ha	332	6	1.5	78	8	Q36143	Q36143 thamnophis
260	7	1.7	1042	4	Q9H4G6	Q9h4g6 homo sapien	333	6	1.5	79	6	Q29452	Q29452 bos taurus
261	7	1.7	1130	4	Q9H1V5	Q9h1v5 homo sapien	334	6	1.5	79	16	Q25333	Q25333 helicobacte
262	7	1.7	1131	16	Q8YT43	Q8yt43 anabaena sp	335	6	1.5	80	2	Q70028	Q70028 streptomyce
263	7	1.7	1133	17	Q96XX7	Q96xx7 sulfolobus	336	6	1.5	80	2	Q9R6M8	Q9rem8 agrobacteri
264	7	1.7	1142	16	Q97J24	Q97j24 clostridium	337	6	1.5	80	8	Q99365	Q99365 elaphe bima
265	7	1.7	1236	5	Q9JPA4	Q9jpa4 rhodocyclus	338	6	1.5	80	10	Q49028	Q49028 gracilaria
266	7	1.7	1269	2	Q43993	Q43993 dictyosteli	339	6	1.5	81	8	Q99362	Q99362 elaphe taen
267	7	1.7	1324	10	Q94GQ7	Q94gq7 oryza sativ	340	6	1.5	81	8	Q99370	Q99370 dinodon ruf
268	7	1.7	1330	6	Q97961	Q97961 vulpes vulp	341	6	1.5	81	8	Q99371	Q99371 dinodon ruf
269	7	1.7	1379	5	Q9VNG9	Q9vng9 drosophila	342	6	1.5	81	8	Q99372	Q99372 zaocys dhum
270	7	1.7	1379	5	Q9TY11	Q9ty11 drosophila	343	6	1.5	81	8	Q99373	Q99373 zaocys dhum
271	7	1.7	1411	2	Q9AJ93	Q9aj93 actinomycetes	344	6	1.5	81	8	Q99374	Q99374 ptiyas korro
272	7	1.7	1429	4	Q9YST6	Q9yst6 homo sapien	345	6	1.5	81	8	Q99375	Q99375 ptiyas korro
273	7	1.7	1437	11	Q07563	Q07563 mus musculu	346	6	1.5	81	8	Q36138	Q36138 thamnophis
274	7	1.7	1437	5	Q9GQ51	Q9gq51 dictyosteli	347	6	1.5	81	8	Q9ZXW5	Q9zxw5 zaocys dhum
275	7	1.7	1630	16	Q8RHH7	Q8rhh7 fusobacteri	348	6	1.5	81	8	Q9ZXR1	Q9zxr1 elaphe taen
276	7	1.7	1886	5	Q9NKU5	Q9nkus leishmania	349	6	1.5	81	12	Q55445	Q55445 sindbis vir
277	7	1.7	1937	2	Q8RJY2	Q8rij2 stigmatella	350	6	1.5	81	12	Q55447	Q55447 sindbis vir
278	7	1.7	2014	5	Q22774	Q22774 caenorhabdi	351	6	1.5	81	12	Q55448	Q55448 sindbis vir
279	7	1.7	2025	10	Q9SHK4	Q9shk4 arabidopsis	352	6	1.5	81	12	Q9W8F2	Q9w8f2 sindbis vir
280	7	1.7	2042	5	Q9W1C5	Q9w1c5 drosophila	353	6	1.5	81	16	Q9PA00	Q9pa00 xylella fas
281	7	1.7	2554	5	Q9NKT1	Q9nkt1 leishmania	354	6	1.5	82	12	Q55446	Q55446 sindbis vir
282	7	1.7	2813	4	Q96JP6	Q96jp6 homo sapien	355	6	1.5	83	4	Q9H3B2	Q9h3b2 homo sapien
283	7	1.7	2813	4	Q8WXQ6	Q8wxq6 homo sapien	356	6	1.5	84	8	Q36106	Q36106 thamnophis
284	7	1.7	2817	4	Q96P79	Q96p79 homo sapien	357	6	1.5	85	5	Q9W5T0	Q9w5t0 drosophila
285	7	1.7	2894	17	Q58791	Q58791 methanococc	358	6	1.5	85	8	Q48086	Q48086 eryx tatari
286	6	1.5	15	3	Q9UR72	Q9ur72 trichoderma	359	6	1.5	85	17	Q9HJF0	Q9hjf0 thermoplasm
287	6	1.5	19	3	Q9S956	Q9s956 zea mays (m	360	6	1.5	88	8	Q36141	Q36141 thamnophis
288	6	1.5	22	11	Q9QWB6	Q9qwb6 mus sp. sgp	361	6	1.5	88	16	Q25107	Q25107 helicobacte
289	6	1.5	24	9	Q9T0O7	Q9t0q7 bacteriopha	362	6	1.5	88	16	Q92K13	Q92k13 rhizobium m
290	6	1.5	25	12	Q9WMG7	Q9wmg7 sigma virus	363	6	1.5	88	16	Q9F2U8	Q9f2u8 streptomyce
291	6	1.5	30	7	Q31234	Q31234 mus musculu	364	6	1.5	89	8	Q36122	Q36122 thamnophis
292	6	1.5	35	8	Q9SA09	Q9sa09 synaphobran	365	6	1.5	89	16	Q36745	Q3chr8 lactococcus
293	6	1.5	39	5	Q16984	Q16984 acheta dome	366	6	1.5	90	8	Q36745	Q36745 epirates s
294	6	1.5	40	10	Q9SSK6	Q9ssk6 arabidopsis	367	6	1.5	90	8	Q8WEQ7	Q8weg7 sanzinia ma
295	6	1.5	40	16	Q8VJ52	Q8vj52 mycobacteri	368	6	1.5	90	8	Q8WEQ6	Q8weg6 boa constri
296	6	1.5	45	6	Q9GK71	Q9gk71 bos taurus	369	6	1.5	90	8	Q8WEQ5	Q8weg5 candoia bib
297	6	1.5	46	6	Q9GK71	Q9gk71 bos taurus	370	6	1.5	90	8	Q8WEQ4	Q8weg4 candoia car
298	6	1.5	46	11	Q9R1N8	Q9r1n8 mus musculu	371	6	1.5	90	8	Q8WEQ3	Q8weg3 candoia car
299	6	1.5	46	11	Q9WVP4	Q9wvp4 mus spretus	372	6	1.5	90	8	Q8WEQ2	Q8weg2 candoia car
300	6	1.5	46	11	Q9WTK9	Q9wtk9 mus musculu	373	6	1.5	90	8	Q8WEQ1	Q8weg1 candoia car
301	6	1.5	49	2	Q9EVP1	Q9evp1 escherichia	374	6	1.5	90	8	Q8W7U6	Q8w7u6 candoia bib
302	6	1.5	52	16	Q9A041	Q9a041 streptococc	375	6	1.5	90	8	Q8W7N8	Q8w7n8 candoia asp
303	6	1.5	54	4	Q13807	Q13807 homo sapien	376	6	1.5	90	8	Q8W7N7	Q8w7n7 candoia car
304	6	1.5	56	2	P97248	P97248 escherichia	377	6	1.5	90	8	Q8W7N6	Q8w7n6 candoia asp
305	6	1.5	58	4	Q969L1	Q969l1 homo sapien	378	6	1.5	90	13	Q91063	Q91063 jordanella
306	6	1.5	59	16	Q9L720	Q9l720 caulobacter	379	6	1.5	90	13	Q90XJ1	Q90xj1 acipenser s
307	6	1.5	60	3	Q12711	Q12711 trichoderma	380	6	1.5	90	13	Q90X15	Q90x15 amia calva
308	6	1.5	61	2	O52860	O52860 bacillus su	381	6	1.5	90	16	Q9K3G8	Q9k3g8 streptomyce

382	6	1.5	92	2	Q52631	Q52631 escherichia
383	6	1.5	92	2	Q52632	Q52632 escherichia
384	6	1.5	92	8	Q36123	Q36123 thamnophis
385	6	1.5	93	13	Q91251	Q91251 profundulus
386	6	1.5	93	17	Q8TWE6	Q8twe6 methanopyru
387	6	1.5	94	8	Q36145	Q36145 thamnophis
388	6	1.5	94	8	Q36094	Q36094 thamnophis
389	6	1.5	95	2	Q49154	Q49154 methyllobact
390	6	1.5	95	2	Q36000	Q36000 thamnophis
391	6	1.5	95	8	Q35147	Q35147 nerodia ery
392	6	1.5	95	15	Q9INC6	Q9inc6 human immun
393	6	1.5	96	8	Q36001	Q36001 thamnophis
394	6	1.5	96	11	Q8R401	Q8r401 rattus norv
395	6	1.5	96	12	Q8QP44	Q8qp44 dengue viru
396	6	1.5	96	15	Q38190	Q38190 human immun
397	6	1.5	97	8	Q36051	Q36051 thamnophis
398	6	1.5	97	8	Q36019	Q36019 thamnophis
399	6	1.5	97	8	Q36021	Q36021 thamnophis
400	6	1.5	97	8	Q36029	Q36029 thamnophis
401	6	1.5	97	8	Q35983	Q35983 thamnophis
402	6	1.5	97	15	Q9Y65	Q9y65 human immun
403	6	1.5	98	5	Q8SYX2	Q8syx2 drosophila
404	6	1.5	98	8	Q36077	Q36077 thamnophis
405	6	1.5	98	8	Q35982	Q35982 thamnophis
406	6	1.5	98	8	Q21564	Q21564 sigmodon oc
407	6	1.5	98	8	Q36028	Q36028 thamnophis
408	6	1.5	98	9	Q80282	Q80282 xanthomonas
409	6	1.5	99	8	Q36124	Q36124 thamnophis
410	6	1.5	99	8	Q9G435	Q9g435 thamnophis
411	6	1.5	99	8	Q36024	Q36024 thamnophis
412	6	1.5	99	12	Q73557	Q73557 laassa virus
413	6	1.5	99	15	Q71241	Q71241 human immun
414	6	1.5	99	16	Q92Y38	Q92y38 rhizobium m
415	6	1.5	99	16	Q8YXN5	Q8yxn5 anabaena sp
416	6	1.5	100	8	Q9TEP8	Q9tep8 natrix natr
417	6	1.5	100	8	Q9TEP7	Q9tep7 elaphe long
418	6	1.5	100	8	Q36144	Q36144 thamnophis
419	6	1.5	100	8	Q36025	Q36025 thamnophis
420	6	1.5	100	8	Q36027	Q36027 thamnophis
421	6	1.5	100	8	Q36003	Q36003 thamnophis
422	6	1.5	100	8	Q35150	Q35150 nerodia fas
423	6	1.5	100	12	Q91FS4	Q91fs4 chilo iride
424	6	1.5	100	13	Q90393	Q90393 cypripinodon
425	6	1.5	101	2	Q46552	Q46552 bacteroides
426	6	1.5	101	8	Q36083	Q36083 thamnophis
427	6	1.5	101	17	Q9Y9N7	Q9y9n7 aeropyrum p
428	6	1.5	102	8	Q9G1Z1	Q9g1z1 thamnophis
429	6	1.5	102	8	Q9G1W2	Q9g1w2 thamnophis
430	6	1.5	102	8	Q9G1V3	Q9g1v3 thamnophis
431	6	1.5	102	8	Q9G1T7	Q9g1t7 thamnophis
432	6	1.5	102	8	Q36078	Q36078 thamnophis
433	6	1.5	102	8	Q36022	Q36022 thamnophis
434	6	1.5	102	8	Q36023	Q36023 thamnophis
435	6	1.5	102	8	Q9B8P0	Q9b8p0 philodryas
436	6	1.5	102	8	Q9B8N9	Q9b8n9 philodryas
437	6	1.5	102	8	Q9B8N8	Q9b8n8 philodryas
438	6	1.5	102	8	Q9B8N7	Q9b8n7 philodryas
439	6	1.5	102	8	Q9B8N6	Q9b8n6 philodryas
440	6	1.5	102	8	Q9B8N3	Q9b8n3 tropidodrya
441	6	1.5	102	8	Q9B8N1	Q9b8n1 oxyrhopus g
442	6	1.5	102	8	Q9G436	Q9g436 thamnophis
443	6	1.5	102	8	Q9G434	Q9g434 thamnophis
444	6	1.5	102	8	Q9G432	Q9g432 thamnophis
445	6	1.5	102	16	Q8X798	Q8x798 escherichia
446	6	1.5	103	8	Q9TB05	Q9tb05 azemiops fe
447	6	1.5	103	8	Q9TB04	Q9tb04 agkistrodon
448	6	1.5	103	8	Q9TB03	Q9tb03 agkistrodon
449	6	1.5	103	8	Q9TB02	Q9tb02 glyodius br
450	6	1.5	103	8	Q9TB01	Q9tb01 agkistrodon
451	6	1.5	103	8	Q9TB00	Q9tb00 glyodius st
452	6	1.5	103	8	Q9TAZ9	Q9taaz glyodius sa
453	6	1.5	103	8	Q9TAZ8	Q9taaz glyodius sh
454	6	1.5	103	8	Q9TAZ7	Q9taaz glyodius st
455	6	1.5	103	8	Q9TAZ6	Q9taaz agkistrodon
456	6	1.5	103	8	Q9TAZ5	Q9taaz ovophis mon
457	6	1.5	103	8	Q9TAZ4	Q9taaz trimeresuru
458	6	1.5	103	8	Q9TAZ3	Q9taaz trimeresuru
459	6	1.5	103	10	Q8S737	Q8s737 oryza sativ
460	6	1.5	103	13	Q90224	Q90224 aplocheilic
461	6	1.5	103	13	Q90312	Q90312 crenichthys
462	6	1.5	103	13	Q91991	Q91991 zoogoneticu
463	6	1.5	103	16	Q98P21	Q98p21 rhizobium 1
464	6	1.5	104	6	Q29169	Q29169 sus scrofa
465	6	1.5	104	13	Q90242	Q90242 aplocheilic
466	6	1.5	104	13	Q91536	Q91536 xenotoca ei
467	6	1.5	105	16	Q8YH98	Q8yh98 bruceella me
468	6	1.5	106	8	Q9B1R1	Q9b1r1 crotalus ho
469	6	1.5	106	8	Q9B426	Q9b426 crotalus ho
470	6	1.5	106	12	Q9YK02	Q9yk02 dengue viru
471	6	1.5	107	2	Q05626	Q05626 streptomyce
472	6	1.5	107	5	P91196	P91196 caenorhabdi
473	6	1.5	107	17	Q979E7	Q979e7 thermoplasm
474	6	1.5	109	5	Q24148	Q24148 drosophila
475	6	1.5	109	9	Q8SCS1	Q8scs1 pseudomonas
476	6	1.5	109	12	Q9WJG7	Q9wjg7 dengue viru
477	6	1.5	109	16	Q92Q07	Q92qg7 rhizobium m
478	6	1.5	111	4	Q9H383	Q9h383 homo sapien
479	6	1.5	112	10	Q9SFC3	Q9sf33 arabidopsis
480	6	1.5	112	10	Q9LYY2	Q9lyy2 arabidopsis
481	6	1.5	112	16	Q8Z6U5	Q8z6u5 salmonella
482	6	1.5	113	11	Q8R0E4	Q8r0e4 mus musculu
483	6	1.5	113	12	Q9YJT5	Q9ytf5 ateline her
484	6	1.5	113	16	Q9KBIT0	Q9kbio bacillus ha
485	6	1.5	113	16	Q06536	Q06536 mycobacteri
486	6	1.5	114	2	Q9REBK0	Q9rbko xanthomonas
487	6	1.5	114	5	Q9Y063	Q9y063 trichinella
488	6	1.5	114	5	Q95UI8	Q9sui8 trichinella
489	6	1.5	114	10	Q9W0G5	Q9w0g5 oryza sativ
490	6	1.5	114	17	Q9YFA7	Q9yfa7 aeropyrum p
491	6	1.5	115	8	Q48070	Q48070 eryx colubr
492	6	1.5	115	10	Q9ATH2	Q9ath2 corylus ave
493	6	1.5	115	10	Q9AWM2	Q9awm2 oryza sativ
494	6	1.5	116	16	Q9FBU5	Q9fbu5 streptomyce
495	6	1.5	116	17	Q8ZYZ8	Q8zyz8 pyrobaculum
496	6	1.5	117	5	Q9NGU5	Q9ngu5 sarcophaga
497	6	1.5	117	10	Q8W539	Q8w539 retama raet
498	6	1.5	118	10	Q9FYI2	Q9fyi2 arabidopsis
499	6	1.5	119	8	Q63527	Q63527 dicrocoeliu
500	6	1.5	119	8	Q48061	Q48061 epicrates s
501	6	1.5	119	8	Q48069	Q48069 eryx colubr
502	6	1.5	120	5	Q8TAZ8	Q8taaz8 heterodera
503	6	1.5	120	9	Q8SCW5	Q8scw5 pseudomonas
504	6	1.5	121	2	Q9AMU8	Q9amu8 bradyrhizob
505	6	1.5	121	4	Q8WUE8	Q8wue8 homo sapien
506	6	1.5	121	10	Q8RYC6	Q8ryc6 arabidopsis
507	6	1.5	121	16	Q9A1R0	Q9a1r0 streptococc
508	6	1.5	121	16	Q9L2K6	Q9l2k6 streptomyce
509	6	1.5	122	8	Q9TEC6	Q9tec6 epicrates a
510	6	1.5	122	8	Q9TEC5	Q9tec5 epicrates f
511	6	1.5	122	8	Q48074	Q48074 eryx elegan
512	6	1.5	122	12	Q9WJG6	Q9wjg6 dengue viru
513	6	1.5	123	8	Q48018	Q48018 boa constri
514	6	1.5	123	8	Q9TEC7	Q9tec7 boa constri
515	6	1.5	123	8	Q48021	Q48021 boa constri
516	6	1.5	123	8	Q48022	Q48022 boa constri
517	6	1.5	123	8	Q48115	Q48115 thamnophis
518	6	1.5	123	8	Q48020	Q48020 boa constri
519	6	1.5	123	12	Q9YK01	Q9yk01 dengue viru
520	6	1.5	123	17	Q9HMY9	Q9hmy9 halobacteri
521	6	1.5	124	17	Q8TNS0	Q8tns0 methanosarc
522	6	1.5	125	6	Q9N0C6	Q9n0c6 macaca fasc
523	6	1.5	125	8	Q95822	Q95822 lachesis mu
524	6	1.5	125	10	Q8S007	Q8s007 oryza sativ
525	6	1.5	125	16	Q8UGX4	Q8ugx4 agrobacteri
526	6	1.5	126	10	Q9LPK9	Q9lpk9 arabidopsis
527	6	1.5	127	2	Q93RNI	Q93rni listeria mo

528	6	1.5	128	8	Q95722	Q95722 agkistrodon	601	6	1.5	146	16	Q9Z943	Q9Z943 chlamydia p
529	6	1.5	128	12	Q98279	Q98279 molluscum c	602	6	1.5	146	16	Q8RAL2	Q8ral2 thermoanaer
530	6	1.5	128	10	Q9YK03	Q9YK03 dengue viru	603	6	1.5	146	17	Q97XH6	Q97xn6 sulfolobus
531	6	1.5	129	10	Q93X29	Q93X29 nicotiana t	604	6	1.5	147	5	Q8SU34	Q8su34 encephalito
532	6	1.5	129	16	Q98R21	Q98r21 mycoplasma	605	6	1.5	147	17	Q9HKK9	Q9hkk9 thermoplasm
533	6	1.5	129	16	Q8YF69	Q8Yf69 brucella me	606	6	1.5	148	9	Q38345	Q38345 lactococcus
534	6	1.5	131	8	Q95733	Q95733 glycydus ha	607	6	1.5	148	12	Q11391	Q11391 rhesus papi
535	6	1.5	131	12	Q8QPN0	Q8qpn0 dengue viru	608	6	1.5	148	12	Q11394	Q11394 rhesus papi
536	6	1.5	131	12	Q8QPM9	Q8qpm9 dengue viru	609	6	1.5	148	12	Q11400	Q11400 rhesus papi
537	6	1.5	131	12	Q8QPM8	Q8qpm8 dengue viru	610	6	1.5	148	16	Q9WXR8	Q9wxr8 thermotoga
538	6	1.5	131	12	Q8QPM7	Q8qpm7 dengue viru	611	6	1.5	148	16	Q92X98	Q92x98 rhizobium m
539	6	1.5	131	12	Q8QPM6	Q8qpm6 dengue viru	612	6	1.5	149	16	Q8U7V3	Q8u7v3 agrobacteri
540	6	1.5	131	12	Q8QPM5	Q8qpm5 dengue viru	613	6	1.5	149	17	Q976D8	Q976d8 sulfolobus
541	6	1.5	131	15	Q80675	Q80675 human immun	614	6	1.5	150	9	Q94MV6	Q94mv6 bacterioph
542	6	1.5	131	15	Q80677	Q80677 human immun	615	6	1.5	150	12	Q11396	Q11396 rhesus papi
543	6	1.5	131	15	Q80679	Q80679 human immun	616	6	1.5	150	12	Q11397	Q11397 rhesus papi
544	6	1.5	131	15	Q80679	Q80679 human immun	617	6	1.5	150	12	Q11398	Q11398 rhesus papi
545	6	1.5	132	8	Q9G1Q0	Q9g1q0 arctica isl	618	6	1.5	150	16	Q98MK9	Q98mk9 rhizobium i
546	6	1.5	132	8	Q9GAB4	Q9gab4 arctica isl	619	6	1.5	150	16	Q98IT3	Q98it3 rhizobium i
547	6	1.5	132	8	Q9GAB3	Q9gab3 arctica isl	620	6	1.5	150	17	Q97B14	Q97b14 thermoplasm
548	6	1.5	132	16	Q927V7	Q927v7 listeria in	621	6	1.5	151	2	Q91475	Q91475 lactococcus
549	6	1.5	132	16	Q8Y4B5	Q8y4b5 listeria mo	622	6	1.5	151	5	Q8WQP7	Q8wqp7 anopheles g
550	6	1.5	132	16	Q50489	Q50489 streptomyce	623	6	1.5	151	10	Q9FW68	Q9fw68 oryza sativ
551	6	1.5	133	16	Q9A2K3	Q9a2k3 caulobacter	624	6	1.5	151	16	Q9CHT0	Q9cht0 lactococcus
552	6	1.5	134	2	Q47122	Q47122 escherichia	625	6	1.5	151	17	Q9HSW0	Q9hsw0 halobacteri
553	6	1.5	134	12	Q39791	Q39791 dengue viru	626	6	1.5	152	2	Q8RQP5	Q8rqp5 thermus the
554	6	1.5	134	16	Q8UGT2	Q8ugt2 agrobacteri	627	6	1.5	152	8	Q48024	Q48024 candaia asp
555	6	1.5	135	17	Q57837	Q57837 pyrococcus	628	6	1.5	152	8	Q48048	Q48048 epicrates e
556	6	1.5	136	6	Q8WMC1	Q8wmc1 bubalus bub	629	6	1.5	152	8	Q48119	Q48119 ungaliophis
557	6	1.5	137	6	Q95MP6	Q95mp6 bos taurus	630	6	1.5	152	10	Q8VXP7	Q8vxp7 cicer retic
558	6	1.5	138	16	Q8XAK9	Q8xak9 escherichia	631	6	1.5	152	16	Q9L222	Q9l222 streptomyce
559	6	1.5	138	17	Q9YBJ7	Q9ybj7 aeropyrum p	632	6	1.5	152	17	Q9YJ78	Q9y78 aeropyrum p
560	6	1.5	139	17	Q30319	Q30319 archaeoglob	633	6	1.5	152	17	Q8TUD9	Q8tud9 methanosarc
561	6	1.5	140	4	Q9PIL9	Q9p1l9 homo sapien	634	6	1.5	153	4	Q8WYZ6	Q8wyz6 homo sapien
562	6	1.5	141	10	Q98S51	Q98s51 guillardia	635	6	1.5	153	16	Q98GW3	Q98gw3 rhizobium i
563	6	1.5	141	12	Q65260	Q65260 african swi	636	6	1.5	154	2	Q93PL4	Q93pl4 pseudomonas
564	6	1.5	141	16	Q8X325	Q8x325 escherichia	637	6	1.5	154	9	Q03959	Q03959 bacterioph
565	6	1.5	141	16	Q8YC88	Q8yc88 brucella me	638	6	1.5	154	14	Q991Z6	Q991z6 uncultured
566	6	1.5	142	2	Q47124	Q47124 escherichia	639	6	1.5	155	10	Q949A8	Q949a8 oryza sativ
567	6	1.5	142	12	Q919G1	Q919g1 blueberry r	640	6	1.5	155	16	Q8YEO0	Q8ye00 brucella me
568	6	1.5	142	16	Q98BR1	Q98br1 rhizobium i	641	6	1.5	155	17	Q9YEB3	Q9yeb3 aeropyrum p
569	6	1.5	142	16	Q8YHO1	Q8yhq1 brucella me	642	6	1.5	156	2	Q9F5B0	Q9f5b0 agrobacteri
570	6	1.5	143	1	Q9C4S8	Q9c4s8 halobacteri	643	6	1.5	156	16	Q92P09	Q92p09 rhizobium m
571	6	1.5	143	2	Q9ZA97	Q9za97 streptococc	644	6	1.5	156	16	Q8XWJ5	Q8xwj5 ralstonia s
572	6	1.5	143	3	Q9U095	Q9u095 schizosacch	645	6	1.5	157	10	Q9LTT7	Q9l1t7 arabidopsis
573	6	1.5	143	9	Q03935	Q03935 bacterioph	646	6	1.5	157	16	Q9KOD0	Q9kqd0 vibrio chol
574	6	1.5	143	16	Q8Y1H3	Q8ylh3 ralstonia s	647	6	1.5	157	16	Q9HVR3	Q9hvr3 pseudomonas
575	6	1.5	143	16	Q8XV31	Q8xv31 ralstonia s	648	6	1.5	157	17	Q9YDV5	Q9ydv5 aeropyrum p
576	6	1.5	143	16	Q8RH81	Q8rh81 fusobacteri	649	6	1.5	157	17	Q8TXR0	Q8txr0 methanopyru
577	6	1.5	144	12	Q11395	Q11395 rhesus papi	650	6	1.5	158	5	Q9G0X4	Q9g0x4 plasmodium
578	6	1.5	144	16	Q9FBS3	Q9fbs3 streptomyce	651	6	1.5	158	5	Q9VK73	Q9vkr73 drosophila
579	6	1.5	145	11	Q54878	Q54878 mus musculu	652	6	1.5	158	16	Q8XZB3	Q8xzb3 ralstonia s
580	6	1.5	145	12	Q72508	Q72508 sinbis vir	653	6	1.5	159	5	Q9N717	Q9n717 leishmania
581	6	1.5	145	12	Q72509	Q72509 sinbis vir	654	6	1.5	159	10	Q23429	Q23429 arabidopsis
582	6	1.5	145	12	Q72510	Q72510 sinbis vir	655	6	1.5	159	12	Q8QP46	Q8qp46 dengue viru
583	6	1.5	145	12	Q72511	Q72511 sinbis vir	656	6	1.5	159	16	Q9CCL6	Q9cc16 mycobacteri
584	6	1.5	145	12	Q72512	Q72512 sinbis vir	657	6	1.5	159	16	Q9XAF5	Q9xat5 streptomyce
585	6	1.5	145	12	Q72513	Q72513 sinbis vir	658	6	1.5	159	16	Q92S42	Q92s42 rhizobium m
586	6	1.5	145	12	Q72514	Q72514 sinbis vir	659	6	1.5	160	16	Q92KH6	Q92kh6 rhizobium m
587	6	1.5	145	12	Q72515	Q72515 sinbis vir	660	6	1.5	161	4	Q96FH9	Q96fh9 homo sapien
588	6	1.5	145	12	Q72516	Q72516 sinbis vir	661	6	1.5	161	10	Q9FW07	Q9fw07 oryza sativ
589	6	1.5	145	12	Q93005	Q93005 sinbis vir	662	6	1.5	161	12	Q9QP59	Q9qp59 cucumber gr
590	6	1.5	145	12	Q93006	Q93006 sinbis vir	663	6	1.5	162	5	Q24353	Q24353 drosophila
591	6	1.5	145	12	Q9WBL4	Q9wb14 sinbis vir	664	6	1.5	162	16	Q98F42	Q98f42 rhizobium i
592	6	1.5	145	12	Q9W992	Q9w992 sinbis vir	665	6	1.5	162	16	Q8U682	Q8u682 agrobacteri
593	6	1.5	145	12	Q9W883	Q9w883 sinbis vir	666	6	1.5	163	5	Q9Y199	Q9y199 caenorhabdi
594	6	1.5	145	12	Q8QTH9	Q8qth9 sinbis vir	667	6	1.5	163	6	Q95MP5	Q95mps bos taurus
595	6	1.5	145	16	Q912X8	Q912x8 pseudomonas	668	6	1.5	163	12	Q9J9Z9	Q9j9z9 rana tempor
596	6	1.5	145	17	Q9HKG7	Q9hkg7 thermoplasm	669	6	1.5	163	12	Q9J9Z7	Q9j9z7 rana tempor
597	6	1.5	146	4	Q9HD48	Q9hd48 homo sapien	670	6	1.5	163	12	Q9J9Z5	Q9j9z5 bufo marinu
598	6	1.5	146	11	Q9DCY8	Q9dcy8 mus musculu	671	6	1.5	163	12	Q9J9Z3	Q9j9z3 bohle ixido
599	6	1.5	146	11	Q9JU45	Q9ju45 mus musculu	672	6	1.5	163	12	Q9J9Z1	Q9j9z1 bufo bufo u
600	6	1.5	146	16	Q8XJX6	Q8xjx6 clostridium	673	6	1.5	163	12	Q9J9Y9	Q9j9y9 bufo bufo u

674	6	1.5	163	12	Q9J9Y7	Q9j9y7 bufo bufo u	747	6	1.5	174	12	Q84937	Q84937 porcine rep
675	6	1.5	163	12	Q9J9Y5	Q9j9y5 catfish iri	748	6	1.5	174	12	Q84950	Q84950 porcine rep
676	6	1.5	163	12	Q9J9Y3	Q9j9y3 bufo marinu	749	6	1.5	174	12	Q84953	Q84953 porcine rep
677	6	1.5	163	12	Q9J9Y1	Q9j9y1 bufo marinu	750	6	1.5	174	12	Q70659	Q70659 porcine rep
678	6	1.5	163	12	Q9J9X9	Q9j9x9 doctor fish	751	6	1.5	174	12	Q70661	Q70661 porcine rep
679	6	1.5	163	12	Q9J9X7	Q9j9x7 epizootic h	752	6	1.5	174	12	Q70664	Q70664 porcine rep
680	6	1.5	163	12	Q9J9X5	Q9j9x5 frog virus	753	6	1.5	174	12	Q70667	Q70667 porcine rep
681	6	1.5	163	12	Q9J9X3	Q9j9x3 guppyfish i	754	6	1.5	174	12	Q70670	Q70670 porcine rep
682	6	1.5	163	12	Q9J9X1	Q9j9x1 leptodactyl	755	6	1.5	174	12	Q70673	Q70673 porcine rep
683	6	1.5	163	12	Q9J9W9	Q9j9w9 bufo marinu	756	6	1.5	174	12	P89041	P89041 porcine rep
684	6	1.5	163	12	Q9J9W7	Q9j9w7 bufo marinu	757	6	1.5	174	12	Q9YLS7	Q9y1s7 porcine rep
685	6	1.5	163	12	Q9J9W5	Q9j9w5 sheelfish i	758	6	1.5	174	12	Q90050	Q90050 porcine rep
686	6	1.5	163	12	Q9J9W3	Q9j9w3 tadpole ede	759	6	1.5	174	12	Q9YS65	Q9ys65 porcine rep
687	6	1.5	163	16	Q8RHA3	Q8rha3 fusobacteri	760	6	1.5	174	12	Q9E8M4	Q9e8m4 porcine rep
688	6	1.5	163	17	Q9YG32	Q9yg32 aeropyrum p	761	6	1.5	174	12	Q99BU0	Q99bu0 porcine rep
689	6	1.5	164	2	O05140	O05140 proteus mir	762	6	1.5	174	12	Q98XX0	Q98xx0 porcine rep
690	6	1.5	164	2	Q8RLV8	Q8rlv8 xenorhabdus	763	6	1.5	174	12	Q88702	Q88702 porcine rep
691	6	1.5	164	16	Q9KQV4	Q9kqu4 vibrio chol	764	6	1.5	174	12	Q9YNY2	Q9yny2 porcine rep
692	6	1.5	164	16	Q8ZGC8	Q8zgc8 yersinia pe	765	6	1.5	174	12	Q88934	Q88934 porcine rep
693	6	1.5	164	16	Q8Z815	Q8z815 salmonella	766	6	1.5	174	12	Q993U6	Q993u6 porcine rep
694	6	1.5	164	17	Q8TUQ1	Q8tjq1 methanosarc	767	6	1.5	174	12	O56259	O56259 porcine rep
695	6	1.5	165	16	Q98DG7	Q98dg7 rhizobium l	768	6	1.5	174	12	Q9WBR3	Q9wbr3 porcine rep
696	6	1.5	165	16	Q8UC24	Q8uc24 agrobacteri	769	6	1.5	174	12	O55493	O55493 porcine rep
697	6	1.5	166	16	Q9CN27	Q9cn27 pasteurella	770	6	1.5	174	12	Q9YJZ6	Q9ymz6 porcine rep
698	6	1.5	166	16	Q93J05	Q93j05 streptomyce	771	6	1.5	174	12	O57287	O57287 porcine rep
699	6	1.5	167	2	Q93G69	Q93g69 escherichia	772	6	1.5	174	12	O73563	O73563 porcine rep
700	6	1.5	167	5	O77278	O77278 drosophila	773	6	1.5	174	12	Q8QQW3	Q8qqw3 porcine rep
701	6	1.5	167	5	Q9W4I4	Q9w4i4 drosophila	774	6	1.5	174	17	Q9YJCZ9	Q9ycz9 aeropyrum p
702	6	1.5	167	16	O8XYV4	O8xyv4 ralstonia s	775	6	1.5	176	11	Q62195	Q62195 mus musculu
703	6	1.5	167	16	O8TY65	O8ty65 methanopyru	776	6	1.5	176	16	Q62195	Q62195 mus musculu
704	6	1.5	168	2	Q47123	Q47123 escherichia	777	6	1.5	177	8	Q9GB05	Q9gb05 trimeresuru
705	6	1.5	168	8	Q9GAZ8	Q9gaz8 trimeresuru	778	6	1.5	177	16	Q8XV48	Q8xv48 ralstonia s
706	6	1.5	168	10	Q9M444	Q9m444 cicer ariet	779	6	1.5	177	16	O8RAFO	O8raf0 thermoanaer
707	6	1.5	168	16	Q9RRC6	Q9rrc6 deinococcus	780	6	1.5	178	2	Q44994	Q44994 borrelia bu
708	6	1.5	169	12	Q91IT9	Q91it9 hepatitis c	781	6	1.5	178	5	O45197	O45197 caenorhabdi
709	6	1.5	169	12	Q917S7	Q917s7 hepatitis c	782	6	1.5	178	10	Q9SVD6	Q9svd6 arabidopsis
710	6	1.5	169	12	Q917S6	Q917s6 hepatitis c	783	6	1.5	178	11	Q922K0	Q922k0 mus musculu
711	6	1.5	169	12	Q917S5	Q917s5 hepatitis c	784	6	1.5	178	16	Q9RN73	Q9rn73 streptomyce
712	6	1.5	169	16	Q9RMJ6	Q9rmj6 deinococcus	785	6	1.5	179	2	Q9AKR3	Q9akr3 ralstonia m
713	6	1.5	169	16	O8X5C9	O8x5c9 escherichia	786	6	1.5	179	16	Q9RW30	Q9rw30 deinococcus
714	6	1.5	170	8	Q94XW9	Q94xw9 agkistrodon	787	6	1.5	180	5	Q20699	Q20699 caenorhabdi
715	6	1.5	170	8	Q94XW6	Q94xw6 crocalus pu	788	6	1.5	181	10	Q9SG96	Q9sg96 arabidopsis
716	6	1.5	170	10	Q9FVY3	Q9fvy3 oryza sativ	789	6	1.5	181	10	Q9LGF0	Q9lgh0 oryza sativ
717	6	1.5	170	17	Q9UX55	Q9ux55 sulfolobus	790	6	1.5	183	11	O54877	O54877 mus musculu
718	6	1.5	171	2	Q93CH4	Q93ch4 photobacter	791	6	1.5	183	12	O92291	O92291 dengue viru
719	6	1.5	171	10	Q9ZU47	Q9zu47 arabidopsis	792	6	1.5	183	12	Q9YK00	Q9yk00 dengue viru
720	6	1.5	171	10	Q9FVN9	Q9fvn9 arabidopsis	793	6	1.5	183	12	Q9YJZ9	Q9yjz9 dengue viru
721	6	1.5	171	10	Q9S1I5	Q9s1i5 arabidopsis	794	6	1.5	183	12	Q9YJZ8	Q9yjz8 dengue viru
722	6	1.5	171	12	Q9W868	Q9w868 porcine ade	795	6	1.5	183	12	Q9W9N2	Q9w9n2 dengue viru
723	6	1.5	171	12	Q91IT4	Q91it4 hepatitis c	796	6	1.5	183	12	Q9W9N2	Q9w9n2 dengue viru
724	6	1.5	171	12	Q91IT2	Q91it2 hepatitis c	797	6	1.5	183	16	Q9AK22	Q9ak22 streptomyce
725	6	1.5	171	12	Q91IS9	Q91is9 hepatitis c	798	6	1.5	183	16	Q8RH71	Q8rh71 fusobacteri
726	6	1.5	171	12	Q91IS7	Q91is7 hepatitis c	799	6	1.5	183	17	Q9YE89	Q9ye89 aeropyrum p
727	6	1.5	171	16	Q9A8J1	Q9a8j1 caulobacter	800	6	1.5	184	2	Q938D6	Q938d6 mycobacteri
728	6	1.5	171	16	Q8RBM2	Q8rbm2 thermoanaer	801	6	1.5	184	2	Q9XB54	Q9xb54 erwinia car
729	6	1.5	172	4	Q96OT0	Q96ot0 homo sapien	802	6	1.5	184	8	Q9GAX3	Q9gax3 agkistrodon
730	6	1.5	172	4	Q8WYR8	Q8wy8 homo sapien	803	6	1.5	185	4	Q9P0P2	Q9p0p2 homo sapien
731	6	1.5	172	10	O24126	O24126 nicotiana t	804	6	1.5	185	4	Q9P001	Q9p001 homo sapien
732	6	1.5	172	10	Q9SHE9	Q9she9 arabidopsis	805	6	1.5	185	4	Q9Y3R1	Q9y3r1 homo sapien
733	6	1.5	172	12	Q99D34	Q99d34 porcine rep	806	6	1.5	185	4	O9U1I4	O9u1i4 homo sapien
734	6	1.5	172	12	Q8X934	Q8x934 escherichia	807	6	1.5	185	8	Q9T6C6	Q9t6c6 ammophila s
735	6	1.5	172	17	Q96YU7	Q96yu7 sulfolobus	808	6	1.5	185	8	Q94XW3	Q94xw3 crocalus wi
736	6	1.5	173	3	Q96TV7	Q96tv7 pleurotus o	809	6	1.5	185	11	Q9CWZ0	Q9cwz0 mus musculu
737	6	1.5	173	5	Q95Y22	Q95y22 leishmania	810	6	1.5	185	11	Q9JIB0	Q9jib0 mus musculu
738	6	1.5	173	8	O8SGY5	O8sgy5 bitis nasie	811	6	1.5	186	4	Q9HD47	Q9hd47 homo sapien
739	6	1.5	173	12	O55479	O55479 porcine rep	812	6	1.5	186	8	Q9FXM4	Q9fxm4 crocalus wi
740	6	1.5	173	12	O85022	O85022 porcine rep	813	6	1.5	186	8	Q8SF21	Q8sf21 acrodipsas
741	6	1.5	173	12	Q9DY96	Q9dy96 porcine rep	814	6	1.5	186	10	Q9FRD0	Q9frd0 oryza sativ
742	6	1.5	173	16	Q913Q5	Q913q5 pseudomonas	815	6	1.5	186	10	Q9FTI8	Q9fti8 oryza sativ
743	6	1.5	174	2	Q49927	Q49927 mycobacteri	816	6	1.5	186	16	Q8YK72	Q8yk72 anabaena sp
744	6	1.5	174	12	O89452	O89452 porcine rep	817	6	1.5	186	16	O8YK72	O8yk72 anabaena sp
745	6	1.5	174	12	Q98VJ7	Q98vj7 porcine rep	818	6	1.5	187	2	Q93UY3	Q93uy3 agrobacteri
746	6	1.5	174	12	Q88707	Q88707 porcine rep	819	6	1.5	187	2	Q939U5	Q939u5 rhodovulum

820	6	1.5	187	3	013565	013565 saccharomyc	893	6	1.5	199	8	Q94S63	Q94s63 atheris squ
821	6	1.5	187	9	Q8SCJ4	Q8scj4 bacterioph	894	6	1.5	199	8	Q94RL9	Q94r19 bitis ariet
822	6	1.5	187	10	Q9FTK5	Q9ftk5 oryza sativ	895	6	1.5	199	8	Q94RL8	Q94r18 bitis ariet
823	6	1.5	188	2	Q9F5D9	Q9f5d9 agrobacteri	896	6	1.5	199	8	Q94RL4	Q94r14 bitis cornu
824	6	1.5	188	8	Q94XX0	Q94xx0 agkistrodon	897	6	1.5	199	8	Q94RL3	Q94r13 bitis gabon
825	6	1.5	188	8	Q94XW8	Q94xw8 sistrurus m	898	6	1.5	199	8	Q94RL2	Q94r12 bitis nasie
826	6	1.5	188	8	Q94XW7	Q94xw7 sistrurus r	899	6	1.5	199	8	Q94RL0	Q94r10 bitis rhino
827	6	1.5	188	8	Q94XW5	Q94xw5 crocotalus ce	900	6	1.5	199	8	Q94RK9	Q94rk9 bitis worth
828	6	1.5	188	8	Q94XW1	Q94xw1 crocotalus to	901	6	1.5	199	8	Q94RK8	Q94rk8 cerastes ce
829	6	1.5	188	10	Q9SJW5	Q9sjw5 arabidopsis	902	6	1.5	199	8	Q94RK7	Q94rk7 cerastes ce
830	6	1.5	188	11	Q9CRA1	Q9cra1 mus musculu	903	6	1.5	199	8	Q94RH8	Q94rh8 daboia russ
831	6	1.5	189	2	Q8VVE6	Q8vve6 salmonella	904	6	1.5	199	8	Q94RH5	Q94rh5 eristicophi
832	6	1.5	189	10	Q65060	Q65060 picea maria	905	6	1.5	199	8	Q94RD7	Q94rd7 macrovipera
833	6	1.5	189	11	Q9WUP0	Q9wup0 mus musculu	906	6	1.5	199	8	Q94RC9	Q94rc9 pseudoceras
834	6	1.5	190	8	Q9T2U6	Q9t2u6 sus scrofa	907	6	1.5	199	8	Q94RC1	Q94rc1 pseudoceras
835	6	1.5	190	11	Q9EQY7	Q9eqy7 mus musculu	908	6	1.5	199	8	Q94R66	Q94r66 vipera ammo
836	6	1.5	190	16	Q8Y0A0	Q8y0a0 ralstonia s	909	6	1.5	199	8	Q94R62	Q94r62 vipera beru
837	6	1.5	191	5	Q9U9S6	Q9u9s6 drosophila	910	6	1.5	199	8	Q94R61	Q94r61 vipera niko
838	6	1.5	191	5	Q9U9S5	Q9u9s5 drosophila	911	6	1.5	199	8	Q94R60	Q94r60 vipera pala
839	6	1.5	191	5	Q9U9S4	Q9u9s4 drosophila	912	6	1.5	199	8	Q94R58	Q94r58 vipera seoa
840	6	1.5	191	5	Q9U9S3	Q9u9s3 drosophila	913	6	1.5	199	8	Q94P05	Q94p05 vipera beru
841	6	1.5	191	8	Q9GB06	Q9gb06 trimeresuru	914	6	1.5	199	12	Q65970	Q65970 cucumber ye
842	6	1.5	191	11	Q9D814	Q9d814 mus musculu	915	6	1.5	199	12	Q91Q51	Q91q51 influenzavi
843	6	1.5	192	11	Q9D5M7	Q9d5m7 mus musculu	916	6	1.5	199	12	Q91Q50	Q91q50 influenzavi
844	6	1.5	192	12	Q81420	Q81420 hepatitis c	917	6	1.5	199	12	Q9Q217	Q9q217 influenzavi
845	6	1.5	192	16	Q98E25	Q98e25 rhizobium l	918	6	1.5	199	12	Q9Q2P4	Q9q2p4 influenzavi
846	6	1.5	194	8	Q9GB02	Q9gb02 trimeresuru	919	6	1.5	199	12	Q9Q205	Q9q205 influenzavi
847	6	1.5	194	11	Q9CZK8	Q9czk8 mus musculu	920	6	1.5	199	12	Q9Q203	Q9q203 influenzavi
848	6	1.5	194	12	P89529	P89529 chickpea st	921	6	1.5	199	12	Q9Q201	Q9q201 influenzavi
849	6	1.5	195	2	Q9ZIW7	Q9ziw7 streptomyce	922	6	1.5	199	12	Q9Q1Z9	Q9q1z9 influenzavi
850	6	1.5	195	12	P89530	P89530 beet wester	923	6	1.5	199	12	Q9Q1Z7	Q9q1z7 influenzavi
851	6	1.5	195	16	O50932	O50932 borrelia bu	924	6	1.5	199	12	Q9Q1Z5	Q9q1z5 influenzavi
852	6	1.5	195	16	Q97KX0	Q97kx0 clostridium	925	6	1.5	199	12	Q9Q1Z3	Q9q1z3 influenzavi
853	6	1.5	195	16	Q8XSR5	Q8xsr5 ralstonia s	926	6	1.5	199	12	Q9Q1Z1	Q9q1z1 influenzavi
854	6	1.5	195	17	Q8THU5	Q8thus methanosarc	927	6	1.5	199	12	Q9Q1Y9	Q9q1y9 influenzavi
855	6	1.5	196	2	O50257	O50257 desulfovibr	928	6	1.5	199	12	Q9Q1Y7	Q9q1y7 influenzavi
856	6	1.5	196	5	Q23205	Q23205 caenorhabdi	929	6	1.5	199	12	Q8QZT1	Q8qzt1 influenzavi
857	6	1.5	196	11	Q9D599	Q9d599 mus musculu	930	6	1.5	199	12	Q8QZT0	Q8qzt0 influenzavi
858	6	1.5	196	16	Q9PKH0	Q9pkh0 chlamydia m	931	6	1.5	199	12	Q8QZH9	Q8qzh9 influenzavi
859	6	1.5	196	16	Q9LIU0	Q9liu0 streptomyce	932	6	1.5	199	12	Q8QZH8	Q8qzh8 influenzavi
860	6	1.5	197	4	Q9NUP9	Q9nup9 homo sapien	933	6	1.5	199	12	Q8QZH7	Q8qzh7 influenzavi
861	6	1.5	197	8	O48035	O48035 coralus ca	934	6	1.5	199	12	Q8QZH6	Q8qzh6 influenzavi
862	6	1.5	197	11	Q91WY7	Q91wy7 rattus norv	935	6	1.5	199	12	Q8QZH5	Q8qzh5 influenzavi
863	6	1.5	197	11	O88952	O88952 mus musculu	936	6	1.5	199	12	Q8QZH4	Q8qzh4 influenzavi
864	6	1.5	197	12	Q65880	Q65880 barley yell	937	6	1.5	199	12	Q8QZH3	Q8qzh3 influenzavi
865	6	1.5	197	17	Q9HIL9	Q9hil9 thermoplasm	938	6	1.5	199	12	Q8QZH2	Q8qzh2 influenzavi
866	6	1.5	198	2	Q9FBA2	Q9fba2 chroococcid	939	6	1.5	199	12	Q8QZH1	Q8qzh1 influenzavi
867	6	1.5	198	2	Q9FBA1	Q9fba1 scytonema s	940	6	1.5	199	12	Q8QZH0	Q8qzh0 influenzavi
868	6	1.5	198	2	Q9FBA0	Q9fba0 xenococcus	941	6	1.5	199	12	Q8QZG9	Q8qzg9 influenzavi
869	6	1.5	198	2	Q9FB96	Q9fb96 geitlerinem	942	6	1.5	199	12	Q8QZG8	Q8qzg8 influenzavi
870	6	1.5	198	2	Q9FB73	Q9fb73 nostoc musc	943	6	1.5	199	12	Q8QZG7	Q8qzg7 influenzavi
871	6	1.5	198	2	Q9FB72	Q9fb72 caloithrix p	944	6	1.5	199	12	Q8QZG6	Q8qzg6 influenzavi
872	6	1.5	198	2	Q9F8S4	Q9f8s4 gloeobacter	945	6	1.5	199	12	Q8QZG5	Q8qzg5 influenzavi
873	6	1.5	198	8	Q9GAY3	Q9gay3 trimeresuru	946	6	1.5	199	12	Q8QZG4	Q8qzg4 influenzavi
874	6	1.5	198	16	Q8XIF4	Q8xif4 clostridium	947	6	1.5	199	12	Q8QZG3	Q8qzg3 influenzavi
875	6	1.5	199	8	Q9MDT4	Q9mdt4 elaphe dion	948	6	1.5	199	12	Q8QZG2	Q8qzg2 influenzavi
876	6	1.5	199	8	Q9MEC0	Q9mec0 elaphe quat	949	6	1.5	199	12	Q8QZG1	Q8qzg1 influenzavi
877	6	1.5	199	8	Q9B1Z9	Q9b1z9 macrovipera	950	6	1.5	199	16	Q9CFI9	Q9cfi9 lactococcus
878	6	1.5	199	8	Q9MJL0	Q9mj10 elaphe hohe	951	6	1.5	199	16	Q97P31	Q97p31 streptococc
879	6	1.5	199	8	Q9MJK9	Q9mj19 elaphe long	952	6	1.5	200	6	Q9BF54	Q9bf54 pteropus gi
880	6	1.5	199	8	Q9MJK8	Q9mj18 elaphe long	953	6	1.5	200	10	Q9M3U2	Q9m3u2 cucumis sat
881	6	1.5	199	8	Q9MJK7	Q9mj17 elaphe pers	954	6	1.5	200	16	Q9KYP9	Q9kyp9 streptomyce
882	6	1.5	199	8	Q9MJK6	Q9mj16 elaphe line	955	6	1.5	201	5	Q9BLP5	Q9blp5 osterlagia
883	6	1.5	199	8	Q9MJK3	Q9mj13 elaphe quat	956	6	1.5	201	8	Q9GAW9	Q9gaw9 trimeresuru
884	6	1.5	199	8	Q9MJK2	Q9mj12 elaphe quat	957	6	1.5	202	8	Q9GAZ4	Q9gaz4 trimeresuru
885	6	1.5	199	8	Q9MJK1	Q9mj11 elaphe quat	958	6	1.5	202	9	Q9MBW1	Q9mbw1 bacterioph
886	6	1.5	199	8	Q9MJK0	Q9mj10 elaphe situ	959	6	1.5	202	12	Q65841	Q65841 beet wester
887	6	1.5	199	8	Q9MJJ9	Q9mj19 elaphe porp	960	6	1.5	202	12	Q65842	Q65842 beet wester
888	6	1.5	199	8	Q94YA2	Q94yaz adenorhinos	961	6	1.5	202	12	Q65837	Q65837 beet wester
889	6	1.5	199	8	Q94Y97	Q94y97 atheris cer	962	6	1.5	202	12	Q65838	Q65838 beet wester
890	6	1.5	199	8	Q94Y96	Q94y96 atheris chl	963	6	1.5	202	12	Q65839	Q65839 beet wester
891	6	1.5	199	8	Q94TJ7	Q94tj7 atheris his	964	6	1.5	202	12	Q65840	Q65840 beet wester
892	6	1.5	199	8	Q94TJ6	Q94tj6 atheris nit	965	6	1.5	202	12	Q65830	Q65830 beet wester

966	6	1.5	202	12	Q65832	Q65832	beet wester
967	6	1.5	202	12	Q65833	Q65833	beet wester
968	6	1.5	202	12	Q65834	Q65834	beet wester
969	6	1.5	202	12	Q91AV9	Q91AV9	beet chloro
970	6	1.5	202	12	Q91AV5	Q91AV5	beet chloro
971	6	1.5	202	12	Q8V9R7	Q8V9R7	beet wester
972	6	1.5	202	12	Q89780	Q89780	beet wester
973	6	1.5	202	12	Q89798	Q89798	beet wester
974	6	1.5	202	16	Q8UCQ4	Q8UCQ4	agrobacteri
975	6	1.5	202	17	Q9YD86	Q9YD86	aeropyrum p
976	6	1.5	203	8	Q9GAX1	Q9GAX1	trimeresuru
977	6	1.5	203	10	Q9AYR8	Q9AYR8	cucumis sat
978	6	1.5	203	16	Q92S96	Q92S96	rhizobium m
979	6	1.5	204	11	Q9JIM3	Q9JIM3	rattus norv
980	6	1.5	204	12	Q83099	Q83099	latino viru
981	6	1.5	204	12	Q9YQY6	Q9YQY6	randid herpe
982	6	1.5	205	2	Q44152	Q44152	acetobacter
983	6	1.5	205	8	Q9GB04	Q9GB04	trimeresuru
984	6	1.5	205	11	Q8VIB5	Q8VIB5	mus musculu
985	6	1.5	205	16	Q981H8	Q981H8	rhizobium l
986	6	1.5	205	16	Q8ZKZ9	Q8ZKZ9	salmonella
987	6	1.5	205	16	Q8XE58	Q8XE58	escherichia
988	6	1.5	205	16	Q8XG06	Q8XG06	salmonella
989	6	1.5	206	10	Q9SWT7	Q9SWT7	hordeum vul
990	6	1.5	206	10	Q9STH2	Q9STH2	arabidopsis
991	6	1.5	206	11	Q99PR6	Q99PR6	cavia porce
992	6	1.5	206	16	Q98N56	Q98N56	rhizobium l
993	6	1.5	206	16	Q99W14	Q99W14	staphylococ
994	6	1.5	206	16	Q8ZLY8	Q8ZLY8	salmonella
995	6	1.5	206	16	Q8Z3N3	Q8Z3N3	salmonella
996	6	1.5	206	17	Q973M7	Q973M7	sulfolobus
997	6	1.5	207	4	Q9HAP6	Q9HAP6	homo sapien
998	6	1.5	207	11	Q88951	Q88951	mus musculu
999	6	1.5	207	11	Q9Z252	Q9Z252	rattus norv
1000	6	1.5	207	16	Q9K5S8	Q9K5S8	bacillus ha

ALIGNMENTS

RESULT 1
ID Q9H2V8 PRELIMINARY; PRT; 439 AA.
AC Q9H2V8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CDA13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PHEOCHROMOCYTOMA;
RA li Y., Huang Q., Peng, Y, Song H., Yu Y., Xu S., Ren S., Chen Z.,
Han Z.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212252; AAG41783.1; -.
DR HSSP; P00797; 2REN.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 439 AA; 48275 MW; 02EC0E0E50F11602 CRC64;

Query Match 95.8%; Score 389; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 MVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTPHPSYIDTYFDTERSSSTR 77
|||||

Db	1	MVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTPHPSYIDTYFDTERSSSTR	60
QY	78	SKGFDVTVKYTGSGWTGFGEDLVTPKGFNTSFLVNIAITIFESENFFLPKIKNGILGL	137
Db	61	SKGFDVTVKYTGSGWTGFGEDLVTPKGFNTSFLVNIAITIFESENFFLPKIKNGILGL	120
QY	138	AAATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGSGTNGSLVLGGIEPSLY	197
Db	121	AAATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGSGTNGSLVLGGIEPSLY	180
QY	198	KGDIMWTPKKEWYQIEILKLEIGQSLNLDREYNADKAIVDSGTTLLRLPKYEDAV	257
Db	181	KGDIMWTPKKEWYQIEILKLEIGQSLNLDREYNADKAIVDSGTTLLRLPKYEDAV	240
QY	258	VEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISYLRDENSRSFRITLLPOL	317
Db	241	VEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISYLRDENSRSFRITLLPOL	300
QY	318	YIDPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIFDRAQKRVGFAASPCAETAGA	377
Db	301	YIDPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIFDRAQKRVGFAASPCAETAGA	360
QY	378	AVSEISGFSTEDVASNCVPAQSLSEPIL 406	
Db	361	AVSEISGFSTEDVASNCVPAQSLSEPIL 389	

RESULT 2
ID Q9NZL1 PRELIMINARY; PRT; 396 AA.
AC Q9NZL1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de la Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL CytoGenet. Cell Genet. 89:177-184(2000).
DR EMBL; AF188277; AAF35836.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 2.
KW Protease.
SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match 77.8%; Score 316; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTP 60
|||||
Db 63 ALPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPKQLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTRSKGFDVTVKYTGSGWTGFGEDLVTPKGFNTSFLVNIAITFE 120
|||||
Db 123 HSYIDTYFDTERSSSTRSKGFDVTVKYTGSGWTGFGEDLVTPKGFNTSFLVNIAITFE 182
QY 121 SENFFLPKIKNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGS 180
|||||
Db 183 SENFFLPKIKNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGS 242

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QY 181 GTNGGSLVLGGIEPSLYKGDITWTPRIKEEMWYQIETLKLEIGGSLNLDCREYNADKAIY 240
    |||||||
Db 243 GTNGGSLVLGGIEPSLYKGDITWTPRIKEEMWYQIETLKLEIGGSLNLDCREYNADKAIY 302
QY 241 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIYL 300
    |||||||
Db 303 DSGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIYL 362
QY 301 RDENSSRSFRITILPQ 316
    |||||||
Db 363 RDENSSRSFRITILPQ 378

RESULT 3
Q9NZL2 PRELIMINARY; PRT; 468 AA.
ID Q9NZL2;
AC Q9NZL2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Aspartyl protease.
BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxID=9606;
[1]
RN R1
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de la Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RL Alzheimer's amyloid precursor protein beta-secretase.";
DR Cyogenet. Cell Genet. 89:177-184(2000).
DR EMBL; AF188276; AAF35835.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

Query Match 65.5%; Score 266; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 2.9e-268;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKQILVDGTSSNFAVAGTP 60
    |||||||
Db 63 ALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKQILVDGTSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTRSKGPDVTYKTYQGSWTFGVGEDLVITIPKGFNTSFLVNIAITFE 120
    |||||||
Db 123 HSYIDTYFDTERSSSTRSKGPDVTYKTYQGSWTFGVGEDLVITIPKGFNTSFLVNIAITFE 182
QY 121 SENFPLPGIKWNGILGLAVATLAKPSSSLETFFDSLVTQANIPNVFSMQMGAGLPVAGS 180
    |||||||
Db 183 SENFPLPGIKWNGILGLAVATLAKPSSSLETFFDSLVTQANIPNVFSMQMGAGLPVAGS 242
QY 181 GTNGGSLVLGGIEPSLYKGDITWTPRIKEEMWYQIETLKLEIGGSLNLDCREYNADKAIY 240
    |||||||
Db 243 GTNGGSLVLGGIEPSLYKGDITWTPRIKEEMWYQIETLKLEIGGSLNLDCREYNADKAIY 302
QY 241 DSGTTLRLPQKVFDAVEAVARASL 266
    |||||||
Db 303 DSGTTLRLPQKVFDAVEAVARASL 328

RESULT 4
Q9JUL18 PRELIMINARY; PRT; 514 AA.
ID Q9JUL18

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AC Q9JL18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease 1.
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi D.K., Sugano S., Sakaki Y.;
RT "Molecular characterization of the mouse Asp1 gene, a homolog of the
RT human ASP1 (Down Syndrome Region aspartyl protease).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216310; AAF36599.1; -.
DR HSSP; P32329; 1YPS.
DR MEROPS; A01.041; -.
DR MGD; MGI:1860440; Bace2.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 514 AA; 55799 MW; A70725F2C1DF5B47 CRC64;

Query Match
Best Local Similarity 14.5%; Score 59; DB 11; Length 514;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 FSMQMGAGLPVAGSGTNGSLVLGIEPSLYKGDWYTPIKEEWWYQIEILKLEIGGQ 224
Db 224 FSMQMGAGLPVAGSGTNGSLVLGIEPSLYKGDWYTPIKEEWWYQIEILKLEIGGQ 282

RESULT 5
Q9R1P7
ID Q9R1P7 PRELIMINARY; PRT; 255 AA.
AC Q9R1P7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease (Fragment).
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Accorino M., Fumagalli P., Taramelli R., Ottolenghi S.;
RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
RT transmembrane protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051150; AAD45964.1; -.
DR MEROPS; A01.041; -.
DR MGD; MGI:1860440; Bace2.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
KW Protease.
FT NON TER 1 1
SQ SEQUENCE 255 AA; 28685 MW; 53DE317815996D63 CRC64;

Query Match
Best Local Similarity 9.4%; Score 38; DB 11; Length 255;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 INLDGREYNADKAIYDSGTTLLRLPKQVFDVAVEAVAR 263

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Db 25 INLDCREYNADKAIVDGTTLLRLPQKVPDAVVEAVAR 62

RESULT 6

Q9BYB9 PRELIMINARY; PRT; 432 AA.
AC Q9BYB9;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-432.
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
RT production.";
RT Neurosci. Lett. 307:9-12(2001).
RL EMBL; AB050438; BAB40933.1; -.
DR HSSP; P32329; 1YPS.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 432 AA; 48212 MW; 96FC81E6F0EED01B CRC64;

Query Match

Best Local Similarity 3.0%; Score 12; DB 4; Length 432;
Matches 12; Conservativity 100.0%; Pred. No. 0.0017;
Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56

Db 90 ILVDTGSSNFAV 101

RESULT 7

Q9BYC0 PRELIMINARY; PRT; 457 AA.
AC Q9BYC0;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-457 (Beta-site APP cleaving enzyme
DE type C).
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
RT production.";
RT Neurosci. Lett. 307:9-12(2001).
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=EXOCRINE PANCREAS;
RA Zaccchetti D., De Pietri Tonelli D., Schnurbus R.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1c) obtained from
RT human pancreas.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB050437; BAB40932.1; -.
DR EMBL; AF338817; AAK38375.1; -.
DR HSSP; P32329; 1YPS.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 457 AA; 51068 MW; C794C9A9E85FE7A2 CRC64;

Query Match

Best Local Similarity 3.0%; Score 12; DB 4; Length 457;
Matches 12; Conservativity 100.0%; Pred. No. 0.0017;
Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56

Db 90 ILVDTGSSNFAV 101

RESULT 8

Q9BYC1 PRELIMINARY; PRT; 476 AA.
AC Q9BYC1;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-476.
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
RT production.";
RT Neurosci. Lett. 307:9-12(2001).
RL EMBL; AB050436; BAB40931.1; -.
DR HSSP; P32329; 1YPS.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 476 AA; 52907 MW; 6C8C87F8A953AF66 CRC64;

Query Match

Best Local Similarity 3.0%; Score 12; DB 4; Length 476;
Matches 12; Conservativity 100.0%; Pred. No. 0.0018;
Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56

Db 90 ILVDTGSSNFAV 101

RESULT 9

Q9ULS1 PRELIMINARY; PRT; 532 AA.
AC Q9ULS1;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-OCT-2001 (TRENBLREL. 18, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE KIAA1149 protein (Fragment).
GN KIAA1149.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirose M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
DR EMBL; AB032975; BAA86463.2; -
DR HSSP; P56272; 1AM5.
DR MEROPS; A01.004; -
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;

Query Match 3.0%; Score 12; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
Db 121 ILVDTGSSNFAV 132
|||||

RESULT 10
Q9P0D2 PRELIMINARY; PRT; 213 AA.
ID Q9P0D2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE HSPC104 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORD BLOOD;
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161367; AAF28927.1; -
DR InterPro; IPR001461; AspproteaseA1.
DR Pfam; PF00026; asp; 1.
FT NON_TER 1
SQ SEQUENCE 213 AA; 24338 MW; EC9D3FA31CFA835C CRC64;

Query Match 2.2%; Score 9; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 SFRITILPQ 316
Db 119 SFRITILPQ 127
|||||

RESULT 11
Q9CUT5 PRELIMINARY; PRT; 266 AA.
ID Q9CUT5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme (Fragment).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014390; BAB29317.1; -
DR MEROPS; A01.004; -
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; AspproteaseA1.
DR Pfam; PF00026; asp; 1.
FT NON_TER 1
SQ SEQUENCE 266 AA; 30201 MW; B913FDA8ADAB4238 CRC64;

Query Match 2.2%; Score 9; DB 11; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 SFRITILPQ 316
Db 121 SFRITILPQ 129
|||||

RESULT 12
Q9M8Y6 PRELIMINARY; PRT; 96 AA.
ID Q9M8Y6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T6K12.8 protein.
GN T6K12.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Ronning C.M., Koo H., Fujii C.Y., Uteback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC T6K12 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC016829; AAF26784.1; -
SQ SEQUENCE 96 AA; 10847 MW; DCD06BE55060EDA2 CRC64;

Query Match 2.0%; Score 8; DB 10; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 DLVTIPKG 106
|||||

Db 66 DLVTIPKG 73

RESULT 13

O9CP14 PRELIMINARY; PRT; 159 AA.
ID O9CP14
AC O9CP14;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Lrp.
GN Lrp OR PM0254.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
REGULATORS.
CC EMBL; AE006060; AAK02338.1; -.
DR InterPro; IPR000485; ASNC_trans_reg.
DR Pfam; PF01037; ASNC_trans_reg; 1.
DR PRINTS; PR00033; HTHASNC.
DR SMART; SM00344; HTH_ASNC; 1.
DR PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 159 AA; 18085 MW; 45A5F6E4CC7F874D CRC64;

Query Match

2.0%; Score 8; DB 16; Length 159;

Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 GTTLRLP 250

Db 129 GTTLRLP 136

RESULT 14

O9LOR0 PRELIMINARY; PRT; 241 AA.
ID O9LOR0
AC O9LOR0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative lipoprotein.
GN SCO4231 OR SCDBA.04C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Krieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).

[4]

RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Krieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Krieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL160331; CAB77325.1; -.
DR InterPro; IPR000531; TonB_boxC.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Lipoprotein.
SQ SEQUENCE 241 AA; 23517 MW; C42774C407869AB5 CRC64;

Query Match

2.0%; Score 8; DB 16; Length 241;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 GGSIVLGG 191

Db 112 GGSIVLGG 119

RESULT 15

O8WOY9 PRELIMINARY; PRT; 244 AA.
ID O8WOY9
AC O8WOY9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Aspartate protease (Fragment).
GN APP.
OS Aphrocalistes vastus.
OC Eukaryota; Metazoa; Porifera; Hexactinellida; Hexasterophora;
OC Lyssacinosida; Rossellidae; Aphrocalistes.
OX NCBI_TaxID=83887;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller W.E.G., Mueller I.M., Grebenjuk V.A.;
RT "Urmetazoa: Origin and evolution of the common ancestor of Metazoa.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ304863; CAC83293.1; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR InterPro; IPR000005; HTHAraC.
DR Pfam; PF00026; asp; 1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW Protease.
FT NON TER
SQ SEQUENCE 244 AA; 26366 MW; 6536902661E0E4C7 CRC64;

Query Match

2.0%; Score 8; DB 5; Length 244;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GGSNFAVA 57

Db 53 GGSNFAVA 60

Search completed: April 1, 2003, 11:53:26
Job time : 107 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:21:58 ; Search time 39 Seconds
(without alignments)
1769.842 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALRALLLPLLAQWLIRA.....RPRDPEVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2687	100.0	518	AAW61362	Aspartic proteinase
2	2687	100.0	518	AAAY41714	Human PRO852 prote
3	2687	100.0	518	AAAY22239	Human CSP56, aspar
4	2687	100.0	518	AAAY13799	Human aspartyl pro
5	2687	100.0	518	AAAB44270	Human PRO852 (UNO4
6	2687	100.0	518	AAAY88424	Human aspartyl pro
7	2687	100.0	518	AAE10628	Human aspartyl pro
8	2687	100.0	518	AAE10656	Human-Asp 1 protei
9	2687	100.0	518	AAU29059	Human PRO polypept
10	2687	100.0	518	AAE06858	Human aspartyl pro

11	2687	100.0	518	22	AAU06602	Human Aspartyl pro
12	2687	100.0	518	22	AAU07201	Human aspartyl pro
13	2687	100.0	518	22	AAE02580	Human aspartyl pro
14	2687	100.0	518	22	AAE02608	Human Aspartyl pro
15	2687	100.0	518	23	ABB78589	Human Asp-1 protei
16	2687	100.0	518	23	ABB78617	Human Asp-1delatM
17	2687	100.0	518	23	ABB06531	Human aspartyl pro
18	2687	100.0	518	23	ABB07453	Human BACE2 amino
19	2506	93.3	481	22	AAE07592	Human COLON cancer
20	2437	90.7	475	22	AAE10657	Secreted recombina
21	2437	90.7	475	22	AAE02609	Human secreted asp
22	2437	90.7	475	23	ABB78618	Secreted recombina
23	2395	89.1	514	22	AAE04204	Amino acid sequenc
24	2293	85.3	439	23	ABB90365	Human polypeptide
25	2207	82.1	423	22	AAE04796	Human aspartyl pro
26	2184	81.3	423	22	AAE08479	Human membrane or
27	2124	79.0	413	22	AAE10658	Acid-processed hu-
28	2124	79.0	413	22	AAE02610	Human acid-process
29	2124	79.0	413	23	ABB78619	Asp-1delatM(his)6
30	1794	66.8	355	22	AAE03925	Human protein sequ
31	1187	44.2	501	21	AAE04769	Rat beta-secretase
32	1186.5	44.2	501	22	AAE04948	Mouse aspartic sec
33	1185	44.1	501	21	AAE04768	Murine beta-secret
34	1185	44.1	501	21	AAE08427	Murine aspartyl pr
35	1185	44.1	501	22	AAE10631	Murine aspartyl pr
36	1185	44.1	501	22	AAE06861	Murine aspartyl pr
37	1185	44.1	501	22	AAU06605	Mouse Aspartyl pro
38	1185	44.1	501	22	AAU07204	Mouse aspartyl pro
39	1185	44.1	501	22	AAE02583	Murine aspartyl pr
40	1185	44.1	501	23	ABB78592	Mouse Asp-2(a) pro
41	1178.5	43.9	501	21	AAE04767	Human beta-secreta
42	1178.5	43.9	501	21	AAE07896	Amino acid sequenc
43	1178.5	43.9	509	23	AAE02697	FLAG-tagged human
44	1175	43.7	488	22	AAE06572	Human memapsin 2.
45	1175	43.7	488	22	AAE01334	Memapsin 2 protein

ALIGNMENTS

AAW61362	AAW61362 standard; Protein; 518 AA.
XX	AAW61362;
AC	25-SEP-1998 (first entry)
XX	Aspartic proteinase ASP1.
DT	ASPL; Aspartic proteinase; Alzheimer's disease; cancer; melanoma.
XX	Homo sapiens.
OS	EP848062-A2.
XX	17-JUN-1998.
PN	01-DEC-1997; 97EP-0309648.
XX	14-DEC-1996; 96GB-0026022.
PR	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM PLC.
XX	Chapman CG, Evans JR, Powell DJ, Southan C;
PI	WPI; 1998-314477/28.
XX	N-PSDB; AAV27962.
DR	New isolated polynucleotide encodes Aspartic protease polypeptide -
XX	used to diagnosis, treat and vaccinate against Alzheimer's disease,
PT	Cancer and melanoma
PT	

6.98 published

Powell

100%

XX Claim 11; Page 7; 19pp; English.
PS
XX The human ASP1 protein is structurally related to other proteins of the
CC Aspartic proteinase family. ASP 1 polypeptides and polynucleotides can
CC be used to diagnosis, treat and vaccinate against Alzheimer's disease,
CC cancer and melanoma.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 19; Length 518;
Best local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALAPALLPLLAQWLLRAPELAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
Db 1 MGALAPALLPLLAQWLLRAPELAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
QY 61 ALALPAPALASPAGANFLAMVDNLQDGRGYLLEMLIGTPPOKQILVDTGSSNFAVAG 120
Db 61 ALALPAPALASPAGANFLAMVDNLQDGRGYLLEMLIGTPPOKQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSTYRSKGFDTVYKYGSGWTGFGVEDLVTPKGFTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSTYRSKGFDTVYKYGSGWTGFGVEDLVTPKGFTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAVATLAKRSSLETFFDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAVATLAKRSSLETFFDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVEAVARASLPEFSDGFWTGSOLACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVFDAVEAVARASLPEFSDGFWTGSOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYVIFD 420
QY 421 RAOKRVGFASPCAEIAGAASEISGPFSTEDVANSNCVPAQSLSEPIIMIVSYALMSVCG 480
Db 421 RAOKRVGFASPCAEIAGAASEISGPFSTEDVANSNCVPAQSLSEPIIMIVSYALMSVCG 480
QY 481 AILLVILVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
Db 481 AILLVILVLLLPFCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 2
ID AAY41714 standard; Protein; 518 AA.
XX AAY41714;
AC AAY41714;
DT 07-DEC-1999 (first entry)
XX
DE Human PRO852 protein sequence.
XX

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.

XX Homo sapiens.
XX OS
XX WO9946281-A2.
XX PN
XX 16-SEP-1999.
XX PD
XX 08-MAR-1999; 99WO-US05028.
XX PF
XX

PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.

3.98

5.98

PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.

XX (GETH) GENENTECH INC.

PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI; 1999-551358/46.

DR N-PSDB; AAZ34056.

XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -

PS Claim 12; Fig 73; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.

XX Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
OY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKQILVDTGSSNFAVAG 120
OY 121 TPHSYIDTYFDTERSSSTRKSGFDVTVKYTOGSGWTGFVGEDLVTTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSSTRKSGFDVTVKYTOGSGWTGFVGEDLVTTIPKGFNTSFLVNIATI 180
OY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFPDSLVTQANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFPDSLVTQANIPNVFSMOMCGAGLPVA 240
OY 241 GSGTNGSLVGLGIEPSLYKGDIMWYPIKEWYQIEIKLEIGGQSLNLDCREYNADKA 300
DB 241 GSGTNGSLVGLGIEPSLYKGDIMWYPIKEWYQIEIKLEIGGQSLNLDCREYNADKA 300
OY 301 IVDSGTTLRLPQKVFDAVVAARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLRLPQKVFDAVVAARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKISI 360
OY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYIIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYIIFD 420

DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYIIFD 420
OY 421 PAQKRVGFAPSPCAEIAAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
DB 421 PAQKRVGFAPSPCAEIAAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
OY 481 ALLVLIVLLLPPRCQRRPRDPEVNDDESSLVRHRWK 518
DB 481 ALLVLIVLLLPPRCQRRPRDPEVNDDESSLVRHRWK 518

RESULT 3

AAY22239 AAY22239 standard; Protein; 518 AA.

XX AAY22239;

DT 20-SEP-1999 (first entry)

XX Human CSP56, aspartyl-type protease, protein sequence.

XX Metastatic marker protein; human; cancer metastasis; breast cancer;

KW colon cancer; diagnosis; therapy; tumour; metastatic potential;

XX CSP56; aspartyl-type protease.

OS Homo sapiens.

XX WO934004-A2.

XX 08-JUL-1999.

XX 24-DEC-1998; 98WO-US27608.

XX 31-DEC-1997; 97US-0070112.

XX (CHIR) CHIRON CORP.

PI Giese K, Xin H;

XX WPI; 1999-430248/36.

DR N-PSDB; AAX84708.

XX New polynucleotides associated with cancer metastasis

XX Claim 4; Page 78-80; 80pp; English.

CC This sequence represents a polypeptide of the invention, and is
CC an aspartyl-type protease, designated CSP56. The polynucleotides (PNS) of
CC the invention encode metastatic marker protein variants. The PNS and
CC polypeptides can be used as markers for cancer metastasis. The products
CC can be used for identifying metastatic tissue or metastatic potential of
CC a tissue, e.g. breast or colon tissue. They can also be used for
CC screening test compounds for the ability to suppress the metastatic
CC potential of a tumour. The products can be used for developing products
CC for the therapy of cancers, particularly breast or colon cancer.

XX Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
OY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKQILVDTGSSNFAVAG 120
OY 121 TPHSYIDTYFDTERSSSTRKSGFDVTVKYTOGSGWTGFVGEDLVTTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSSTRKSGFDVTVKYTOGSGWTGFVGEDLVTTIPKGFNTSFLVNIATI 180

QY 181 FESENFLLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTQANI PNVFSMOMCGAGLPVA 240
|||||
Db 181 FESENFLLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTQANI PNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
|||||
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQQLACWTNSETPWSYFPKISI 360
|||||
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQQLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
|||||
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
|||||
Db 421 RAQKRVGFPAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
|||||
Db 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 4

AAV13799
ID AAV13799 standard; Protein; 518 AA.

XX AAV13799;

DT 21-SEP-1999 (first entry)

DE Human aspartyl protease, CSP56.

KM CSP56; human; aspartyl protease; diagnosis; neoplasia; tumour;

KW breast tumour; colon tumour.

OS Homo sapiens.

PN WO9933963-A1.

PD 08-JUL-1999.

PF 14-DEC-1998; 98WO-US26547.

PR 31-DEC-1997; 97US-0070112.

PA (CHIR) CHIRON CORP.

PI Giese KW, Xin H;

DR WPI; 1999-430240/36.

DR N-PSDB; AAX89297.

PT Human CSP56 protein for diagnosis of neoplasia

PS Claim 2; Fig 2A; 51pp; English.

CC This represents a human CSP56 protein, a novel aspartyl protease. The
CC CSP56 protein can be used in methods for diagnosing neoplasia, for
CC determining the metastatic potential of a tumour, and for screening test
CC compounds for the ability to suppress the metastatic potential of a
CC tumour. The tumours are preferably from breast or colon.

SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAPELAPAPFTTLRVAATAATNRVVAFTPGDTPAERHADGL 60

Db 1 MGALARALLPLLAQWLLRAPELAPAPFTTLRVAATAATNRVVAFTPGDTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
|||||
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERRSSYRSKGFDTVTKYTQGSWTGFVEDLVTIPKGFNTSFLVNIATI 180
|||||
Db 121 TPHSYIDTYFDTERRSSYRSKGFDTVTKYTQGSWTGFVEDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTQANI PNVFSMOMCGAGLPVA 240
|||||
Db 181 FESENFLLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTQANI PNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
|||||
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQQLACWTNSETPWSYFPKISI 360
|||||
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQQLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
|||||
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
|||||
Db 421 RAQKRVGFPAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
|||||
Db 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 5

AAB44270
ID AAB44270 standard; Protein; 518 AA.

AC AAB44270;

DT 08-FEB-2001 (first entry)

DE Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.

KM Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
KW expressed sequence tag; detection; cancer.

OS Homo sapiens.

PN WO200053756-A2.

PD 14-SEP-2000.

PF 18-FEB-2000; 2000WO-US04341.

PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2000-611443/58.
DR N-PSDB; AAC78500.
XX
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
XX
PS Claim 12; Fig 73; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytosolic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 2687; DB 21; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
ID AAY88424 standard; Protein; 518 AA.
XX
XX AAY88424;
AC
XX
XX 03-AUG-2000 (first entry)
DT
XX
XX Human aspartyl protease 1 (Asp1) amino acid sequence.
DE
XX
XX Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;
KW Alzheimer's disease; beta secretase site.
XX
XX Homo sapiens.
OS
XX WO200017369-A2.
PN
XX 30-MAR-2000.
PD
XX
XX 23-SEP-1999; 99WO-US20881.
PF
XX
XX 24-SEP-1998; 98US-0101594.
PR
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
PA
XX
XX Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;
PI
XX
XX WPI; 2000-303209/26.
DR
XX N-PSDB; AAA15661.
DR
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at
PT the beta secretase site to produce amyloid beta peptide -
XX
XX
PS Claim 54; Fig 1; 183pp; English.
XX
XX
CC This sequence represents the human aspartyl protease amino acid sequence.
CC The invention relates to a protease capable of cleaving the beta
CC secretase site of amyloid precursor protein (APP). The protease contains
CC a sequence encoding the amino acid sequence DTG and a sequence encoding
CC DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
CC causes an autosomal dominant form of Alzheimer's disease. APP localises
CC to the cell surface membrane and have a single C-terminal transmembrane
CC domain. Proteolytic processing of APP produces the amyloid beta protein,
CC which is possibly very important in Alzheimer's disease. The invention
CC includes a nucleotide sequence encoding the protease, a vector containing
CC the nucleotide sequence, and a cell line comprising the vector. Methods
CC for screening for inhibitors of beta secretase activity are also given in
CC the invention. The human aspartase protein and nucleotide sequences and
CC the methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease.
XX
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 2687; DB 21; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
PS Example 14; Page 155-156; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human Asp 1
CC protein lacking a transmembrane (TM) domain and containing (His)6
CC tag. This sequence is generated from human Asp 1 protein by the
CC deletion of its C-terminal TM domain and addition of hexa-histidine
CC tag at its C-terminus.
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 2687; DB 22; length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQJACWTNSETPMWSTPEKISI 360
Db 301 IVDSGTTLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQJACWTNSETPMWSTPEKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIFD 420
QY 421 RAQKRVGAASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGAASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 AILLVLIVLLLPFRQRRPRDPEVNDDESSLVRRWK 518
Db 481 AILLVLIVLLLPFRQRRPRDPEVNDDESSLVRRWK 518
RESULT 9
AAU29059 ID AAU29059 standard; Protein; 518 AA.
XX
AC AAU29059;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #36.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR N-PSDB; AAS45960.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
PS Claim 11; Fig 72; 774pp; English.
XX
CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLLAQWLLRAPELAPAPFTLLRVAATNRVVAFTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAPELAPAPFTLLRVAATNRVVAFTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDGSGRGYLLEMLIGTPPOKQLIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDGSGRGYLLEMLIGTPPOKQLIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYPTDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPIKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYPTDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPIKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGSLVGGIEPSLYKGDIMWYTIKEENYQIEILKLEIGGSLNDCREYNADKA 300
Db 241 GSGTNGSLVGGIEPSLYKGDIMWYTIKEENYQIEILKLEIGGSLNDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDFWTGSQOLACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDFWTGSQOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420
Db 361 YLRDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420

QY 421 RAQKRVGFAASPCAETIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPILTWIVSYALMSVCG 480
Db 421 RAQKRVGFAASPCAETIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPILTWIVSYALMSVCG 480
QY 481 ALLVLIVLLLLPFRQORRPDRDPEVNVNDESSLVRRHWK 518
Db 481 ALLVLIVLLLLPFRQORRPDRDPEVNVNDESSLVRRHWK 518
RESULT 10
AAE06858
ID AAE06858 standard; Protein; 518 AA.
XX
AC AAE06858;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human aspartyl protease 1 (Hu-Asp1) protein.
XX
KW Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy; chromosome 21.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= Signal_peptide
FT 21..518
FT /note= "Mature human aspartyl protease 1 (Hu-Asp1) "
FT Domain 469..492
FT /label= Transmembrane_domain
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00799.
XX
PR 09-MAY-2001; 2001WO-IB00799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX
XX WPI; 2001-483072/52.
DR N-PSDB; AAD13020.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Example 2; Fig 1; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and

CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is human aspartyl protease 1 (Hu-Asp1).
CC Hu-Asp 1 gene is localised on chromosome 21.

XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
OY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
OY 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
OY 181 FESENFLLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTOANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTOANIPNVFSMQMGAGLPVA 240
OY 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
OY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
OY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNVECYRFGISPSSTNALVIGATMEGFYVIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNVECYRFGISPSSTNALVIGATMEGFYVIFD 420
OY 421 RAQKRVGFASPACAEIAGAASEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPACAEIAGAASEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
OY 481 ALLVLIVLILLPFCQRRPRDEVVNDESSLVRHRWK 518
Db 481 ALLVLIVLILLPFCQRRPRDEVVNDESSLVRHRWK 518

RESULT 11
AAU06602
ID AAU06602 standard; Protein; 518 AA.
XX
AC AAU06602;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human Aspartyl protease 1 (Asp1).
XX
KM Human; Aspartyl protease; Asp1; Asp2; beta-secretase; nootropic;
KM neuroprotective; amyloid protein precursor; App; Alzheimer's disease;
KM amyloid-beta; Abeta.
XX
OS Homo sapiens.
XX
PN WO200149098-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00798.
XX
PR 09-MAY-2001; 2001WO-IB00798.
XX

PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

DR WPI, 2001-502549/55.
DR N-PSDB; AAS11516.

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity

PS Example 2; Fig 1; 185pp; English.

CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-Sw-beta-secretase peptide sequence (NDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridise to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is human Asp1.

XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
OY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
OY 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
OY 181 FESENFLLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTOANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTOANIPNVFSMQMGAGLPVA 240
OY 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
OY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
OY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNVECYRFGISPSSTNALVIGATMEGFYVIFD 420

|||||
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
Db 421 RAQKRVGFASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
QY 481 AILVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518
Db 481 AILVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518
RESULT 12
AAU07201
ID AAU07201 standard; Protein; 518 AA.
XX
AC AAU07201;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human aspartyl protease 1 (Asp-1).
XX Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00797.
XX
PR 09-MAY-2001; 2001WO-IB00797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX
XX WPI; 2001-502548/55.
DR N-PSDB; AAS11701.
DR
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
XX Example 2; Fig 1; 185bp; English.
XX
XX The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing
CC an APP cleavage site recognisable by a mammalian beta-secretase, and
CC further comprising two lysine residues at the carboxyl terminus of the
CC amino acid sequence of the mammalian APP or APP fragment. The
CC polypeptides are used for assaying for modulators of beta-secretase
CC activity; identifying agents that inhibit the APP processing activity
CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of
CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in

CC Northern and Southern blots. The present sequence represents the
CC amino acid sequence of human Asp-1.
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 2687; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALAPALLPLLAQWLRAAPELAPAPFTPLRVAAATNRVVAFTPGPGTPAERHADGL 60
Db 1 MGALAPALLPLLAQWLRAAPELAPAPFTPLRVAAATNRVVAFTPGPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTFVGEDLVTI PKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTFVGEDLVTI PKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIETILKLEIGGQSLNLDREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIETILKLEIGGQSLNLDREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
Db 421 RAQKRVGFASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
QY 481 AILVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518
Db 481 AILVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518
RESULT 13
AAE02580
ID AAE02580 standard; Protein; 518 AA.
XX
AC AAE02580;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human aspartyl protease 1 (Asp 1).
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;
KW beta-secretase; chromosome 21.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Peptide /label= Signal_peptide
FT Peptide /label= 22..62
FT Peptide /label= Asp_1_prepropeptide
FT Peptide /label= 23..62
FT Peptide /label= Asp_1_propeptide
FT Protein 63..518
FT Protein /label= Mature_human_Asp_1_protein
FT Active-site /note= "Specifically claimed"
FT 87..89

FT /label= Active_site_1
FT Active-site 110..113
FT /label= Active_site_2
FT Active-site 303..305
FT /label= Active_site_3
FT Domain 469..492
FT /label= Transmembrane_domain
FT Domain 493..518
FT /label= Cytoplasmic_domain
FT Region 497..518
FT /note= "Peptide #1"
XX WO200123533-A2.
XX
XX
XX PD 05-APR-2001.
XX
XX PF 22-SEP-2000; 2000WO-US26080.
XX
XX PR 23-SEP-1999; 99US-0155493.
XX PR 23-SEP-1999; 99WO-US20881.
XX PR 13-OCT-1999; 99US-0416901.
XX PR 06-DEC-1999; 99US-0169232.
XX
XX PA (PHAA) PHARMACIA & UPJOHN CO.
XX
XX PI Gurney M, Bienkowski MJ;
XX
XX DR WPI; 2001-290516/30.
XX DR N-PSDB; AAD06738.
XX
XX PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX PT protein, useful for the treatment of Alzheimer's disease -
XX
XX PS Claim 29, Fig 1; 189pp; English.
XX
XX CC The present invention relates to enzymes for cleaving the alpha-
XX CC secretase site of the amyloid precursor protein (APP) and methods of
XX CC identifying those enzymes. The methods may be used to identify enzymes
XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
XX CC protein. The enzymes may be used to treat or modulate the progress of
XX CC Alzheimer's disease. The present sequence is human aspartyl protease 1
XX CC (Asp 1). Asp 1 has alpha-secretase protease and beta-secretase
XX CC protease activities. Asp 1 gene is located on chromosome 21.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNEAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKLQILVDTGSSNEAVAG 120
QY 121 TPFSYIDTYFDTERSSSTRSKGPDVTVKYTOGSGWTFVGEDLVITPKGNTSFLVNIATI 180
Db 121 TPFSYIDTYFDTERSSSTRSKGPDVTVKYTOGSGWTFVGEDLVITPKGNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTOANIPNVFSMQMGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTOANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGGOSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360

QY 361 YLRDENSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420
Db 361 YLRDENSRSRFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFAASPCAEIAGAVSEISGPFSTEDVASNCVPAQSLSEPIIWMVSYALMSVCG 480
Db 421 RAQKRVGFAASPCAEIAGAVSEISGPFSTEDVASNCVPAQSLSEPIIWMVSYALMSVCG 480
QY 481 AILLVILVLLLPFRCCQRRPRDPEVNVNDESSLVRHRWK 518
Db 481 AILLVILVLLLPFRCCQRRPRDPEVNVNDESSLVRHRWK 518

RESULT 14
AAE02608
ID AAE02608 standard; Protein; 518 AA.
XX
XX AC AAE02608;
XX
XX DT 10-AUG-2001 (first entry)
XX
XX DE Human Aspartyl protease-1 (Asp-1) deltaTM (His)6 protein.
XX
XX KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
XX KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
XX KW beta-secretase; Asp-1 deltaTM (His)6 protein.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO200123533-A2.
XX
XX PD 05-APR-2001.
XX
XX PF 22-SEP-2000; 2000WO-US26080.
XX
XX PR 23-SEP-1999; 99US-0155493.
XX PR 23-SEP-1999; 99WO-US20881.
XX PR 13-OCT-1999; 99US-0416901.
XX PR 06-DEC-1999; 99US-0169232.
XX
XX PA (PHAA) PHARMACIA & UPJOHN CO.
XX
XX PI Gurney M, Bienkowski MJ;
XX
XX DR WPI; 2001-290516/30.
XX
XX PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX PT protein, useful for the treatment of Alzheimer's disease -
XX
XX PS Example 14; Page 183-184; 189pp; English.
XX
XX CC The present invention relates to enzymes for cleaving the alpha-
XX CC secretase site of the amyloid precursor protein (APP) and methods of
XX CC identifying those enzymes. The methods may be used to identify enzymes
XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
XX CC protein. The enzymes may be used to treat or modulate the progress of
XX CC Alzheimer's disease. The present sequence is human Aspartyl protease-1
XX CC (Asp-1) deltaTM (His)6 protein which is used for the expression of
XX CC pre-pro-human-Aspartyl protease 1 (Asp1). This protein is obtained by
XX CC replacing C-terminal transmembrane and cytoplasmic domains with a
XX CC hexahistidine purification tag in the human Aspartyl protease 1.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLRVAATNRVVAPTPGPTPAERHADGL 60

QY	61	ALALEPALASPAGANFLAMVDNLQDSCGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGANFLAMVDNLQDSCGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG	120
QY	121	TPHSYIDTYFDTERRSSTYRSKGFVDVTYKKTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERRSSTYRSKGFVDVTYKKTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
QY	181	FESENFELPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGLPVA	240
Db	181	FESENFELPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGLPVA	240
QY	241	GSGTNGSLVLGIEPSLYKGDIMWTPRIKEENYYOIEILKLEIGQSINLDCREYNADKA	300
Db	241	GSGTNGSLVLGIEPSLYKGDIMWTPRIKEENYYOIEILKLEIGQSINLDCREYNADKA	300
QY	301	IYDSGTTLLRLPQKVFDAVVEAVARASLIPESDGFMTGSQOLACWTNSETPMSYEPKISI	360
Db	301	IYDSGTTLLRLPQKVFDAVVEAVARASLIPESDGFMTGSQOLACWTNSETPMSYEPKISI	360
QY	361	YLRDENSRSFRITILPOLYIQPMGAGLNEYECYRFGISPSSTNALVIGATVMEGEFYIFD	420
Db	361	YLRDENSRSFRITILPOLYIQPMGAGLNEYECYRFGISPSSTNALVIGATVMEGEFYIFD	420
QY	421	RAQKRVGFPAASPCAIEIAGAAVSEISGFSTEDVASNCVPAQSLSEPIIWTIVSYALMSVCG	480
Db	421	RAQKRVGFPAASPCAIEIAGAAVSEISGFSTEDVASNCVPAQSLSEPIIWTIVSYALMSVCG	480
QY	481	AILLVLLVLLLLPFCQRRPRDPEVNVNDESSLVHRWK	518
Db	481	AILLVLLVLLLLPFCQRRPRDPEVNVNDESSLVHRWK	518

RESULT 15	
ABB78589	
ID	ABB78589 standard; Protein; 518 AA.
XX	
AC	ABB78589;
XX	
DT	16-JUL-2002 (first entry)
XX	
DE	Human Asp-1 protein sequence SEQ ID NO:2.
XX	
KW	Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
KW	proteolytic; chromosome 21.
XX	
OS	Homo sapiens.
XX	
PN	GB2367060-A.
XX	
PD	27-MAR-2002.
XX	
PF	29-OCT-2001; 2001GB-0025934.
XX	
PR	23-SEP-1999; 99US-155493P.
PR	23-SEP-1999; 99US-0404133.
PR	23-SEP-1999; 99WO-US20881.
PR	13-OCT-1999; 99US-0416901.
PR	06-DEC-1999; 99US-169232P.
PR	22-SEP-2000; 2000GB-0023315.
XX	
PA	(PHAA) PHARMACIA & UPJOHN CO.
XX	
PI	Bienkowski MJ, Gurney M;
XX	
DR	WPI; 2002-396337/43.
DR	N-PSDB; ABL52456.
XX	
PT	Human aspartyl protease 1 substrates useful in assays to detect
PT	aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT	disease -
XX	

PS Claim 7; Fig 1; 182pp; English.

The present invention describes a human aspartyl protease 1 (hu-Asp1) substrate (I) which comprises a peptide of no more than 50 amino acids, and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1 proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with (I) under acidic conditions; and (b) determining the level of hu-Asp1 proteolytic activity; (2) a purified polynucleotide (III) comprising a nucleotide sequence that hybridises under stringent conditions to the non-coding strand complementary to a defined 1804 nucleotide sequence (see AB552456) where the nucleotide sequence encodes a polypeptide having Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane domain; (3) a purified polynucleotide (III') comprising a sequence that hybridises under stringent conditions to (III) (the nucleotide sequence encodes a polypeptide further lacking a pro-peptide domain corresponding to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV) comprising (III) or (III'); and (5) a host cell (V) transformed or transfected with (III), (III') and/or (IV). The hu-Asp1 protease substrate (I) may be used as an enzyme substrate in assays to detect aspartyl protease activity, (II) and therefore diagnose diseases associated with aberrant hu-Asp1 expression and activity such as Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present sequence represents hu-Asp1 from the present invention.

Sequence 518 AA;

Query Match	100.0%;	Score 2687;	DB 23;	Length 518;
-------------	---------	-------------	--------	-------------

Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGALRALLLPLLAQWMLRAAPELAPFTLLPLRVAATNRVVAFTPGGTPAERHADGL	60
Db	1	MGALARALLPLLAQWMLRAAPELAPFTLLPLRVAATNRVVAFTPGGTPAERHADGL	60
QY	61	ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG	120
QY	121	TPHSYIDTYFDTERSSSTYRSKGFVDVYKYTGGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSSTYRSKGFVDVYKYTGGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
QY	181	FESENFELPGIKWNGILGLAYATLAKRSSLETFDSDLVTOANIPNVFSMOMCGAGLPVA	240
Db	181	FESENFELPGIKWNGILGLAYATLAKRSSLETFDSDLVTOANIPNVFSMOMCGAGLPVA	240
QY	241	GSGTNGSLVLGIEBPSLYKGDIMWYTPRIKEWYYQIEILKLEIGGOSLNDCREYNADKA	300
Db	241	GSGTNGSLVLGIEBPSLYKGDIMWYTPRIKEWYYQIEILKLEIGGOSLNDCREYNADKA	300
QY	301	IYDSGTTILRLPQKVFDVAVEAVARASLIPESDGFWTGSQOLACWNTSETPMSYFPKISI	360
Db	301	IYDSGTTILRLPQKVFDVAVEAVARASLIPESDGFWTGSQOLACWNTSETPMSYFPKISI	360
QY	361	YLRDENSRSFRITILPOLYIQPMMGAGINYEYRFGISPSSTNALVIGATMEGFYVIFD	420
Db	361	YLRDENSRSFRITILPOLYIQPMMGAGINYEYRFGISPSSTNALVIGATMEGFYVIFD	420
QY	421	RAQKRVGFAASPCAETIAGAAVSEISGPESTEDVASNCVPAQSLSEPIIWTIVSYALMSVCG	480
Db	421	RAQKRVGFAASPCAETIAGAAVSEISGPESTEDVASNCVPAQSLSEPIIWTIVSYALMSVCG	480
QY	481	AILLVILVLLLLPFRCCQRRPRDPEVNDSSLVHRWK 518	
Db	481	AILLVILVLLLLPFRCCQRRPRDPEVNDSSLVHRWK 518	

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Job time : 42 secs

Job time : 42 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:31:43 ; Search time 16 Seconds
(without alignments)
952.567 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALARALLPLLAQWLRA.....RPRDPEVVDSSSLVRHWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2687	100.0	518	3 US-08-999-723-2	Sequence 2, Appli
2	2687	100.0	518	4 US-09-434-427-2	Sequence 2, Appli
3	2687	100.0	518	4 US-09-548-372D-2	Sequence 2, Appli
4	2687	100.0	518	4 US-09-548-367D-2	Sequence 2, Appli
5	2395	89.1	514	4 US-09-717-432-2	Sequence 2, Appli
6	2395	89.1	514	4 US-09-912-484-2	Sequence 2, Appli
7	1186.5	44.2	501	4 US-09-713-158-2	Sequence 2, Appli
8	1185	44.1	501	4 US-09-548-372D-8	Sequence 8, Appli
9	1185	44.1	501	4 US-09-548-367D-8	Sequence 8, Appli
10	1178.5	43.9	501	4 US-09-548-372D-4	Sequence 4, Appli
11	1178.5	43.9	501	4 US-09-548-367D-4	Sequence 4, Appli
12	1172.5	43.6	501	4 US-09-009-191-2	Sequence 2, Appli
13	1160.5	43.2	774	4 US-09-009-191-4	Sequence 4, Appli
14	1139	42.4	453	4 US-09-548-372D-30	Sequence 30, Appli
15	1139	42.4	453	4 US-09-548-367D-30	Sequence 30, Appli
16	1139	42.4	459	4 US-09-548-372D-32	Sequence 32, Appli
17	1139	42.4	459	4 US-09-548-367D-32	Sequence 32, Appli
18	1127	41.9	433	4 US-09-548-372D-26	Sequence 26, Appli
19	1127	41.9	433	4 US-09-548-367D-26	Sequence 26, Appli
20	1127	41.9	446	4 US-09-548-372D-22	Sequence 22, Appli
21	1127	41.9	446	4 US-09-548-367D-22	Sequence 22, Appli
22	1127	41.9	459	4 US-09-548-372D-24	Sequence 24, Appli
23	1127	41.9	459	4 US-09-548-367D-24	Sequence 24, Appli
24	1123	41.8	425	4 US-09-548-372D-28	Sequence 28, Appli
25	1123	41.8	425	4 US-09-548-367D-28	Sequence 28, Appli
26	1071.5	39.9	476	4 US-09-548-372D-73	Sequence 73, Appli
27	1071.5	39.9	476	4 US-09-548-367D-73	Sequence 73, Appli

28	1068	39.7	476	4 US-09-548-372D-6	Sequence 6, Appli
29	1068	39.7	476	4 US-09-548-367D-6	Sequence 6, Appli
30	1028.5	38.3	428	4 US-09-548-372D-51	Sequence 51, Appli
31	1028.5	38.3	428	4 US-09-548-367D-51	Sequence 51, Appli
32	1028.5	38.3	434	4 US-09-548-372D-53	Sequence 53, Appli
33	1028.5	38.3	434	4 US-09-548-367D-53	Sequence 53, Appli
34	308.5	11.5	412	4 US-08-007A-12	Sequence 12, Appli
35	308.5	11.5	412	4 US-08-974-691-4	Sequence 4, Appli
36	308.5	11.5	412	4 US-08-915-095A-12	Sequence 12, Appli
37	308.5	11.5	412	4 US-08-798-096-12	Sequence 12, Appli
38	308.5	11.5	412	4 US-08-095A-12	Sequence 12, Appli
39	289	10.8	410	1 US-08-088-633-2	Sequence 2, Appli
40	289	10.8	410	1 US-08-245-756-2	Sequence 2, Appli
41	289	10.8	410	1 US-08-441-750-2	Sequence 2, Appli
42	289	10.8	410	2 US-08-441-751-2	Sequence 2, Appli
43	289	10.8	410	5 PCT-US92-02521-2	Sequence 2, Appli
44	287	10.7	396	1 US-08-208-007A-13	Sequence 13, Appli
45	287	10.7	396	4 US-09-032-523-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1									
US-08-999-723-2 Application US/0899723A									
Sequence 2, Application 6025180									
Patent No. 6025180									
GENERAL INFORMATION:									
APPLICANT: Powell, David G.									
APPLICANT: Southan, Christopher									
APPLICANT: Chapman, Conrad G.									
APPLICANT: Evans, Joanne R.									
TITLE OF INVENTION: ASPI									
FILE REFERENCE: GH70262									
CURRENT APPLICATION NUMBER: US/08/999, 723A									
CURRENT FILING DATE: 1997-10-06									
NUMBER OF SEQ ID NOS: 2									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 2									
LENGTH: 518									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-08-999-723-2									
Query Match									
Best Local Similarity 100.0%; Score 2687; DB 3; Length 518;									
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MGALARALLPLLAQWLRAAPBLAPFTPLRVAAATNRVVAFTPGPTPAERHADGL	60						
DB	1	MGALARALLPLLAQWLRAAPBLAPFTPLRVAAATNRVVAFTPGPTPAERHADGL	60						
QY	61	ALALEPALASPAGANFLAVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG	120						
DB	61	ALALEPALASPAGANFLAVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG	120						
QY	121	TPHSYIDTYFDTERSSFYRSKGFDTVTKYTOGSMWTFVGEDLVITPKGFNTSFLVNIAT	180						
DB	121	TPHSYIDTYFDTERSSFYRSKGFDTVTKYTOGSMWTFVGEDLVITPKGFNTSFLVNIAT	180						
QY	181	FESSENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA	240						
DB	181	FESSENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA	240						
QY	241	GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGOSLNLDCREYNADKA	300						
DB	241	GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEEWYQIEILKLEIGGOSLNLDCREYNADKA	300						
QY	301	IYDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDFWTSQACWTNSETPWSYFPKISI	360						
DB	301	IYDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDFWTSQACWTNSETPWSYFPKISI	360						
QY	361	YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD	420						

DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
QY 421 RAOKRVGFPAASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
DB 421 RAOKRVGFPAASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 ALLVLIVLLLPRCQRRPRDPEVNVDESSLVRHRWK 518
DB 481 ALLVLIVLLLPRCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 2
US-09-434-427-2
; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-434-427-2

Query Match 100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSYRSKGFDTVKYTOGSGWTFVGEDLVITPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSYRSKGFDTVKYTOGSGWTFVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
QY 421 RAOKRVGFPAASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
DB 421 RAOKRVGFPAASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480

QY 481 ALLVLIVLLLPRCQRRPRDPEVNVDESSLVRHRWK 518
DB 481 ALLVLIVLLLPRCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 3
US-09-548-372D-2
; Sequence 2, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 3.1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-2

See 73 issued

Query Match 100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSYRSKGFDTVKYTOGSGWTFVGEDLVITPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSYRSKGFDTVKYTOGSGWTFVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
QY 421 RAOKRVGFPAASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
DB 421 RAOKRVGFPAASPCAEIAGA VSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 ALLVLIVLLLPRCQRRPRDPEVNVDESSLVRHRWK 518
DB 481 ALLVLIVLLLPRCQRRPRDPEVNVDESSLVRHRWK 518

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RESULT 4
US-09-548-367D-2
; Sequence 2, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIORITY FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-2
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Query Match      100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPRLVAATNRVAVPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPRLVAATNRVAVPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYEDTERSSSTYRSKGFDTVTKYTOGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYEDTERSSSTYRSKGFDTVTKYTOGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDLSVTQANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDLSVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPRIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVLGGIEPSLYKGDWYTPRIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQLAQWNTSETPWSYFPKISI 360
DB 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQLAQWNTSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
DB 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAPSPCAEIAAGAVSEISGFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
DB 421 RAQKRVGFAPSPCAEIAAGAVSEISGFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 AILLVLIIVLLLPFRCCRRPRDPEVNVDESSLVRHRWK 518
DB 481 AILLVLIIVLLLPFRCCRRPRDPEVNVDESSLVRHRWK 518
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RESULT 5
US-09-717-432-2
; Sequence 2, Application US/09717432
; Patent No. 6291223
; GENERAL INFORMATION:
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; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: CHRISTIE, GARY
; APPLICANT: POWELL, DAVID J.
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; PRIORITY FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-717-432-2
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Query Match      89.1%; Score 2395; DB 4; Length 514;
Best Local Similarity 88.6%; Pred. No. 2.6e-216;
Matches 459; Conservative 20; Mismatches 35; Indels 4; Gaps 1;
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QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPRLVAATNRVAVPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPRLVAATNRVAVPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAG 116
QY 121 TPHSYIDTYEDTERSSSTYRSKGFDTVTKYTOGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
DB 117 APHSYIDTYEDTERSSSTYRSKGFDTVTKYTOGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 176
QY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDLSVTQANIPNVFSMOMCGAGLPVA 240
DB 177 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDLSVTQANIPNVFSMOMCGAGLPVA 236
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPRIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
DB 237 GSGTNGGSLVLGGIEPSLYKGDWYTPRIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 296
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQLAQWNTSETPWSYFPKISI 360
DB 297 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQLAQWNTSETPWSYFPKISI 356
QY 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
DB 357 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 416
QY 421 RAQKRVGFAPSPCAEIAAGAVSEISGFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
DB 417 RAQKRVGFAPSPCAEIAAGAVSEISGFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 476
QY 481 AILLVLIIVLLLPFRCCRRPRDPEVNVDESSLVRHRWK 518
DB 477 AILLVLIIVLLLPFRCCRRPRDPEVNVDESSLVRHRWK 514
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RESULT 6
US-09-912-484-2
; Sequence 2, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaotong
; APPLICANT: Powell, David J.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974
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; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/717,432
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-912-484-2

Query Match 89.1%; Score 2395; DB 4; Length 514;
Best Local Similarity 88.6%; Pred. No. 2.6e-216;
Matches 459; Conservative 20; Mismatches 35; Indels 4; Gaps 1;

QY 1 MGALRALLLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALRALLLLVLAQWLLSAVPALAPAPFTLLPLQVAGATNHRASAVPGLGTPPELPRADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAG 120
Db 61 ALALEPVRAT----ANFLAMVDNLQDSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAG 116
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTOGSGWTGFGVEDLVITPKGFNTSFLVNIATI 180
Db 117 APHSYIDTYFDSESSSTYHSKGFDTVKYTOGSGWTGFGVEDLVITPKGFNSFLVNIATI 176
QY 181 FESENFPLPGIKWNGILGLAYATLAKSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
Db 177 FESENFPLPGIKWNGILGLAYAAALAKSSSLETFPDSLVAQAKIPDIFSMOMCGAGLPVA 236
QY 241 GSGTNGGSLVLGIEPSLYKGDIMWTPRIKEWYQIEILKLEIGGSLNLDCREYNADKA 300
Db 237 GSGTNGGSLVLGIEPSLYKGDIMWTPRIKEWYQIEILKLEIGGSLNLDCREYNADKA 296
QY 301 IVDSGTTLLRLPQKVFDAVEAVARASLIPFSDGFWTGSQACWTNSETPWSYFPKISI 360
Db 297 IVDSGTTLLRLPQKVFDAVEAVARTSLIPFSDGFWTGAQACWTNSETPMAYFPKISI 356
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFD 420
Db 357 YLRDENASSRSFRITILPOLYIQPMGAGNYECYRFGISSSTNALVIGATWMEGFYVIFD 416
QY 421 RAQKRVGFPAASPCAIEAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILMIVSYALMSVCG 480
Db 417 RAQRRVGFPAVSPCAIEIGTIVSEISGPFSTEDIASNCVPAQALNEPIILMIVSYALMSVCG 476
QY 481 AILLVLIVLLLLPFCQRRPRDPEVNVDESSLVRHRWK 518
Db 477 AILLVLIVLLLLPLCHRAPRDPEVNVDESSLVRHRWK 514

RESULT 7
US-09-713-158-2
; Sequence 2, Application US/09713158
; Patent No. 6361975
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: POWELL, DAVID J.
; APPLICANT: CHRISTIE, GARY
; TITLE OF INVENTION: MOUSE ASPARTIC SECRETASE-2 (MASP-2)
; FILE REFERENCE: GP-70660
; CURRENT APPLICATION NUMBER: US/09/713,158
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/165,800
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: MUS MUSCULUS

US-09-713-158-2

Query Match 44.2%; Score 1186.5; DB 4; Length 501;
Best Local Similarity 46.0%; Pred. No. 7.7e-103;
Matches 238; Conservative 83; Mismatches 167; Indels 29; Gaps 8;

QY 7 ALLPLLAQWLLRAAPELAPAPFT----LPLRVAATNRVVAPTPGPTPAERHADGLA 61
Db 2 AQAIPWLLLV--GSGMLPAQGTGLGIRLPLRSGLA-----GPPLGLRLPRETDEES-- 51
QY 62 LALPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPOKQILVDTGSSNFAVAGT 121
Db 52 -----EPPGRGSFVENVNLRGKSGQGYVEMTVGSPQTLNILLVDTGSSNFAVGAA 104
QY 122 PHSYIDTYFDTERSSSTYRSKGFDTVKYTOGSGWTGFGVEDLVITPKGFNTSFLVNIATIF 181
Db 105 PHPFLHRYQORQLSSTYRDLRKGVVVPYTOGKMEGELGTDLVSIHPGNVTVRANIAAIT 164
QY 182 ESENFPLPGIKWNGILGLAYATLAKSSSLETFPDSLVTQANIPNVFSMOMCGAGLPV-- 239
Db 165 ESDKFFINGSNWEGILGLAYAEIARPDDSLPEFPDSLVKQTHIPNIFSLQCGAGFPLNQ 224
QY 240 -AGSGTNGGSLVLGIEPSLYKGDIMWTPRIKEWYQIEILKLEIGGSLNLDCREYNAD 298
Db 225 TEALASVGGSMIIGIDHSLYTGSLWYTPIRREWYEVIIIVREINGODLKMDCKEYNYD 284
QY 299 KAIVDSGTTLLRLPQKVFDAVEAVARASLIPFSDGFWTGSQACWTNSETPWSYFPKI 358
Db 285 KSIYDSGTTNRLPKKVFEAAVKSIKAASSTEKEFPDFWLGEQLVWCQAGTTPWNIFPVI 344
QY 359 SLYLRDENSSRSFRITILPOLYIQPMGAGLNY-ECYRFGISPSSTNALVIGATWMEGFYV 417
Db 345 SLYLMEGVTNOSFRITILPOLYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYV 404
QY 418 IFDRAQKRVGFPAASPCAIEAGAAVSEISGPFSTEDVASNCVPAQSLSEPIILMIVSYALMS 477
Db 405 VFDRARKRIGFAVSACHVDEPRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAA 464
QY 478 VCGAILLVIVLLLLPFCQRRPRDPEVNVDESSL 512
Db 465 IC-ALFMLPLCLMVCQWRCLRLRHQHDPEADDISLL 500

RESULT 8
US-09-548-372D-8
; Sequence 8, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-548-372D-8
Query Match 44.1%; Score 1185; DB 4; Length 501;
Best Local Similarity 46.0%; Pred. No. 1.1e-102;
Matches 237; Conservative 83; Mismatches 169; Indels 26; Gaps 7;

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QY      9 LIPLLAQWLLRAAPELAAPFT-----LPLRVAATNRVAAPTPPGPTPAERHADGLALA   63
Db      1 MAPALHWLLLVWGSGMLPAGCTHLGIRLPFRSGLA-----GPPLGLRLPRETDEES-----   51
QY      64 LEPALASPAGAANFLAVNDNLQGDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVACTPH   123
Db      52 -----EEPGRGGSFVEWDNLRGKSGQGGYYVEMTVGSPQTNLITLVDTGSSNFAVGAAH   106
QY      124 SYIDTYFDTERSTYSRSKGFDTVKYTQGSWTGFVEDLVTIPIKGNTSLVNIAITFES   183
Db      107 PFLHRYYQRQLSSTYRDLRKGVVPYPTQGMKEGELGTDLVSIPHGPNVTVRANIAAITES   166
QY      184 ENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVSQMCGAGIPV---A   240
Db      167 DKFFINGSNMEGILGLAAEAETARPDSLEPFDFSLVQTHIPNI FSLQLCGAGPLNQTE   226
QY      241 GSGTNGSLVLGGIEPSLYKGDIMWYTPIKEEWYQIETIKLEIGQSINLDCREYNADKA   300
Db      227 ALASVGSMIIIGSIDHSLYTGSLMYTPIRREWEYEVIIVREINGODLKMDCKEYNYDKS   286
QY      301 IVDSGTTLRLRPQKVFDVAIVEAVARASLIPEFSDFWTGSOLACWTNSTETPMSEYFPKISI   360
Db      287 IVDSGTTLRLPKKVFEAEAVKSIKAAASSTEKFDPGFMLGEQLVCWQA GTTPMNI FPVISL   346
QY      361 YLRDENSSRSFRITILPOLYIQPMGAGLNY-ECYRFGISPTNALVIGATWEGFYVIF   419
Db      347 YLMGEVTNQSFRTILPQYL RPVEDVATSQDDCYKFAVSQSSTGTVMGAIVMEGFYVVF   406
QY      420 DRAQKRVGFAASPCAETAGAAVSEISGPFSTEDVASNCVPAQSLSEPILMWYSALMSVC   479
Db      407 DRARKRIGFAVSACHVDEERTTAAVEGPFVTADMEDCGYNIPQTDESTLMTATVMAAIC   466
QY      480 GAILLVLLVLLLPRCQR--RPRDPEVVNDESSL   512
Db      467 -ALFMLPLCLMVCCWRCLRCIRHQHDDFADDISL   500

RESULT 9
US-09-548-367D-8
; Sequence 8, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-548-367D-8
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Query Match          44.1%; Score 1185; DB 4; Length 501;
Best Local Similarity 46.0%; Pred. No. 1.le-102;
Matches 237; Conservative 83; Mismatches 169; Indels 26; Gaps 7;
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QY	64	LEPALASPAGANFLAMVDNLQDGSRGYYLEMLIGTPPOKLOILVDTGSSNFAVAGTPH	123
Db	52	-----EPPGRKGSFVEMVDNLRKSGGQGYVEMTVGSPQOTLINILVDTGSSNFAVGAAPH	106
QY	124	SYIDTYFDTERSSSTYRSKGFVDVTVKYYTOGSWTGFVGEDLVTI PKGENTSFLVNIATIFES	183
Db	107	PFLHRYQOQLSSTYRDLRKGVVVPYTOQKEGELGTDLVSI PHGPNVTVRANIAAITES	166
QY	184	ENFFLPGIKMGILGLAYATLAKPSSSIETFFDSLVTQANI PNVFSMOMCGAGIPV---A	240
Db	167	DKFFINGSNWEGILGLAYAEIARPDSDSEPPFDSLvkQTHI PNIFSLQLCGAGPPLNQTE	226
QY	241	GSGTNGSLVLGIEPSLYKGDIMWTPRIKEWYVYQIEILKEIGQSLNLDCREYNADKA	300
Db	227	ALASVGSMSIIGGIDHSLYTGSLWYTPRIREWYEVIVRVEINGQDLKMDCKEYNYDKS	286
QY	301	IYDSGTTLLRLPOKVFDAVVEAVARASLIPEFSDFWTSQLA CWTNSETPWSYEPKISI	360
Db	287	IYDSGTNNLRLPKVFEAAVKSIIKAASSTEEKFPDGFWLGEQLV CWAQTTPMNI FPVISL	346
QY	361	YLRENSRSFRITILPOLYIQPMMGAGLNY-ECYRFGISPTNALVIGATVMEGEFYIF	419
Db	347	YLMGEVYNOSFRITILPQOYLRPEVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGEFYVF	406
QY	420	DRAQKRVGFPAASPCAIEIAGA AVSEISGPFSTEDVASNCVPAQSLSEPI LMTVSALMSVC	479
Db	407	DRARKRIGFAVSACHVHDEFRTAAVEGEFVTADMEDCGYNI PQTDESTLMTIAYVMAAIC	466
QY	480	GAILLVILVLLLPFCOR--RPRDPEVYNDESSL 512	
Db	467	-ALEMFLPLCIWVCQWRCLRCHQHDHDFADDISL 500	

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RESULT 10
US-09-548-372D-4
; Sequence 4, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-4

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Query Match          43.9%; Score 1178.5; DB 4; Length 501;
Best Local Similarity 46.2%; Pred. No. 4.3e-102;
Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;

QY      7  ALLPLIAQWLLRAPELAPAF-----LPLRVAATNRVVAPTPGGTPAERHADGLA 61
      | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db      2  AQALFWLLMM---GAGVLPAHGTHGIRLPLRSGLG-----GAPL-----GLR 42

QY      62  LALE--PALASPAGAAFLAMVDNLQDSDGGRGYLLEMLIGTPPOKLIQILVDTGSSNFAYA 119
      | | | | | : | | | | | : | | | | | : | | | | | | | | | | | |
Db      43  LPRETDEEPEEPGRGRGSFVEMVDNLRGKSGQGGYVEMTVGSDPPQTLNILLVDTGSSNFAYG 102

QY     120  GTFHSYIDTFYDTERSSSTYRSKGFVDTVTKYTQGSWTFGEVGEDLVITIPKGFNTSFLVNIAT 179

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Db 103 AAPHPELHRYQROLSSYTRDLRKGVYVPYTOGKMEGELGTDLVSI PHGPNTVTRANIAA 162
QY 180 IFESENFELPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVEFSMOMGAGLPV 239
Db 163 ITESDKFEFINGSNWEIGILGLAYAEIARPDSDLPEPFDSLVKQTHVFNLSLQLCGAGFPL 222
QY 240 AGS---GTNGSLVLGGIEPSLYKGDIMWTPIKEWYYQIEILKLEIGGOSLNDCREYN 296
Db 223 NOSEVLASVGGSMIIGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGODLKMDCKEYN 282
QY 297 ADKAIVDSGTTLLRLPKQVFDVAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFP 356
Db 283 YDKSIVDSGTTNLRPLPKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFP 342
QY 357 KISIVLDENSSRSFRITILPOLYIQPMGAGLNY-ECYRFGISPSTNALVIGATWMEGF 415
Db 343 VLSLYLMEVTNQSFRITILPQOYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 402
QY 416 YVIFDRAQKRVGFAASPCAIEAGAVSEISGPFSTEDVASNCVPAQSLSEPIIMIVSYAL 475
Db 403 YVIFDRAKRIKIGFAVSACHVDEFRTAVEGPFVTLDMEDCGYNIPTDESTLMTIAYVM 462
QY 476 MSVCGAILLVILVLLLPFRQOR--RPRDPEVNDDESSL 512
Db 463 AAIC-ALFMLPLCLMVCQWRCLRCLRQOHDDFADDISLL 500

RESULT 11

US-09-548-367D-4
; Sequence 4, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-4

Query Match 43.9%; Score 1178.5; DB 4; Length 501;
Best Local Similarity 46.2%; Pred. No. 4.3e-102;
Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;

QY 7 ALLPLLAQWLLRAAPELAPAPT-----LPLRVAATNRVAVPTPGPGTPAERHADGLA 61
Db 2 AQALPWLMLM---GAGVLPAHGTQHGIRLPLRSGLG-----GAPL-----GLR 42
QY 62 LALE--PALASPAGANFLAMVDNLQDSGGRYYLEMLIGTPPOKLQILVDTGSSNFAYA 119
Db 43 LPRETDEEPERGRSGFVEMVDNLRGSGGGYYVEMTVGSPQTLNIIIVDTGSSNFAVG 102
QY 120 GTPHSYIDTYFDTERSSTYRSKGFVTVKTYTGSGSWTGFGEDLVITIPKGFNTSFLVNIAT 179
Db 103 AAPHPELHRYQROLSSYTRDLRKGVYVPYTOGKMEGELGTDLVSI PHGPNTVTRANIAA 162
QY 180 IFESENFELPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI PNVEFSMOMGAGLPV 239

Db 163 ITESDKFEFINGSNWEIGILGLAYAEIARPDSDLPEPFDSLVKQTHVFNLSLQLCGAGFPL 222
QY 240 AGS---GTNGSLVLGGIEPSLYKGDIMWTPIKEWYYQIEILKLEIGGOSLNDCREYN 296
Db 223 NOSEVLASVGGSMIIGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGODLKMDCKEYN 282
QY 297 ADKAIVDSGTTLLRLPKQVFDVAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFP 356
Db 283 YDKSIVDSGTTNLRPLPKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFP 342
QY 357 KISIVLDENSSRSFRITILPOLYIQPMGAGLNY-ECYRFGISPSTNALVIGATWMEGF 415
Db 343 VLSLYLMEVTNQSFRITILPQOYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 402
QY 416 YVIFDRAQKRVGFAASPCAIEAGAVSEISGPFSTEDVASNCVPAQSLSEPIIMIVSYAL 475
Db 403 YVIFDRAKRIKIGFAVSACHVDEFRTAVEGPFVTLDMEDCGYNIPTDESTLMTIAYVM 462
QY 476 MSVCGAILLVILVLLLPFRQOR--RPRDPEVNDDESSL 512
Db 463 AAIC-ALFMLPLCLMVCQWRCLRCLRQOHDDFADDISLL 500

RESULT 12

US-09-009-191-2
; Sequence 2, Application US/09009191
; Patent No. 6319689
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID
; APPLICANT: CHAPMAN, CONRAD
; APPLICANT: MURPHY, KAY
; APPLICANT: SMITH, TRUDI
; TITLE OF INVENTION: ASP2
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,191
; FILING DATE: 20-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9701684.4
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-191-2

Query Match 43.6%; Score 1172.5; DB 4; Length 501;
Best Local Similarity 46.1%; Pred. No. 1.6e-101;
Matches 239; Conservative 82; Mismatches 165; Indels 33; Gaps 9;

[illegible]

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; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-009-191-4

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Query Match	43.2%;	Score 1160.5;	DB 4;	Length 774;
Best Local Similarity	47.5%;	Pred. No. 4.3e-100;		
Matches 224;	Conservative 80;	Mismatches 137;	Indels 31;	Gaps 5;

QY	76	NELAMVNDLQODSGRGYYLEMLIGTPPOKLOILVDTGSSNFAVAGTPHSHYIDTYFDTERS	133
Db	2	SFEVEMVDNLRGKSGGGYYVEMTVGSPQTLNILDVTGSSNFAVGAAPHPLHRYQROLS	61
QY	136	STYRSKGFDTVTKYTOGGSWTGFVGEDLVITPKGENTSFLVNIATIFESENFFLPGIKMG	195
Db	62	STYRDLRKGVPEPTYOGKWEGLGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWEG	121
QY	196	ILGLAYATLAKPSSSLETFPDSLVTQANI PNVEFSMOMCGAGLPVAGS--GTNGGSLVG	252
Db	122	ILGLAYAEIARPDLSLEFPFDSLVKQTHVPNLFSLOLCGAGFLNQSSEVLASVGSMTIG	181
QY	253	GIEPSLYKGDIMWYTPRIKEEMWYQJIEILKLEIGGOSLNDCREYNADKAIVDSGTLRLP	312
Db	182	GIDHSLYTGSLWYTPIRREWWYEVAIIVRVEINGQDLKMDCKEYNYDKSIYDSGTLNLRLP	241
QY	313	QKVEDAVEAVARASLIPFESDGFMTGSOLACWTNSETPWSYFPKISLYLRDENSRSRFR	372
Db	242	KKYFEAAVKSIKASPREKFPDGFMLGEOQLVCWQAAGTTPWNI FVVISLYLMGEVTNQSR	301
QY	373	ITILPOLYIQPMGAGLNY-ECYRPGIS PSTNALVIGATVMEGFYVIFDRAQKRVGFAAS	431
Db	302	ITILPOQYLRPVEDVATSQDDCKFAISQSSTGTVMGAVIMEGFYVIFDRARKRIGFAVS	361
QY	432	PCAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPILMIVSYALMSVCGAILLVILLL	491
Db	362	ACHVHDEFRITAVEGPFVITLDMEDCGYNIPODESTLMTIAYVMAAIC-ALFMLPLCLMV	420
QY	492	LPFRCCQRRPRDP-EVYNDESSLV-----RHRW 517	
Db	421	QWRCLRCLROTMDPFADDISLKGKGFWEKDRDSPGTTTPPWFTLTVSRHRW 472	

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RESULT 14
US-09-548-372D-30
; Sequence 30, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 453
; TYPE: PR1

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:34:29 ; Search time 37 Seconds
(without alignments)
855.905 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALARALLPLLAQWLRA.....RPRDPEVNVDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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14:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2687	100.0	518	US-09-978-295A-196	Sequence 196, App
2	2687	100.0	518	US-09-886-143-2	Sequence 2, Appli
3	2687	100.0	518	US-09-978-697-196	Sequence 196, App
4	2687	100.0	518	US-09-978-192A-196	Sequence 196, App
5	2687	100.0	518	US-09-999-832A-196	Sequence 196, App
6	2687	100.0	518	US-09-978-189-196	Sequence 196, App
7	2687	100.0	518	US-10-174-590-72	Sequence 72, Appl
8	2687	100.0	518	US-10-176-758-72	Sequence 72, Appl
9	2687	100.0	518	US-10-175-737-72	Sequence 72, Appl
10	2687	100.0	518	US-10-173-706-72	Sequence 72, Appl
11	2687	100.0	518	US-10-175-738-72	Sequence 72, Appl
12	2687	100.0	518	US-10-175-752-72	Sequence 72, Appl
13	2687	100.0	518	US-10-176-482-72	Sequence 72, Appl
14	2687	100.0	518	US-10-176-757-72	Sequence 72, Appl
15	2687	100.0	518	US-10-176-913-72	Sequence 72, Appl
16	2687	100.0	518	US-10-180-552-72	Sequence 72, Appl
17	2687	100.0	518	US-10-180-557-72	Sequence 72, Appl
18	2687	100.0	518	US-10-173-700-72	Sequence 72, Appl
19	2687	100.0	518	US-10-174-572-72	Sequence 72, Appl

20	2687	100.0	518	US-10-174-579-72	Sequence 72, Appl
21	2687	100.0	518	US-10-174-582-72	Sequence 72, Appl
22	2687	100.0	518	US-10-174-588-72	Sequence 72, Appl
23	2687	100.0	518	US-10-175-739-72	Sequence 72, Appl
24	2687	100.0	518	US-10-175-740-72	Sequence 72, Appl
25	2687	100.0	518	US-10-175-743-72	Sequence 72, Appl
26	2687	100.0	518	US-10-176-488-72	Sequence 72, Appl
27	2687	100.0	518	US-10-176-492-72	Sequence 72, Appl
28	2687	100.0	518	US-10-176-747-72	Sequence 72, Appl
29	2687	100.0	518	US-10-176-750-72	Sequence 72, Appl
30	2687	100.0	518	US-10-176-985-72	Sequence 72, Appl
31	2687	100.0	518	US-10-176-987-72	Sequence 72, Appl
32	2687	100.0	518	US-10-176-991-72	Sequence 72, Appl
33	2687	100.0	518	US-10-176-992-72	Sequence 72, Appl
34	2687	100.0	518	US-10-176-993-72	Sequence 72, Appl
35	2687	100.0	518	US-10-184-658-72	Sequence 72, Appl
36	2687	100.0	518	US-10-173-695-72	Sequence 72, Appl
37	2687	100.0	518	US-10-173-697-72	Sequence 72, Appl
38	2687	100.0	518	US-10-173-705-72	Sequence 72, Appl
39	2687	100.0	518	US-10-174-576-72	Sequence 72, Appl
40	2687	100.0	518	US-10-174-585-72	Sequence 72, Appl
41	2687	100.0	518	US-10-174-586-72	Sequence 72, Appl
42	2687	100.0	518	US-10-175-747-72	Sequence 72, Appl
43	2687	100.0	518	US-10-176-481-72	Sequence 72, Appl
44	2687	100.0	518	US-10-176-485-72	Sequence 72, Appl
45	2687	100.0	518	US-10-176-487-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-09-978-295A-196
; Sequence 196, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249

1	PRIOR FILING DATE: 1997-11-03
2	PRIOR APPLICATION NUMBER: 60/065311
3	PRIOR FILING DATE: 1997-11-13
4	PRIOR APPLICATION NUMBER: 60/066364
5	PRIOR FILING DATE: 1997-11-21
6	PRIOR APPLICATION NUMBER: 60/077450
7	PRIOR FILING DATE: 1998-03-10
8	PRIOR APPLICATION NUMBER: 60/077632
9	PRIOR FILING DATE: 1998-03-11
10	PRIOR APPLICATION NUMBER: 60/077641
11	PRIOR FILING DATE: 1998-03-11
12	PRIOR APPLICATION NUMBER: 60/077649
13	PRIOR FILING DATE: 1998-03-11
14	PRIOR APPLICATION NUMBER: 60/077791
15	PRIOR FILING DATE: 1998-03-12
16	PRIOR APPLICATION NUMBER: 60/078004
17	PRIOR FILING DATE: 1998-03-13
18	PRIOR APPLICATION NUMBER: 60/078886
19	PRIOR FILING DATE: 1998-03-20
20	PRIOR APPLICATION NUMBER: 60/078936
21	PRIOR FILING DATE: 1998-03-20
22	PRIOR APPLICATION NUMBER: 60/078910
23	PRIOR FILING DATE: 1998-03-20
24	PRIOR APPLICATION NUMBER: 60/078939
25	PRIOR FILING DATE: 1998-03-20
26	PRIOR APPLICATION NUMBER: 60/079294
27	PRIOR FILING DATE: 1998-03-25
28	PRIOR APPLICATION NUMBER: 60/079656
29	PRIOR FILING DATE: 1998-03-26
30	PRIOR APPLICATION NUMBER: 60/079664
31	PRIOR FILING DATE: 1998-03-27
32	PRIOR APPLICATION NUMBER: 60/079689
33	PRIOR FILING DATE: 1998-03-27
34	PRIOR APPLICATION NUMBER: 60/079663
35	PRIOR FILING DATE: 1998-03-27
36	PRIOR APPLICATION NUMBER: 60/079728
37	PRIOR FILING DATE: 1998-03-27
38	PRIOR APPLICATION NUMBER: 60/079786
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73	PRIOR FILING DATE: 1998-04-15

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67	PRIOR APPLICATION NUMBER: 60/085339
68	PRIOR FILING DATE: 1998-05-13
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72	PRIOR FILING DATE: 1998-05-13
73	PRIOR APPLICATION NUMBER: 60/085582

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAFTPGGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAFTPGGTPAERHADGL 60
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Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTI PKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTI PKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFASPACAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPACAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDDEVVNDESSLVRHRWK 518
Db 481 AILLVLIIVLLLPFCQRRPRDDEVVNDESSLVRHRWK 518

RESULT 2
US-09-886-143-2
; Sequence 2, Application US/09886143
; Patent No. US20020159991A1
; GENERAL INFORMATION:
; APPLICANT: Cordell, Barbara
; APPLICANT: Schimmoller, Frauke
; APPLICANT: Liu, Yu-Wang
; APPLICANT: Quon, Diana Hom
; TITLE OF INVENTION: Modulation of A Levels by
; TITLE OF INVENTION: Secretase BACE2
; FILE REFERENCE: SCIOS.022A
; CURRENT APPLICATION NUMBER: US/09/886,143
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/215,729
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-143-2

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAFTPGGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAFTPGGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
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Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTI PKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
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QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWTNSETPWSYFPKISI 360
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QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFASPACAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFASPACAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDDEVVNDESSLVRHRWK 518
Db 481 AILLVLIIVLLLPFCQRRPRDDEVVNDESSLVRHRWK 518

RESULT 3
US-09-978-697-196
; Sequence 196, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAPELAPAPFTLLPLRVAAATNRVVAPTPGPTPAERHADGL 60
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Db 61 ALALBPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPKLQILVDTGSSNFAVAG 120
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Db 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDSLVTQANIPNVFSMOMCGAGLPVA 240
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Db 241 GSGTNGGSLVLGGIEPSLYKGDITWYTPIKEWYYQIEILKEIGGOSLNLDCREYNADKA 300
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Db 301 IVDSGTTLLRLPQKVFDAVVEAARASLIPEFSDGFMTGSQLA CWTNSETPWSYFPKISI 360
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Db 361 YLRDENSSRSFRITILLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAAVSEISGPSTEDVASNCVPAQSLSEPIILMIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAEIAGAAVSEISGPSTEDVASNCVPAQSLSEPIILMIVSYALMSVCG 480
QY 481 ALLVLIVLLLPRCQRRPRDPEVYNDESSLVRHRWK 518
Db 481 ALLVLIVLLLPRCQRRPRDPEVYNDESSLVRHRWK 518

RESULT 4
US-09-978-192A-196
; Sequence 196, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2687; DB 9; length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALAPALLPLLAQWLRAAPELAPAPFTLPRLVAAATNRVAVPTPGPTPAERHADGL 60
DB 1 MGALAPALLPLLAQWLRAAPELAPAPFTLPRLVAAATNRVAVPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFVDYTVKYTGSGSWTGFVGEDLVTIIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSTYRSKGFVDYTVKYTGSGSWTGFVGEDLVTIIPKGFNTSFLVNIATI 180

QY 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTOANI PNVESQMCGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDLSLVTOANI PNVESQMCGAGLPVA 240
QY 241 GSGTNGGSLVGGIEPSLYKGDIMWTPRIKEEMYYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVGGIEPSLYKGDIMWTPRIKEEMYYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
Db 361 YRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFD 420
QY 421 RAKRVGFAPCAEIAAGAVSEISGFSTEDVASNCVPAQSLSEPIIMVSYALMSVCG 480
Db 421 RAKRVGFAPCAEIAAGAVSEISGFSTEDVASNCVPAQSLSEPIIMVSYALMSVCG 480
QY 481 AILLVILVLLLPFCQRRPRDEPVNDESSLVRHRWK 518
Db 481 AILLVILVLLLPFCQRRPRDEPVNDESSLVRHRWK 518

RESULT 5
US-09-999-832A-196
; Sequence 196, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAAPELAPAPFTPLRVAAATNRVVAFTPGPGTPAERHADGL 60
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Db 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYEDTERSSTYRSKGFDTVTKYTQGSWTFVGEDLVTI PKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYEDTERSSTYRSKGFDTVTKYTQGSWTFVGEDLVTI PKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IYDSGTTLLRLPOKVPDAVVEAVARASLIPEFSDGFMTGSQOLACWTNSETPWSYFPKISI 360
Db 301 IYDSGTTLLRLPOKVPDAVVEAVARASLIPEFSDGFMTGSQOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIYFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIYFD 420
QY 421 RAQKRVGFASPCAIEIAGAVERSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
Db 421 RAQKRVGFASPCAIEIAGAVERSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCG 480
QY 481 AILLVILVLLLPFRCCRRPRDPEVYNDESSLVRHRMK 518
Db 481 AILLVILVLLLPFRCCRRPRDPEVYNDESSLVRHRMK 518

RESULT 6
US-09-978-189-196
; Sequence 196, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAPELAPAPFTLLPLRVAATNRVVAAPTGPPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAPELAPAPFTLLPLRVAATNRVVAAPTGPPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVVKYTOGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSSTYRSKGFDTVVKYTOGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
DB 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
DB 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIILWISYALMSVCG 480
DB 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIILWISYALMSVCG 480
QY 481 AILLVLIIVLLLPFRCCQRRPRDPEVNVDESSLVRHRWK 518
DB 481 AILLVLIIVLLLPFRCCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 7
US-10-174-590-72
; Sequence 72, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRIOR application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-72

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAPELAPAPFTLLPLRVAATNRVVAAPTGPPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAPELAPAPFTLLPLRVAATNRVVAAPTGPPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVVKYTOGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSSTYRSKGFDTVVKYTOGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
DB 181 FESENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
DB 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
DB 361 YLRDENSSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIILWISYALMSVCG 480
DB 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIILWISYALMSVCG 480
QY 481 AILLVLIIVLLLPFRCCQRRPRDPEVNVDESSLVRHRWK 518
DB 481 AILLVLIIVLLLPFRCCQRRPRDPEVNVDESSLVRHRWK 518

RESULT 8

US-10-176-758-72
; Sequence 72, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-72

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPBLAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPBLAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAVNDLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAVNDLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTRSKGFDVTVKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSSTRSKGFDVTVKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
DB 181 FESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
DB 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIWIYSYALMSVCG 480
DB 421 RAQKRVGFAASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIWIYSYALMSVCG 480
QY 481 ALLVLIVLILLPFRCCRRPRDPEVNDDESSLVRHRWK 518
DB 481 ALLVLIVLILLPFRCCRRPRDPEVNDDESSLVRHRWK 518

RESULT 9
US-10-175-737-72
; Sequence 72, Application US/10175737
; Publication No. US20030013153A1

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-72

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPBLAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
DB 1 MGALARALLPLLAQWLLRAAPBLAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAVNDLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAVNDLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTRSKGFDVTVKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDTERSSSTRSKGFDVTVKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
DB 181 FESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
DB 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDSGTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFAASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIWIYSYALMSVCG 480
DB 421 RAQKRVGFAASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIWIYSYALMSVCG 480
QY 481 ALLVLIVLILLPFRCCRRPRDPEVNDDESSLVRHRWK 518
DB 481 ALLVLIVLILLPFRCCRRPRDPEVNDDESSLVRHRWK 518

RESULT 10
US-10-173-706-72
; Sequence 72, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173, 706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-72

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGAANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQIILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGAANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQIILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTGFGEDLVITPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTGFGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFEDSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFEDSLVTQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIILKLEIGGOSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIIFD 420
QY 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIILWISYALMSVCG 480
Db 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIILWISYALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSLVRRHWK 518
Db 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSLVRRHWK 518

RESULT 11
US-10-175-738-72
; Sequence 72, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175, 738
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-72

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGAANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQIILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGAANFLAMVDNLQDSDGRGYLLEMLIGTPPKLQIILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTGFGEDLVITPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTGFGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFEDSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFEDSLVTQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIILKLEIGGOSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWYTPIKEWYQIILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVPDAVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYIIFD 420
QY 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIILWISYALMSVCG 480
Db 421 RAQKRVGFPAASPCAIEIAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIILWISYALMSVCG 480
QY 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSLVRRHWK 518
Db 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSLVRRHWK 518

RESULT 12
US-10-175-752-72
; Sequence 72, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria

```
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION: US/10/175,752
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-72
```

```
Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
OY 61 ALALEPALASPAGANFLAVNDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAVNDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
OY 121 TPHSYIDTYFDTERSSSTRYSKGFDTVKYTGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTRYSKGFDTVKYTGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
OY 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
OY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
OY 301 IVDSGTTLLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
OY 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYECYRFGISPTNALVIGATWEGFYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYECYRFGISPTNALVIGATWEGFYVIFD 420
OY 421 RAQKRVGFAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
OY 481 ALLLVILVLLLPFRCCRRPRDPEVNVDESSLVRHRWK 518
Db 481 ALLLVILVLLLPFRCCRRPRDPEVNVDESSLVRHRWK 518
```

```
RESULT 13
US-10-176-482-72
; Sequence 72, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION: US/10/176,482
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-72
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```
Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
OY 61 ALALEPALASPAGANFLAVNDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAVNDNLQDSDGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120
OY 121 TPHSYIDTYFDTERSSSTRYSKGFDTVKYTGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSSTRYSKGFDTVKYTGSGWTGFGVEDLVTIPKGFNTSFLVNIATI 180
OY 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQMGAGLPVA 240
OY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPPIKEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
OY 301 IVDSGTTLLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
OY 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYECYRFGISPTNALVIGATWEGFYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYECYRFGISPTNALVIGATWEGFYVIFD 420
OY 421 RAQKRVGFAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
OY 481 ALLLVILVLLLPFRCCRRPRDPEVNVDESSLVRHRWK 518
Db 481 ALLLVILVLLLPFRCCRRPRDPEVNVDESSLVRHRWK 518
```

```
RESULT 14
US-10-176-757-72
; Sequence 72, Application US/10176757
; Publication No. US20030022297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C86
```

```

; CURRENT APPLICATION NUMBER: US/10/176,757
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-176-757-72

```

Query Match	100.0%;	Score 2687;	DB 9;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 2.3e-217;		
Matches 518;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MGALARALLPLLAQWLLRAPELAPAPFTLLPLRVAATNRVVAFTPGPGTPAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAPELAPAPFTLLPLRVAATNRVVAFTPGPGTPAERHADGL	60
QY	61	ALALEPALASPAGAANFLAMVDNLQDGGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAANFLAMVDNLQDGGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG	120
QY	121	TPHSYIDTYEDTERSSTYRSKGFDVTXKYTOGSWTGFGVEDLVTI PKGNTSFLVNIATI	180
Db	121	TPHSYIDTYEDTERSSTYRSKGFDVTXKYTOGSWTGFGVEDLVTI PKGNTSFLVNIATI	180
QY	181	FESENEFLPGIKWNGIIGLAYATLAKPSSLETFEFDLSVLTQANI PNVSFMOGAGLPVA	240
Db	181	FESENEFLPGIKWNGIIGLAYATLAKPSSLETFEFDLSVLTQANI PNVSFMOGAGLPVA	240
QY	241	GSGTNGGSLVLGGIEPSLYKGDIMWTPIKEWYYOIEILKLEIGGQSLNLDCREYNADKA	300
Db	241	GSGTNGGSLVLGGIEPSLYKGDIMWTPIKEWYYOIEILKLEIGGQSLNLDCREYNADKA	300
QY	301	IYDGGTLLRLPQKVFDVAVEAVARASLIPERSDGFWTGSQLAQWNTNSETPWSYEPKISI	360
Db	301	IYDGGTLLRLPQKVFDVAVEAVARASLIPERSDGFWTGSQLAQWNTNSETPWSYEPKISI	360
QY	361	YLRDENSRSFRITILPQLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIIFD	420
Db	361	YLRDENSRSFRITILPQLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIIFD	420
QY	421	RAQKRVGFPAASPCAEIAGAAYSEISGPFSTEDVASNCPVPAQSLSEPIIWIYSYALMSVCG	480
Db	421	RAQKRVGFPAASPCAEIAGAAYSEISGPFSTEDVASNCPVPAQSLSEPIIWIYSYALMSVCG	480
QY	481	ALLVLIVLLLLPFCORRPRDPEVNVNDESSLVRHRWK	518
Db	481	ALLVLIVLLLLPFCORRPRDPEVNVNDESSLVRHRWK	518

```

RESULT 15
US-10-176-913-72
; Sequence 72, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C66
; CURRENT APPLICATION NUMBER: US/10/176,913
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file Wrapper or Palm

```

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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-176-913-72

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Query Match	100.0%;	Score 2687;	DB 9;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 2.3e-217;		
Matches 518;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MGALARALLPBLAQMWLLRRAPELAPAPFTLPRLVAAATNRVAAPTBPGETPAEHNADGL	60
Db	1	MGALARALLPBLAQMWLLRRAPELAPAPFTLPRLVAAATNRVAAPTBPGETPAEHNADGL	60
QY	61	ALALEPALASPAGANFLAMVDNIQGDSGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGANFLAMVDNIQDSDRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG	120
QY	121	TPHSYIDTYEPDTERSSSTYRSKGFDTVTKYTQGSWTGFVEDLVTI PKGFNTSFLVINIATI	180
Db	121	TPHSYIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVEDLVTI PKGFNTSFLVINIATI	180
QY	181	FESENFPLPGIKMNGILGLAYATLAKPSSSLETFFDLSLTVOANI PNVSFOMCGAGLPVA	240
Db	181	FESENFPLPGIKMNGILGLAYATLAKPSSSLETFFDLSLTVOANI PNVSFMQMGAGLPVA	240
QY	241	GSGTNGSLVLGGIEPSLYKGDIMWTPIKEEMYYYQIBLKLEIGQSINLDCREYNADKA	300
Db	241	GSGTNGSGLVGIEPSLYKGDIMWTPIKEEMYYYQIELKLEIGQSINLDCREYNADKA	300
QY	301	IVDSGTTLLRLPOKVFDVAVEAVARASLIPEFSDFGFWTSQLACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPOKVFDVAVEAVARASLIPEFSDFGFWTSQLACWTNSETPWSYFPKISI	360
QY	361	YLRDENSRSFRITILLPOLYIQPMWGAGLNVECYRFGISPTSNALVIGATVMEGFYIFD	420
Db	361	YLRDENSRSFRITILLPOLYIQPMWGAGLNVECYRFGISPSTNALVIGATVMEGFYIFD	420
QY	421	PAQRVGFAPAAPCAEIAGAAVSEISGPSTEDVASNCVPPOSISEPILWIVSYALMSVCG	480
Db	421	PAQRVGFAPAAPCAEIAGAAVSEISGPFSTEDVASNCVPPOSISEPILWIVSYALMSVCG	480
QY	481	AILLVLLVLLLIPFCQRRPRDPDEVVNDESSLVRHRWK	518
Db	481	AILLVLLVLLLIPFCQRRPRDPDEVVNDESSLVRHRWK	518

Search completed: April 1, 2003, 11:42:39
Job time : 40 secs

GenCore version 5.1.4_p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:31:03 ; Search time 21 Seconds
(without alignments)
2371.316 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALRALLLPLLAQWLRA.....RPRDPEVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178.5	43.9	501	2 A59090	aspartic proteinase
2	367.5	13.7	383	2 JC7573	pepsinogen C - Afr
3	363.5	13.5	377	1 PEMQCCJ	gastricsin (EC 3.4
4	355.5	13.2	384	2 A39314	gastricsin (EC 3.4
5	355	13.2	389	2 JE0371	pepsin C (EC 3.4.2
6	353	13.1	388	2 A29937	gastricsin (EC 3.4
7	351.5	13.1	388	2 JC7246	pepsinogen C - com
8	324.5	12.1	394	2 B43356	gastricsin (EC 3.4
9	320	11.9	385	2 JC7575	pepsinogen A - bul
10	320	11.9	402	1 REMSK	renin (EC 3.4.23.1
11	313.5	11.7	509	2 S66516	oryzasin (EC 3.4.2
12	313	11.6	392	1 A24608	gastricsin (EC 3.4
13	310	11.5	383	2 A41443	pepsin (EC 3.4.23.
14	308.5	11.5	412	1 KHHUD	cathepsin D (EC 3.
15	306.5	11.4	410	1 KHMDS	cathepsin D (EC 3.
16	305.5	11.4	401	1 REMSS	renin (EC 3.4.23.1
17	305	11.4	384	2 JC7574	pepsinogen A - Afr
18	305	11.4	407	1 KHRTD	cathepsin D (EC 3.
19	302	11.2	405	2 A25379	saccharopepsin (EC
20	301.5	11.2	398	2 S66465	cathepsin E (EC 3.
21	300.5	11.2	387	2 C38302	pepsin (EC 3.4.23.
22	299	11.1	398	2 I51185	cathepsin D (EC 3.
23	298.5	11.1	387	2 D38302	pepsin (EC 3.4.23.
24	298.5	11.1	400	2 I47099	renin (EC 3.4.23.1
25	297	11.1	388	1 PEHU	pepsin A (EC 3.4.2
26	296	11.0	388	2 A30142	pepsin A (EC 3.4.2
27	296	11.0	388	2 B30142	pepsin A (EC 3.4.2
28	294.5	11.0	388	1 S19684	pepsin A (EC 3.4.2
29	292	10.9	506	2 T07915	probable aspartic

30	291	10.8	388	1 S19682	pepsin A (EC 3.4.2
31	291	10.8	402	1 REBTK	renin (EC 3.4.23.1
32	291	10.8	406	1 REHUK	renin (EC 3.4.23.1
33	290.5	10.8	396	2 S36865	cathepsin E (EC 3.
34	289	10.8	387	2 E38302	pepsin (EC 3.4.23.
35	288	10.7	387	2 B38302	pepsin (EC 3.4.23.
36	288	10.7	388	1 PEMQAJ	pepsin A (EC 3.4.2
37	287.5	10.7	632	2 T45858	hypothetical prote
38	287	10.7	391	2 A43356	cathepsin E (EC 3.
39	287	10.7	396	2 A34401	cathepsin E (EC 3.
40	286.5	10.7	334	2 JC4870	pepsin A (EC 3.4.2
41	286	10.6	382	1 PECH	pepsin A (EC 3.4.2
42	286	10.6	388	1 PEMQAR	pepsin A (EC 3.4.2
43	285.5	10.6	387	2 JC7245	pepsinogen A - com
44	285	10.6	396	2 T47207	aspartic proteinase
45	284.5	10.6	386	1 PEPG	pepsin A (EC 3.4.2

ALIGNMENTS

RESULT 1									
A59090									
aspartic proteinase (EC 3.4.23.-) BACE precursor - human									
N;Alternate names: beta-secretase; beta-site APP cleaving enzyme									
C;Species: Homo sapiens (man)									
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000									
C;Accession: A59090									
R;Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Teplow, M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Roga Science 286, 735-741, 1999									
A;Title: Beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transm F;46-501/Product: acid proteinase BACE #status predicted <PRO>									
F;461-477/Domains: transmembrane #status predicted <TRN>									
F;93,289/Active site: Asp #status predicted									
F;153,172,223,354/Binding site: carboxylate (Asn) (covalent) #status predicted									
F;330-380/Disulfide bonds: #status predicted									
A;Accession: A59090									
A;Status: not compared with conceptual translation									
A;Molecule type: mRNA									
A;Residues: 1-501 <VAS>									
A;Cross-references: GB:AF190725; NID:g6118538; PIDN:AAF04142.1; PID:g6118539									
C;Genetics:									
A;Gene: BACE									
C;Superfamily: beta-secretase									
C;Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; p F;1-21/Domains: signal sequence #status predicted <SIG>									
F;22-45/Domains: propeptide #status predicted <PRO>									
F;46-501/Product: acid proteinase BACE #status predicted <MAT>									
F;461-477/Domains: transmembrane #status predicted <TRN>									
F;93,289/Active site: Asp #status predicted									
F;153,172,223,354/Binding site: carboxylate (Asn) (covalent) #status predicted									
F;330-380/Disulfide bonds: #status predicted									
Query Match									
Best Local Similarity 43.9%; Score 1178.5; DB 2; Length 501;									
Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;									
QY	7	ALLPLLAQWLRAPELAPFT-----LPLRVAAATNRVVAPTPGPTPAERHADGLA	61						
Db	2	AQALPWLMM---GAGVPAHGTGHRPLRSGLC-----GAPL-----GLR	42						
QY	62	LALF--PALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLIQILVDTGSSNFAVA	119						
Db	43	LPRETDEEPEEPGRGRGSFVEMVDNLRGKSGGYVEMTVGSPQTLNILDVTSNFAVG	102						
QY	120	GTPHSYIDTYFDTERSSITYRSKGFVDVTVKYTGSGWTFVGEDLVTPKGFNTSFLVNIAT	179						
Db	103	AAPHPLHRYRQRLSSTYRDLRKGVVVPYTGKWEGLGTDLVSIPIHGPNTVRANIAA	162						
QY	180	IFESSENFLLPGIKWNGILGAYATLAKPSSSLTFPDSLVTQANIPIVFSMQGAGLPV	239						
Db	163	ITESDKFINGSNWEGILGAYAEIARPDSDLPEPDSLVKQTHVPLFSLQCGAGFPL	222						
QY	240	AGS---GTNGSLVVGTEPSLYKGDWYTPPIKEWYYQIEILKEIGGSLNDCREYN	296						

Db 223 NQSEVLASVGSGSMIIGIDHSLYTGSLWYTPIRREWYEVIIIVREINGODLKMDCKEYN 282

QY 297 ADKAIVDSGTTLRLPQKVFDAVVAVARASLIPEFSDGFMTGSOLACWTNSETPWSYFP 356

Db 283 YDKSIVDSGTNLRLPKVFEEAAVKSIIKAASSTEKEFPDGFMLGEOVCWQAGTTPWNIFFP 342

QY 357 KISITLRDENSRSFRITILPOLYIQPMGAGLNY-ECYRFGISPDSTNALVIGATVMEGF 415

Db 343 VISLYLMGEVTNQSFRTITLPQOYLREVEDVATSQDDCYKFAISQSSGTVMGAVIMEGF 402

QY 416 YVIFPRAOKRVGFAPASPCAEIAGAVERSEISGFPESTEDVASNCVPAQSLSEPILMVSYAL 475

Db 403 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTESTLMTIAYVM 462

QY 476 MSVCGAILLVLLVLLLPFRCCQR-RPRDPEVNDDESSL 512

Db 463 AAIC-ALFMPLPLCLMVCQWRCLRCLROQHDDEADISLL 500

RESULT 2

JC7573

pepsinogen C - African clawed frog

N/Alternate names: progastriecin

C/Species: Xenopus laevis (African clawed frog)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001

C/Accession: JC7573; PC7118

R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.

J. Biochem. 129, 147-153, 2001

A/Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens

A/Reference number: JC7573; MUID:21064922; PMID:11134969

A/Contents: Stomach

A/Accession: JC7573

A/Molecule type: mRNA

A/Residues: 1-383 <IKU>

A/Cross-references: DDBJ:AB045379

A/Accession: PC7118

A/Molecule type: protein

A/Residues: 17-68 <IK2>

C/Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like a

C/Genetics:

A/Gene: Pgc

C/Superfamily: pepsin

C/Keywords: stomach; zymogen

Query Match 13.7%; Score 367.5; DB 2; Length 383;

Best Local Similarity 28.9%; Pred. No. 8.7e-20;

Matches 132; Conservative 70; Mismatches 154; Indels 101; Gaps 25;

QY 1 MGALARALLPLLAQWLIRAPELAPFPTPLRVAATNRVAPTPGPGTPABRHADGL 60

Db 1 MKFLILALVCIQISEGIR-----VPLKFRKSMREVMRENGIKAPLVDPAT--KYVMQY 52

QY 61 ALALEPALASPAGANFLAMVDNLQDGSGRGYLLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Db 53 ATAYEP-----LSNYMDM-----SYGGEISIGTPPQNFLVLPDGTGSSNLWVAS 95

QY 121 TPHSYIDT-----YFDTERSSYRSKGFDTYVKYTOGSWTGFVGEDLVTIKGFNTSF 173

Db 96 T---YCQSQACTNHPLFNPSQSSTYSSNQQFSLOYGTGSLTGILGYDVTIQ----- 145

QY 174 LVNIATIFESENFPL-----PG-----IKWNGILGLAYATLAKPSSSLETFPDSLVTQANI 224

Db 146 --NVA--ISQGEFGLSETEPGTNFVYAQFDGILGLAYPSIAVGAT--TVMQGM--QQNL 198

QY 225 PN--VFSMQMCGAGLPVAGSGTNGSLVLGIEPSLYKGDWYTPIKEWYQIEILKLE 282

Db 199 LNQPIFGFYLSGQ-----SSQNGGEVAFGGVDQNYTGTQIYWTPTSETYQWQIGIGFS 252

QY 283 IGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFDAVVAVARASLIPERSDGFMTGSOL 342

Db 253 INGQATGW-CSQ--GCQAIVDGTSLTAPQSVFSSLIQSIG-----AQQDQNGQYV 301

QY 343 ACWTNSETPWSYFPKISITLYLRDENSRSFRITILPOLYI-QPMGAGLNYECYRFGIS-- 399

Db 302 VSGSNIQN-----LPTISFTI-----SGVSFPLP--PSAYVLQOSSG-----YC-TIGIMPT 345

QY 400 --PSTNA---LVIGATVMEGFYVIFDRAQKRVGFAS 431

Db 346 YLPSQNGQPLWILGDVFLREYYSVYDLGNNGVGFATA 382

RESULT 3

PEMOCJ

gastricisin (EC 3.4.23.3) precursor - Japanese macaque (fragment)

N/Alternate names: pepsin C

C/Species: Macaca fuscata (Japanese macaque)

C/Date: 13-Aug-1986 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999

C/Accession: S19683; A00986; A22402; S16066

R;Kageyama, T.; Tanabe, K.; Koiwai, O.

Eur. J. Biochem. 202, 205-215, 1991

A/Title: Development-dependent expression of isozymogens of monkey pepsinogens and stru

A/Reference number: S19681; MUID:92037645; PMID:1935977

A/Accession: S19683

A/Molecule type: mRNA

A/Residues: 1-377 <KAG>

A/Cross-references: EMBL:X59754; NID:g38072; PIDN:CAA42426.1; PID:g38073

R;Kageyama, T.; Takahashi, K.

J. Biol. Chem. 261, 4406-4419, 1986

A/Title: The complete amino acid sequence of monkey progastriecin.

A/Reference number: A00986; MUID:86168133; PMID:3514597

A/Accession: A00986

A/Molecule type: protein

A/Residues: 6-330,'V',332-349,'VY',350-377 <KA2>

R;Kageyama, T.; Takahashi, K.

J. Biochem. 97, 1235-1246, 1985

A/Title: Monkey pepsinogens and pepsins. VII. Analysis of the activation process and de

pepsinogens.

A/Reference number: A22402; MUID:85289106; PMID:3928607

A/Accession: A22402

A/Molecule type: protein

A/Residues: 6-65 <KA3>

C/Comment: This enzyme has more restricted specificity than pepsin A.

C/Comment: The enzyme is activated in a two-step process that gives rise to two end pro.

C/Superfamily: pepsin

C/Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach

F;1-5/Domain: signal sequence (fragment) #status predicted <SIG>

F;6-377/Product: progastriecin #status experimental <ZYM>

F;6-45/Domain: activation peptide #status experimental <APT>

F;46-377/Product: Gly-gastricisin #status experimental <MIN>

F;49-377/Product: Ser-gastricisin #status experimental <MAT>

F;31-32/Cleavage site: Phe-Leu (pepsin) #status experimental

F;45-46/Cleavage site: Phe-Gly (pepsin) #status experimental

F;48-49/Cleavage site: Leu-Ser (pepsin) #status experimental

F;80,265/Active site: Asp #status predicted

F;93-98,256-260,299-332/Disulfide bonds: #status experimental

Query Match 13.5%; Score 363.5; DB 1; Length 377;

Best Local Similarity 28.9%; Pred. No. 1.7e-19;

Matches 118; Conservative 65; Mismatches 118; Indels 107; Gaps 19;

QY 56 HADGLALALEPALASPAGANFLAMVDNLQDGSGRGYLLEMLIGTPPQKLQILVDTGSSN 115

Db 44 HFGDLVSYPEP-----MAYMD-----AAVFGELISIGTPPQNFLVLPDGTGSSN 85

QY 116 FAV-----AGTPHSYIDTYFPDTERSSYRSKGFDTYVKYTOGSWTGFVGEDLVTIK 167

Db 86 LWPVSVYQCQSQACTSHS---RPNPSESSYSTSTNGQTFSLQYSGSGLTGFFGYDTLTV-- 139

QY 168 GFNTSFLVNIATIFESENFPLPG-----IKWNGILGLAYATLAKPSSSLETFPDSLVTQA 222

Db 140 --QSIQVBNQEFGLSEN--EPGTNFVYAQFDGIMGLAYPTLSVDGAT--TAMQGMVQEG 192

QY 223 NIPN-VFSMQMCGAGLPVAGSGTNGSLVLGIEPSLYKGDWYTPIKEWYQIEILKL 281

Db 193 ALTSPIFSVYLSDQ-----QGSSGGAVVGVGVDSSLYTGTQIYWAPVTQELYWQIGIEEF 246

QY 282 EIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQ 341
Db 247 LIGGQASGW-CSE--GCQAIVDGTGTSLLTPQQYMSALLQA-----TGAQ 288
QY 342 LACWTNSETPWSYF-----PKISIVLRDENSRSFRITILPOLYIQPMGAGLNY 391
Db 289 -----EDEYGFVLVNCNSIQNLPTLTFII-----NGVEFPLPSSSYI-----LNN 328
QY 392 ECY-RFGISP-----STNALVIGATVMEGFYVIFDRAQKRVGFAAS 431
Db 329 NGYCTVGVETPYLSAQNSQPLMILGDVFLRSYSVYDLNNRVGFPATA 376

RESULT 4
A39314
gastricsin (EC 3.4.23.3) precursor - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 22-Jun-1999
C/Accession: A39314
R/Yakabe, E.; Tanji, M.; Ichinose, M.; Goto, S.; Miki, K.; Kurokawa, K.; Ito, H.; Kageya
J. Biol. Chem. 266, 22436-22443, 1991
A/Title: Purification, characterization, and amino acid sequences of pepsinogens and pep
A/Reference number: A39314; MUID:92042186; PMID:1939266
A/Accession: A39314
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-384 <YAK>
A/Cross-references: GB:M73750; NID:g213687; PIDN:AAA49530.1; PID:g213688
C/Superfamily: pepsin
C/Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 13.2%; Score 355.5; DB 2; Length 384;
Best Local Similarity 26.5%; Pred. No. 6.8e-19;
Matches 120; Conservative 73; Mismatches 136; Indels 123; Gaps 21;
QY 23 ELADAPFTLPRLVAAATNRV-----APTPGPTPAERHADGLALALPALASPAGAN 76
Db 12 QLSGGITKIVPLKKFKSMREVMRDHGIKAPVDPAT--KYNNPATAFEP-----LAN 61
QY 77 FLAVVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGTPHSYIDT-----Y 129
Db 62 YMDM-----SYGGEISIGTPPQNPLVLFDTGSSNLWV---PSTYCQSQACTNHPQ 108
QY 130 FDTERRSSTYRSKGFVDTVKKTQGSWTGFVGEDLVTI PKGFNTSFLVNIAITIFESENFLL 188
Db 109 FNPSSQSSSYSSNQQFSLQYGTGSLTGLGYDVOIQ-----NIA--ISQGFGLS 157
QY 189 ---PG-----IKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPN--VFSMQMGAGLP 238
Db 158 VTEPGTNFVYAQFDGILGLAYPSIAEGCAT--TWMQGM-QQNLINQPLFAFYLSG---- 210
QY 239 VAGSGTNGSLVLGGIEPSLYKDIWYTPIKEWYYQIEILKLEIGQSLNLDCREYNAD 298
Db 211 -QQNSONGGEVAFGGVDQNYSGQIYWTPTSETYWGIGFSSVNGQATGW-CSQ--GC 266
QY 299 KAIVDSGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQ-----LACWTNSET 350
Db 267 QGIYDGTSLTAPQSVFSSLMQSI-----GAQODQNGQYAVSCSNISL 311
QY 351 PWSYFP-----KISIVLRDENS---SRSFRITILPOLYIQPMGAGLNYECYRFGIS 399
Db 312 PTISFTISGVSFPLPSPAYVLQQNSGYCTIGIMPTYLPSQNGQPLW----- 357
QY 400 PSTNALVIGATVMEGFYVIFDRAQKRVGFAAS 431
Db 358 -----ILGDVFLRQYYSVYDLGNNOVGFAAA 383

RESULT 5
JE0371
pepsin C (EC 3.4.23.-) precursor - chicken
N/Alternate names: pepsinogen C
C/Species: Gallus gallus (chicken)

C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C/Accession: JE0371
R/Sakamoto, N.; Saiga, H.; Yasugi, S.
Biochem. Biophys. Res. Commun. 250, 420-424, 1998
A/Title: Analysis of temporal expression pattern and cis-regulatory sequences of chicken
A/Reference number: JE0370; MUID:98440813; PMID:9753645
A/Accession: JE0371
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-389 <SAK>
C/Superfamily: pepsin
C/Keywords: aspartic proteinase; hydrolase

Query Match 13.2%; Score 355; DB 2; Length 389;
Best Local Similarity 28.7%; Pred. No. 7.6e-19;
Matches 114; Conservative 58; Mismatches 121; Indels 104; Gaps 16;
QY 75 ANFLAMVDNLQDSDGRGYLLEMLIGTPPOKLQILVDTGSSNFAVAGT-----PHSYI 126
Db 56 SNFATAVEPLANNMDMSYGEISIGTPQNPLVLFDTGSSNLWVPSTLCQSQACANHN-- 113
QY 127 DTYFDTERSSTYRSKGFVDTVKKTQGSWTGFVGEDLVTI PKGFN-----TS 172
Db 114 --EFDPNESSTFSTQDEFFSLQYSGSLTGIFGPDVTYI-QGISITNQEFGLSETEPGTS 170
QY 173 FLVNIATIFESENFLLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPN--VFSM 230
Db 171 FLYS-----PFDGILGLAFPSI---SAGGATTVMQKMLQENLIDFPVFSF 212
QY 231 QMCGAGLPVAGSGTNGSLVLGGIEPSLYKDIWYTPIKEWYYQIEILKLEIGQSLNL 290
Db 213 YLSGQ-----EGSQGELVFGGVDPNLYTGQITWTPVTQTTWQIGIEDFAVGGQSSGW 266
QY 291 DCREYNADKAIVDSGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQIACWTNSET 350
Db 267 -CSQ--GCQGIYDGTGTSLLTPNQVFTLMQYIG-----AQADD--SGQYVASCNIE- 314
QY 351 PWSYFPKI-----SIYLRDENS---SRSFRITILPOLYIQPMGAGLNYECY 394
Db 315 ---YMTITFVISGTFPPLPSPAYMLQNSNDYCTVGIESTYLPSTQGTQPLW----- 362
QY 395 RFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAAS 431
Db 363 -----ILGDVFLRVYYSIYDMGNNOVGFAATA 388

RESULT 6
A29937
gastricsin (EC 3.4.23.3) precursor - human
N/Alternate names: pepsin C; pepsinogen C
C/Species: Homo sapiens (man)
C/Date: 17-Oct-1988 #sequence_revision 17-Oct-1988 #text_change 31-Mar-2000
C/Accession: A29937; A31811; PX0028; I54213; A91125; A23458
R/Hayano, T.; Sogawa, K.; Ichihara, Y.; Fujii-Kuriyama, Y.; Takahashi, K.
J. Biol. Chem. 263, 1382-1385, 1988
A/Title: Primary structure of human pepsinogen C gene.
A/Reference number: A29937; MUID:88087276; PMID:3335549
A/Accession: A29937
A/Molecule type: DNA
A/Residues: 1-388 <HAY>
R/Taggart, R.T.; Cass, L.G.; Mohandas, T.K.; Derby, P.; Barr, P.J.; Pals, G.; Bell, G.I
J. Biol. Chem. 264, 375-379, 1989
A/Title: Human pepsinogen C (progastricsin). Isolation of cDNA clones, localization to
A/Reference number: A31811; MUID:89079679; PMID:2909526
A/Accession: A31811
A/Molecule type: mRNA
A/Residues: 1-388 <TAG>
A/Cross-references: GB:J04443; NID:g551175; PIDN:AAA60074.1; PID:g551176
R/Athauda, S.B.P.; Tanji, M.; Kageyama, T.; Takahashi, K.
J. Biochem. 106, 920-927, 1989
A/Title: A comparative study on the NH2-terminal amino acid sequences and some other pr
A/Reference number: PX0023; MUID:90130402; PMID:2515193
A/Accession: PX0028

A;Molecule type: protein
A;Residues: 17-101 <ATH>
R;Pats, G.; Azuma, T.; Mohandas, T.K.; Bell, G.I.; Bacon, J.; Samloff, I.M.; Walz, D.A.;
Genomics 4, 137-148, 1989
A;Title: Human pepsinogen C (progastricsin) polymorphism: evidence for a single locus loc
A;Reference number: 154213; MUID:89290840; PMID:2567697.
A;Accession: 154213
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-388 <RES>
A;Cross-references: GB:M23077; NID:g189830; PIDN:AAA60063.1; PID:g387015; GB:J03063
A;Note: parts of this sequence, including the amino end and carboxyl ends of the mature
R;Foltmann, B.; Jensen, A.L.
Eur. J. Biochem. 128, 63-70, 1982
A;Title: Human progastricsin. Analysis of intermediates during activation into gastricsin
A;Reference number: A91125; MUID:83079318; PMID:6816595
A;Accession: A91125
A;Molecule type: Protein
A;Residues: 17-39, 'ED', 42-51, 'S', 53-64 <FOL>
A;Note: pro-form; 29-Leu was also found
A;Note: activation at pH 2 is proposed to involve conformation change, cleavage after Ph
C;Genetics:
A;Gene: GDB:PGC
A;Cross-references: GDB:119485; OMIM:169740
A;Map position: 6p21.3-6p21.1
A;Introns: 20/2; 70/3; 110/1; 149/3; 216/2; 256/2; 305/3; 338/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase; protein digestion; stomach; zymogen
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-59/Domain: propeptide #status experimental <PRO>
F;60-388/Product: gastricsin #status experimental <MAT>

Query Match	13.1%;	Score 353;	DB 2;	Length 388;
Best Local Similarity	29.1%;	Pred. No. 1.1e-18;		
Matches 120;	Conservative 65;	Mismatches 120;	Indels 108;	Gaps 21;

```

Qy      52 PAERHADC-LALALEPALASPAGAAFLAMVDNLQDSGRGYLLEMLIGTPPQKQILVD 110
      || :: | | :: | | | | :: | | | | | | | | | | | | | | | | |
Db      50 PAWKYRFGDLSTYEP-----MAYMD-----AAFYGEISIGTPPQNFLVFD 91

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QY      111 TGSSNFAV-----AGTPHSYIDTYPDETSSTYRSKGEDVTVKYTGSGSWTGEVGEDL 162
        |||||      | ||||      : ||||| : || ||||| ||
Db      92  TGSSNFWPSVYCQSQACTSHS---RFPNSESTYSTNGQTFSLQYGSGLTGFGGYDT 147

```

```
QY      163 VTIPKGFNTSFLVNIAITIFESENFLLPG-----IKWNGILGLAYATLAKPSSSELETFEFD 217
       :|: | | ||| |::||| | |: |
Db      148 LTV-----QSIVPNQOEFGLSEN--EPGTNFFVAQFODGIMGLAYPALSVDEAT--TAMOG 198
```

QY 218 LVTOANIPN-VFSMOMCAGLPVAGSGTNGSLVLGIEPLSYKGDIMWTPRIKEENWYOI 276
: : : : ||| : | : : : | : : : | : : :
Db 199 MVEGALTSPIFVSVLYLSNQ-----QGSSCGAVFGVDSSLTYGTQIYMARPVTDELWYOI 252

```

QY      277 ELKLEIGGOSLNLDCREYNADKAIYDSGTTLLRLPQKVFDAVEAVARASLIPEESDGF 336
      | : ||||: | | : ||||: ||| : ||: | : ||: |
Db      253 GIEEFLLIGGASGM-CSE--GCOAIVDTGTSLTLVPOQYMSALLQA----- 295

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QY      337 WTGSQIACWTNSETPWSYF-----PKISIVLRDENSRSFRITILPOLYIQEMNG 386
      ||:| | : | | : | |
Db      296 -TGAQ-----EDEYGFVNCNSIQNLPSLFRIT-----NGVEFPLPPSSYI----- 336

```

```
QY      387 AGINVECY-RFGISP----STNA---LVIGATWMEGFVIFDRAQRKRVGEFAAS 431
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db     337 --LSNNGYCTGVVEPTLYSSONGQPWLILGDVFRLRSYSVYDLGNRRVGFAATA 387
```

RESULT 7
JC7246
pepsinogen C - common marmoset
C/Species: Callithrix jacchus (common marmoset)
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C/Accession: J07246
R;Kageyama, T.
J. Biochem. 127, 761-770, 2000

A;Title: New world monkey pepsinogens A and C, and prochymosins. Purification, characterisation and properties of the enzymes.
A;Reference number: JC7245
A;Accession: JC7246
A;Molecule type: mRNA
A;Residues: 1-388 <KAG>
A;Cross-references: DDBJ:AB038385
A;Experimental source: strain NW791
C;Comment: This protein, a zymogen of pepsins, is the major proteolytic enzyme in vertebrate stomachs.
C;Superfamily: pepsin
C;Keywords: gastric juice; zymogen

Query Match	13.1%;	Score 351.5;	DB 2;	Length 388;
Best Local Similarity	30.1%;	Pred. No. 1.4e-18;		
Matches 112; Conservative	56;	Mismatches 115;	Indels 89;	Gaps 17;

```

QY      92  YYLEMLIGTPQQLQILVDTGSSNFAV-----AGTPHSYIDTYEDTERESTYRSKGF 143
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      73  YFGEISIGTPPQNFVLVFDTGSSNLWPSVYCQSQACTSHS----RFPNSASTYSSNGQ 128

```

```
QY      144 DVTAKYTQGSWTGTFVGEDLVTPKGFNTSFLVNIAITFESENFFLP-----IKWNGILG 198
        ::| | | | | :| | | | |
Db     129 TFSLTQVSGSLTGFFGYDTLTV-----QSIVPNQOEFGLSEN--EPGTNFVVAQFDGIMG 181
```

```
QY 199 LAYATLAKPSSLETFDFDSLVTQANIPN-VFSMÖMGAGLPVAGSGTNGSLVLCIEPS 257
    ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 182 LAYPALSMGAT--TAMÖGMLÖEGALTSPVFSFYLSNQ-----QGSSGAVIFGGVDSS 233
```

```
QY      258 LYKGDWYTPIKEEWYYOIEILKLEIGOSLNLDCREYNADKAIVDSCTLLRLPQKVED 317
        |||:::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      234 LYTGGIYWAPVTLQELYMQIGIEEFLIGGASGM--GCQAIVDTGTSLLTVPQQYS 290
```

```

QY      318 AVEAEVARSALIPESDGFMTGSQGLACWTNSETPWSYF-----PKISYLRDENS 367
          ||: ||: ||: | : | :
Db      291 AFLEA-----TGAQ-----EDEYGFVNCDSIQNLPTLFTII----- 323

```

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QY      368 SRSFRITILPOLYIQPMGAGLNEYCY-RFGISP-----STNALVIGATVMEGFYVF 419
          . : | | | | : | | | | : | | : | : |
Db      324 -NGVEFPLPPSSYI-----LSNNGCYTVGVEPTYLSSQNSQPLWILGDVFLRSYSVF 375

```

QY 420 DRAQKRVGFAS 431
| | | | :
Db 376 DLGNRRVGFATA 387

RESULT 8
B43356

N;Alternate names: pepsin C
C;Species: *Cavia porcellus* (guinea pig)
C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 22-Jun-1999

R; Kageyama, T.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Koiwai, O.; Tanji, M. J. Biol. Chem. 267, 16450-16459, 1992

A; Title: Gastric procathepsin E and progastricsin from guinea pig. Purification, molecu

A/Accession: B43356
A/Status: preliminary
A/Molecule type: mRNA

A:Cross-references: GB:M88652, NID:g191296; PIDN:AAA37053.1; PID:g191297
A:Note: sequence extracted from NCBI backbone (NCBIN:110805, NCBI:P:110806)
C:Superfamily: pepsin

Query Match	12.1%;	Score 324.5;	DB 2;	length 394;
Best Local Similarity	29.0%;	Pred. No. 1.5e-16;		
Matches 107;	Conservative 63;	Mismatches 116;	Indels 83;	Gaps 18;

```
QY 92 YLLEMLIGTEPQKLQILVDTGSSNF-----AVAGTPHSYIDTYFEDTERSSITYRSKGF 143
|: :: ||||| :| ||||| ::| | | | | : ||||| :
Db 79 YFGQISLGTBPQSFQVLFDTGSSNLWVPYSYCSSLACTTH---TRENPRDSSITYATDQ 134
```


QY 144 DVTVKYTGSGWTGFVGEDLVTI-----PK-GFNTSFLVNIATIFESENFLLPG-----IK 192
Db 135 SFSLEYGTGSLTGVFGYDTMTIQDIQPKQEFGLS-----ETE-----PGSDFVYAE 181
QY 193 WNGILGLAVATLAKPSSSLETFFDSLVTQANI-PNVFSMQMGAGLPVAGS--GTNGSL 249
Db 182 FDGILGLGVPGLSEGGAT--TAMQGLREGALISQSLFSVYL-----GSQGSDEGQL 231
QY 250 VLGIEPSLYKGDIMWYTPIKEWYQIETIKLEIGGOSLNLDCREYNADKAIVDSGTTLL 309
Db 232 ILGGVDESLYTGDIWYTPVTOELYWQIGIEGFLIDGSASGWCSSR--GCQGIWDTGTSL 288
QY 310 RLPOKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITYLRDENS 369
Db 289 TVPSDYLTSLVQAIGAE--NEYGEYF-----VSCSSIQDLPTLTFVISGV----- 332
QY 370 SFRITILPOLYIQP-----MMGAGLNEYCYRFGISPTN--ALVIGATWMEGFYVIFDRA 422
Db 333 --EFPLSPAYILSGENYCMVGLSESTY-----VSPGGGEPPWILGDVFLRSYYSVYDLA 384
QY 423 QKRVGFPAAS 431
Db 385 NNRVGFATA 393

RESULT 9
JC7575
pepsinogen A - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
C;Accession: JC7575
R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.
J. Biochem. 129, 147-153, 2001
A;Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens
A;Reference number: JC7573; MUID:21064922; PMID:11134969
A;Contents: Stomach
A;Accession: JC7575
A;Molecule type: mRNA
A;Residues: 1-385 <IKU>
A;Cross-references: DDBJ:AB045376
C;Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like
A;Genetics:
A;Gene: Pga
C;Superfamily: pepsin
C;Keywords: stomach; zymogen

Query Match 11.9%; Score 320; DB 2; Length 385;
Best Local Similarity 27.8%; Pred. No. 3.1e-16;
Matches 111; Conservative 67; Mismatches 147; Indels 74; Gaps 15;

QY 50 GTPAERRADGLALALEPALASPAGANFLAVDNLQGDSSGRGYLEMLIGTPPOKLOILV 109
Db 39 GDYLKKHHNPATKYFPSLAQASG-----EPLQNYMDIEYFGTISIGTPPOSTVIF 90
QY 110 DTGSSNFAVAGTPHSYIDT-----YFDTERRSSTYRSKGFVTVKYTQGSWTGFVGEDL 162
Db 91 DTGSSNLWV--PSVYCSPACTNHMFNPQOSSTFOATNTPVSIQYGTGSMGFLGYDT 147
QY 163 VTIPKGFNTSFLVNIATIFESE-NPFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQ 221
Db 148 VOVG---NIQITNQIFGLSQSEPGSFLYSPFDGILGLAFLSLA--SSQATPVFDNMNQ 202
QY 222 ANIP-NVFSMQMGAGLPVAGSGTNGSLVLGIEPSLYKGDIMWYTPIKEWYQIETLK 280
Db 203 GLIPDPLFSVYL-----SSQGSQGSFVLFGVDTSYTGNLNWPPLTAETYWQITVDS 255
QY 281 LEIGGOSLNLDCREYNADKAIVDSGTTLLRLPOKVFDAVVEAVARASLIPEFSDGFWTGS 340
Db 256 ISIGGOVIACS---GSCSAIVDTGTSLLAGSPSTPI-ANIQYVIGAN---QDSNGQYV-- 305
QY 341 QLACWTNSETPWSYFP-----KISITYLRDENS--RSFRITILPOLYIQPMGAGLN 390
Db 306 -INCNNISNMPTVVFTEINGVQYPLPASAYVRQSQSCTSGFQAMNLP----- 351

QY 391 YECYREGISPSTNALVIGATWMEGFYVIFDRAQKRVGFA 429
Db 352 -----TSSGDLWILGDVFIREYVVFDRANNYVAMA 382

RESULT 10
REMSK
renin (EC 3.4.23.15) precursor, renal - mouse
N;Alternate names: angiotensin-forming enzyme; angiotensinogenase; renin 1
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
C;Accession: A00989; S07636; A22766; A22058; I57576; A05137; JH0083
R;Holm, I.; Ollio, R.; Panthier, J.J.; Rougeon, F.
EMBO J. 3, 557-562, 1984
A;Title: Evolution of aspartyl proteases by gene duplication: the mouse renin gene is o
A;Reference number: A00989; MUID:84182525; PMID:6370686
A;Accession: A00989
A;Molecule type: DNA
A;Residues: 1-402 <HOL>
A;Cross-references: EMBL:X00850
R;Kim, W.S.; Murakami, K.; Nakayama, K.
Nucleic Acids Res. 17, 9480, 1989
A;Title: Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.
A;Reference number: S07636; MUID:90067953; PMID:2685761
A;Accession: S07636
A;Molecule type: mRNA
A;Residues: 1-402 <KIM>
A;Cross-references: EMBL:X16642; NID:g53930; PIDN:CAA34636.1; PID:g53931
R;Mullins, J.J.; Burt, D.W.; Windass, J.D.; McTurk, P.; George, H.; Brammar, W.J.
EMBO J. 1, 1461-1466, 1982
A;Title: Molecular cloning of two distinct renin genes from the DBA/2 mouse.
A;Reference number: A90968; MUID:84207899; PMID:6327270
A;Accession: A22766
A;Molecule type: mRNA
A;Residues: 269-314, 'D', 316 <MUL>
R;Panthier, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984
A;Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative re
A;Reference number: A22058; MUID:84298161; PMID:6089205
A;Accession: A22058
A;Molecule type: DNA
A;Residues: 1-30 <PAN>
R;Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.
Mol. Cell. Biol. 4, 2321-2331, 1984
A;Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analy
A;Reference number: I57576; MUID:85085936; PMID:6392850
A;Accession: I57576
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <RES>
A;Cross-references: GB:K02800; NID:g200689; PIDN:AAA40044.1; PID:g200690
C;Comment: The only known function of renal renin is to release angiotensin I from angi
creased sodium retention by the kidney.
C;Comment: Renal renin is synthesized by the juxtaglomerular cells of the kidney in res
C;Genetics:
A;Gene: Ren-1
A;Introns: 31/2; 81/3; 123/1; 162/3; 228/2; 268/2; 316/3; 349/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; blood pressure control; glycoprotein; hydrolase; kidne
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-64/Domain: propeptide #status predicted <PRO>
F;65-402/Product: renin #status predicted <MAT>
F;69,139,320/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;102,287/Active site: Asp #status predicted

Query Match 11.9%; Score 320; DB 1; Length 402;
Best Local Similarity 28.6%; Pred. No. 3.3e-16;
Matches 126; Conservative 66; Mismatches 181; Indels 68; Gaps 21;

QY 10 LPLIAQWLIRAAPELADAPFTLPLRVAAATNRVVAPTPG-PGTPAERRHADGLALALE--- 65
Db 6 MPLWALLLL-----WSPCTFSLPTRATFERIPKMPVSVREILEERGVDTRLSAEWGV 60

[illegible]

RESULT 11
S66516

oryzasin (EC 3.4.23.-) precursor - rice
N/Alternate names: aspartic proteinase 1
C/Species: Oryza sativa (rice)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C/Accession: S66516; S66517
R/Asakura, T.; Watanabe, H.; Abe, K.; Arai, S.
Eur. J. Biochem. 232, 77-83, 1995
A/Title: Rice aspartic proteinase, oryzasin, expressed during seed ripening and germinat
A/Reference number: S66516; MUID:96048031; PMID:7556174
A/Accession: S66516
A/Molecule type: DNA
A/Residues: 1-509 <ASA>
A/Cross-references: EMBL:D32165; NID:g511665; PIDN:BAA06876.1; PID:g1030715
A/Accession: S66517
A/Molecule type: mRNA
A/Residues: 1-509 <ASZ>
A/Cross-references: EMBL:D32144; NID:g1255684; PIDN:BAA06875.1; PID:g1711289
C/Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a
C/Genetics:
A;introns: 119/3; 140/1; 171/3; 209/2; 265/3; 279/1; 300/3; 338/3; 360/2; 412/3; 452/3;
C/Superfamily: oryzasin; saposin repeat homology
C/Keywords: aspartic proteinase; hydrolase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-68/Domain: propeptide #status predicted <PRO>
F;68-509/Product: aspartic proteinase 1 #status predicted <MAT>
F;316-361/Domain: saposin repeat homology #status atypical <SAP1>
F;370-420/Domain: saposin repeat homology #status atypical <SAP2>
F;103,290/Active site: Asp #status predicted

Query Match	11.7%;	Score 313.5;	DB 2;	Length 509;
Best Local Similarity	23.0%;	Pred. No. 1.4e-15;		
Matches 127;	Conservative 75;	Mismatches 179;	Indels 171;	Gaps 19;

[illegible]

OY	116	--FAVAGTPHYSIDTYFDTERSSSTYRSKGFVDVTVKYTQGSWTFVGEDLVTI PKGENTSF	173
Db	116	CYFSIACFHS---RYKSGSSTYQKNCKPAIQYGTGSIAGFSSEDSVTVGD-----	165
OY	174	LVNIAITFESENFF---LPGI---KWNGILGLAYATLAKPSSLETFEDSLVTOANI	224
Db	166	----LVVKDQEFIEATKEPGLTFMWAKFDGILGLGFQEIISVGDA-----V	206
OY	225	PNVFSMQMCG-AGLPVAGSGTN-----GSSLVLGGIEPSLYKGDIWYTPIKEWWYQI	276
Db	207	PWMYKWEQGLVSEPVPFSFWENRSHDEGEGERIVFGMDPSHYKHNTYVPVSQKGWQF	266
OY	277	EILKLEIGQSINLDCREYNADKAIVDSGTTLLRLPKQVFDAVVEAVARASLIPE----	331
Db	267	EMGDVLIGKTTGF-CA--SGCSAIAДСГTSLLAGPTAI ITEINEKIGATGVWSQECKTV	323
OY	332	-----FSDGF-----	336
Db	324	VSOYGQQILLDLLLAETQPSKICSQVGLCTFDKGHGVSAGIKSVVDDEAGESENSGLQSGPMC	383
OY	337	-----WTGSQLACWTNSETPMSY-----FPKISIYLRD	364
Db	384	NACEMAVVMQNOLAQNKQTODLINYNQLCDKLPSPMGESSVDCGSLASMPESISFTIGA	443
OY	365	ENSRSFRITILPOLYIQPMMGAGLNIECY---RFGISPTNAL-VIGATWMEGFYIF	419
Db	444	K-----KFALKPEEYIL-KVGEGAALAQICISGFTAMDIPPPRGPLMLGDVFMGAYHTVF	496
OY	420	DRAQKRVGFAAS	431
Db	497	DYGMKRVGFSAKS	508

RESULT 12

gastriecin (EC 3.4.23.3) precursor - rat
N/Alternate names: pepsinogen C
N/Contains: pepsin A (EC 3.4.23.1) precursor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence revision 05-Aug-1994 #text_change 18-Jun-1999
C/Accession: A33510; A24608; C22434; A05145; A61298
R/ishihara, T.; Ichihara, Y.; Hayano, T.; Katsura, I.; Sogawa, K.; Fujii-Kuriyama, Y.;
J. Biol. Chem. 264, 10193-10199, 1989
J/Title: Primary structure and transcriptional regulation of rat pepsinogen C gene.
A/Reference number: A33510; MUID:89255508; PMID:2722863
A/Accession: A33510
A/Molecule type: DNA
A/Residues: 1-392 <ISH>
A/Cross-references: GB:M25985
R/ichihara, Y.; Sogawa, K.; Morohashi, K.; Fujii-Kuriyama, Y.; Takahashi, K.
Eur. J. Biochem. 161, 7-12, 1986
A/Title: Nucleotide sequence of a nearly full-length cDNA coding for pepsinogen of rat
A/Reference number: A24608; MUID:87054020; PMID:3780741
A/Accession: A24608
A/Molecule type: mRNA
A/Residues: 1-392 <ICH>
A/Cross-references: GB:X04644; NID:g56880; PIDN:CAA28305.1; PID:g56881
R/ichihara, Y.; Sogawa, K.; Takahashi, K.
J. Biochem. 98, 483-492, 1985
A/Title: Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, and
A/Reference number: A22434; MUID:86059312; PMID:2415509
A/Accession: C22434
A/Molecule type: protein
A/Residues: 1-19, 'X', 21-23, 'X', 25-29 <IC2>
R/Arai, K.M.; Muto, N.; Tani, S.; Akahane, K.
Biochim. Biophys. Acta 788, 256-261, 1984
A/Title: The N-terminal sequence of rat pepsinogen.
A/Reference number: A05145; MUID:84257697; PMID:6743670
A/Accession: A05145
A/Molecule type: protein
A/Residues: 17-30, 'Q', 32-102, 'A', 104-108, 'L', 110-112 <ARA>
A/Experimental source: Wistar strain
R/ichihara, Y.; Sogawa, K.; Takahashi, K.

J. Biochem. 92, 603-606, 1982
A/Title: Rat gastric prepepsinogen: in vitro synthesis and partial amino-terminal signal
A/Reference number: A61298; MUID:83030750; PMID:6182139
A/Accession: A61298
A/Molecule type: protein
A/Residues: 1,'XX',4-6,'X',8-9,'X',11,'X',13-14,'XXX',18-19,'X',21,'X',23,'XX',26,'X' <I
C/Comment: This enzyme has more restricted specificity than pepsin A. It is the major fo
C/Genetics:
A/Introns: 20/2; 73/3; 113/1; 152/3; 219/2; 259/2; 309/3; 342/3
A/Note: there are at least two very similar genes for gastricsin in rat
C/Superfamily: Pepsin
C/Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach
F/1-16/Domain: signal sequence #status experimental <SIG>
F/17-392/Product: pepsinogen #status experimental <MAT>
F/17-62/Domain: activation peptide #status experimental <ACT>
F/94,280/Active site: Asp #status predicted
F/107-112,270-275,314-347/Disulfide bonds: #status predicted

Query Match 11.6%; Score 313; DB 1; Length 392;
Best Local Similarity 29.5%; Pred. No. 1.1e-15;
Matches 105; Conservative 56; Mismatches 139; Indels 56; Gaps 16;

QY 92 VYLEMLIGTPPOKLQILVDTGSSNPAY-----AGTPHSYIDTYFDTERSSTYRSKGF 143
Db 76 YFGEISIGTPPOQNFVLVFDTGSSNLWSSVYCQSEACTTHA---RFNPSKSTYYTEGQ 131
QY 144 DVTVKXYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFLPG-----IKWNGILG 198
Db 132 TFSLQYGTGSLTGFGYDTLTV-----QSIQVPNQEFGLSEN--EFGTNFVYAQFDGIMG 184
QY 199 LAVATLAKPSSSLETFFDSLVTQANIPNVFSMQMGAGLPVAGS--GTNGSLVLGIEP 256
Db 185 LAVPGLS--SGGATTALQGMGE-----GALSQPLFGVYL---GSQGSNGGQIVFGGVDK 235
QY 257 SLVKGDIMWTPRIKEWYQIEILKLEIGQSLLNDCREYNADKAIVDSGTTLRLPQKVF 316
Db 236 NLTYGEITWVPVTOELYWQITIDDFLIGDQASGW-CSSQGC-QGIVDTGTSLLVMPAQYL 293
QY 317 DAVVEAVARASLIPEFSDGFMTGSQIACWTNSETPWSYFPKISIVLRDENSRSFRITIL 376
Db 294 SELIQITGAQE--GEYGEYF-----VSCDSVSS-----LPTLSFVL-----NGVQFPLS 335
QY 377 POLY-IQPMWGAGLNEYCYRFGISPSSTNALVIGATWMEGFYVIFDRAQKRVGFAAS 431
Db 336 PSSYIIQEDNFCMVGLEISILTSESGQPLWILGDVFLRSYVAIFDMGNKKVGLATS 391

RESULT 13
A41443
pepsin (EC 3.4.23.-) precursor, embryonic - chicken
C/Species: Gallus gallus (chicken)
C/Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 21-Jul-2000
C/Accession: A41443
R/Hayashi, K.; Agata, K.; Mochii, M.; Yasugi, S.; Eguchi, G.; Mizuno, T.
J. Biochem. 103, 290-296, 1988
A/Title: Molecular cloning and the nucleotide sequence of cDNA for embryonic chicken pep
A/Reference number: A41443; MUID:88227903; PMID:3131317
A/Accession: A41443
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-383 <HAY>
A/Cross-references: GB:D00215; NID:g2760810; PIDN:BAA00153.1; PID:g222853
C/Superfamily: pepsin
C/Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 11.5%; Score 310; DB 2; Length 383;
Best Local Similarity 26.8%; Pred. No. 1.7e-15;
Matches 106; Conservative 63; Mismatches 136; Indels 90; Gaps 15;

QY 56 HA--DGLALALEPALASPAGANFLAWDNLQGDSDGRGYLEMLIGTPPOKLQILVDTGS 113
Db 55 HAFPDVLTVTEPLT-----NTLDM-----EYVGTISIGTPPOQDFTVVDTS 97

QY 114 SNFAVAG-----TPHSYIDTYFDTERSSTYRSKGFDTVVKYTOGSWTGFVGEDLVTPKGF 169
Db 98 SNLWTVSVSCTSPACQSHQMFNPQSOSTYKSTGQNLSTHYGTGDMEGTVGCDTVTVASLM 157
QY 170 NTSFLVNIATIFESENFFLPGLKWNIGLGLAYATLAKPSSSLETFFDSLVTQANI-PNVF 228
Db 158 DTMQFLGLST-SEPGQFV-YKFDGILGLYPSLA--ADGITPVFDNMVNESLLEQNLF 213
QY 229 SMOGAGLPVAGSGTNGSLVLGIEPSLYKGDIMWTPRIKEWYQIEILKLEIGQSL 288
Db 214 SVYLSREPM-----GSMVVFGEIDESYFTGSINWIPVSYQGYWQISMSDIIVNKQEI 265
QY 289 NLDCREYNADKAIIVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQIACWTNS 348
Db 266 ACS-----SGCAIIDTGTSLVAGPASPDIINDIQSAVG-----ANQ 300
QY 349 ETPWSYFPKISIVLRDENSRSFRITILPOLYIQPMWGAGLNY-----ECY 394
Db 301 NTYGEY-----SVNCSHILAMPDVVF--VIG-GIQYPVPALAYTEQNGQGTGM 345
QY 395 RFGISPSSTNALVIGATWMEGFYVIFDRAQKRVGFA 429
Db 346 SSFQNSSADLWILGDVFIRVYYSIFDRANRVGLA 380

RESULT 14
KHHUD
cathepsin D (EC 3.4.23.5) precursor [validated] - human
N/Alternate names: preprocathepsin D
C/Species: Homo sapiens (man)
C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 15-Sep-2000
C/Accession: A25771; S30749; PC2066; I59236; I57716
R/Faust, P.L.; Kornfeld, S.; Chirgwin, J.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 4910-4914, 1985
A/Title: Cloning and sequence analysis of cDNA for human cathepsin D.
A/Reference number: A25771; MUID:85270436; PMID:3927292
A/Accession: A25771
A/Molecule type: mRNA
A/Residues: 1-412 <FAU>
A/Cross-references: EMBL:M11233; NID:g181179; PIDN:AAB59529.1; PID:g181180
R/Westley, B.R.; May, F.E.B.
Nucleic Acids Res. 15, 3773-3786, 1987
A/Title: Oestrogen regulates cathepsin D mRNA levels in oestrogen responsive human brea
A/Reference number: S30749; MUID:87231068; PMID:3588310
A/Accession: S30749
A/Molecule type: mRNA
A/Residues: 1-412 <WES>
A/Cross-references: EMBL:X05344; NID:g29677; PIDN:CAA28955.1; PID:g29678
R/May, F.E.B.; Smith, D.J.; Westley, B.R.
Gene 134, 277-282, 1993
A/Title: The human cathepsin D-encoding gene is transcribed from an estrogen-regulated
A/Reference number: PC2066; MUID:94085791; PMID:8262386
A/Accession: PC2066
A/Molecule type: DNA
A/Residues: 1-23 <MAY>
A/Cross-references: GB:LI2980; NID:g291930; PIDN:AAA16314.1; PID:g455429
A/Experimental source: MCF-7 cell
R/Cavaillès, V.; Augereau, P.; Rochefort, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 203-207, 1993
A/Title: Cathepsin D gene is controlled by a mixed promoter, and estrogens stimulate on
A/Reference number: I59236; MUID:93126342; PMID:8419924
A/Accession: I59236
A/Status: translation not shown; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-22 <CAV1>
A/Cross-references: GB:S52557; NID:g263124; PIDN:AAD13868.1; PID:g4261568
R/Augereau, P.; Miralles, F.; Cavaillès, V.; Gaudelet, C.; Parker, M.; Rochefort, H.
Mol. Endocrinol. 8, 693-703, 1994
A/Title: Characterization of the proximal estrogen-responsive element of human cathepsi
A/Reference number: I57716; MUID:95021301; PMID:7935485
A/Accession: I57716
A/Status: translation not shown; translated from GB/EMBL/DBJ
A/Molecule type: DNA

A;Residues: 1-22 <CAV2>
 A;Cross-references: GB:S74689; NID:g786350; PIDN:AAD14156.1; PID:g4261856
 R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Erickson, J.W.
 submitted to the Brookhaven Protein Data Bank, April 1993
 A;Reference number: A51839; PDB:1LYA
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 65-161;170-241
 R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Erickson, J.W.
 submitted to the Brookhaven Protein Data Bank, April 1993
 A;Reference number: A51840; PDB:1LYB
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms, with inhibitor residues 65-161;170-241
 R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Hosur, M.V.; Sowder II, R.C.; Cachau, R.E.; Col
 Proc. Natl. Acad. Sci. U.S.A. 90, 6796-6800, 1993
 A;Title: Crystal structures of native and inhibited forms of human cathepsin D: implicat
 A;Reference number: A48229; MUID:93342076; PMID:8393577
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms
 C;Comment: Cathepsin D is a ubiquitous lysosomal proteinase.
 C;Comment: In addition to the propeptide, residues 163-168 and 411-412 are proteolytical
 C;Comment: The carbohydrate bound to 134-Asn contains a mannose-6-phosphate that is boun
 C;Genetics:
 A;Gene: GDB:CTSD
 A;Cross-references: GDB:120512; OMIM:116840
 A;Map position: 11p15.5-11p15.5
 C;Function:
 A;Description: limited specificity endopeptidase
 A;Pathway: intracellular protein degradation
 C;Superfamily: pepsin
 C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-64/Domain: propeptide #status predicted <PRO>
 F;65-162,169-410/Product: cathepsin D #status experimental <MAT>
 F;267,329-356/Region: phosphotransferase recognition
 F;91-160,110-117,286-290,329-366/Disulfide bonds: #status experimental
 F;97,295/Active site: Asp #status experimental
 F;134,263/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match	11.5%;	Score 308.5;	DB 1;	Length 412;
Best Local Similarity	27.1%;	Pred. No. 2.5e-15;		
Matches 121;	Conservative 75;	Mismatches 180;	Indels 71;	Gaps 22;
QY 9	LLPLLAQWLLRAPELAPAPFTLPLRVAATNRVVAPTPG-----PGTPAERHADGLAL	62		
Db 6	LLPLAL--CLLAAP--ASALVRIPLHKFTSIRRTMSEVGGSVEDLLAKGPVSKYSQAVPA	61		
QY 63	ALPEPALSPAGANFLAMVDNLQDSGRGYYLEMLIGTTPQKQLIVDTGSSNFAVAGTP	122		
Db 62	VTEGPI--PEVLKNYM-----DAQYYGEIGIGTPPQCFYVFDTGSSNLMVPSIH	109		
QY 123	HSYIDT-----YFPTERSSTYRSKGDVTVKYTGGSWTGFGVEGLVTIP--KGFNSTFL	174		
Db 110	CKLIDIA CWIHHKYNDSKSTYVKNGTSPDIIHGSSLSGYLSQDTVSVPQCSASSASAL	169		
QY 175	--VNIAITFESSENFLLPGI-----KWNIGILGLAYATLAKPSSSLETFEFDLSLTQANI-PN	226		
Db 170	GGVYERQVFGFEGATKQPGITFIAAKEDGILGMAYPRIS--VNNVLEVFEDNLMOQKLVQDN	227		
QY 227	VFSMQMCGAGLPVAGSGTNGSLVIGTIEPSLYKGDIMWYTPIKEENYYQIEILKEIGQ	286		
Db 228	IFSFY-----LSRDPDAQPGGELMLGTDSDSKYKGSLSYLVNTRKAYWQVHLDOVEV-AS	281		
QY 287	SLNLDGREYNADKAIIVDSGTTLLRLPKQYFDVAVVEAVARASLIPEFSDGFWTGSQACWT	346		
Db 282	GLTL-CKE--GCEAIVDTGTSIMVGP--VDEVRELQKAIGAVPLIOGEY----MIPC--	329		
QY 347	NSETPWSYFPKISIIYLRDENSSRSFRITLLPOLYIQPMGAGLNYECYRF--GISPSTN	403		
Db 330	--EKYSTLLPAITLKL---GGKGKYL--PEDYTLKVSQAGKTLCLSGFGWMDIPPPSG	380		
QY 404	AL-VIGATWMEGFYVIFDRAQKRVGFA	429		
Db 381	PLWILGDVFIGRYTVFDRDNNRVGFA	407		

RESULT 15

KHMSD
cathepsin D (EC 3.4.23.5) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 18-Jun-1999
C/Accession: I48278; S14704; S12587
R/Hetman, M.; Perschl, A.; Safftig, P.; Von Figura, K.; Peters, C.
DNA Cell Biol. 13, 419-427, 1994
A/Title: Mouse cathepsin D gene: molecular organization, characterization of the promot
A/Reference number: I48278; MUID:94280622; PMID:8011168
A/Accession: I48278
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-410 <RES>
A/Cross-references: EMBL:X68378; NID:g50302; PIDN:CAA48453.1; PID:g817945
R/Diedrich, J.F.; Staskus, K.A.; Retzel, E.F.; Haase, A.T.
Nucleic Acids Res. 18, 7184, 1990
A/Title: Nucleotide sequence of a cDNA encoding mouse cathepsin D.
A/Reference number: S14704; MUID:91088345; PMID:2263503
A/Accession: S14704
A/Molecule type: mRNA
A/Residues: 1-410 <DIE>
A/Cross-references: EMBL:X53337; NID:g50300; PIDN:CAA37423.1; PID:g50301
R/Grusby, M.J.; Mitchell, S.C.; Glimcher, L.H.
Nucleic Acids Res. 18, 4008, 1990
A/Title: Molecular cloning of mouse cathepsin D.
A/Reference number: S12587; MUID:90326544; PMID:2374732
A/Accession: S12587
A/Molecule type: mRNA
A/Residues: 1-410 <GRU>
A/Cross-references: EMBL:X52886; NID:g50298; PIDN:CAA37067.1; PID:g50299
C/Genetics:
A/introns: 23/2; 76/3; 118/1; 157/3; 233/2; 274/2; 322/3; 355/3
C/Function:
A/Description: limited specificity endopeptidase
A/Pathway: intracellular protein degradation
C/Superfamily: pepsin
C/Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
F/1-20/Domain: signal sequence #status predicted <Sig>
F/21-64/Domain: propeptide #status predicted <PRO>
F/65-410/Product: cathepsin D, single-chain form #status predicted <MAT>
F/91-160,110-117,284-288,327-364/Disulfide bonds: #status predicted
F/97,293/Active site: Asp #status predicted
F/134,261/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	11.4%;	Score 306.5;	DB 1;	Length 410;
Best Local Similarity	27.5%;	Pred. No. 3.4e-15;		
Matches 103;	Conservative 64;	Mismatches 123;	Indels 85;	Gaps 15;
QY 92	YYLEMLIGTPPOKLQILVDTGSSNFAVAGTPHSHYIDT-----YFDTERSSTYRSKGF	145		
Db 79	YGGDIGIGTPPOCFTVFVDTGSSNLMWPSIHCKILDIACWVHHKXNSDKSSTVYKNGTSF	138		
QY 146	TVKVTQGSWTFVGEDLVITPKGFNTSFLVNIAT--IFESENFFLPGL-----KMWGIL	197		
Db 139	DIHGGSSLSGYLSQDTVSVPCKSDSKARGIKVEKQIF-GEATKQCGIVFAAKFDGIL	197		
QY 198	GLAYATLAKPSSSLETFFDSLVITQANI-PNVFSMQMGAGLPVAGSGTNGSLVLGIEP	256		
Db 198	GMGYPHIS--VNNVLPVFDNLMQQLVDKNIFSFY-----LNRDPEGQGGELMLGGTDS	250		
QY 257	SLYKGDWYTPRIKEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKV	316		
Db 251	KYYHGEISYLVNTRKAYWQVHMDQLEVNE-LTL-CK--GGCEAIVDTGTSLLVGPVEEV	306		
QY 317	DAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIVLRDENSSRSFRITIL	376		
Db 307	KELQKALGAVPLI-----QGEYMIPEKVVSSL	333		
QY 377	POLYIQPMMGAGLNVEC---YRFGIS-----PSTNALVIGATVMEG	414		
Db 334	PTVYLK--LG-GKNYELHPDKYILKVSQGGKTIICLSGFMGMDIPRPSGLMILGDFVIGS	390		
QY 415	FYVIFDRAQKRVGFA	429		

Db 391 YTVFDRDNNRVGFA 405

Search completed: April 1, 2003, 11:34:51
Job time : 24 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:22:48 ; Search time 14 Seconds
(without alignments)
1534.624 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALARALLPLLAQWLRA.....RPRDPVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2687	100.0	518	BAE2_HUMAN	Q9Y5Z0 homo sapien
2	1187	44.2	501	BACE_RAT	P56819 rattus norv
3	1185	44.1	501	BACE_MOUSE	P56818 mus musculu
4	1178.5	43.9	501	BACE_HUMAN	P56817 homo sapien
5	363.5	13.5	377	PEPC_MACFU	P03955 macaca fusc
6	353	13.1	388	PEPC_HUMAN	P20142 homo sapien
7	351.5	13.1	388	PEPC_CALJA	Q9n2d3 callithrix
8	324.5	12.1	394	PEPC_CAVPO	Q64411 cavia porce
9	320	11.9	402	RENI_MOUSE	P06281 mus musculu
10	313.5	11.7	509	APR1_ORYSA	Q42456 oryza sativ
11	313	11.6	392	PEPC_RAT	P04073 rattus norv
12	310	11.5	383	PEPC_CHICK	P16476 gallus gall
13	308.5	11.5	412	CATD_HUMAN	P07339 homo sapien
14	306.5	11.4	410	CATD_MOUSE	P18242 mus musculu
15	305.5	11.4	401	RENS_MOUSE	P00796 mus musculu
16	305	11.4	407	CATD_RAT	P24268 rattus norv
17	302	11.2	324	PEPI_GADMO	P56272 gadus morhu
18	302	11.2	405	CARP_YEAST	P07267 saccharomyc
19	301.5	11.2	398	CATE_YEAST	P16228 rattus norv
20	300.5	11.2	387	PEP2_RABIT	P27821 oryctolagus
21	300.5	11.2	397	CATE_MOUSE	P70269 mus musculu
22	299	11.1	398	CATD_CHICK	Q05744 gallus gall
23	298.5	11.1	387	PEP4_RABIT	P28713 oryctolagus
24	298.5	11.1	400	RENI_SHEEP	P52115 ovis aries
25	297	11.1	388	PEPA_HUMAN	P00790 homo sapien
26	294.5	11.0	388	PEP2_MACFU	P27677 macaca fusc
27	291	10.8	388	PEP4_MACFU	P27678 macaca fusc
28	291	10.8	402	RENI_RAT	P08424 rattus norv
29	291	10.8	406	RENI_HUMAN	P00797 homo sapien
30	290.5	10.8	396	CATE_RABIT	P43159 oryctolagus
31	289	10.8	387	PEP3_RABIT	P27822 oryctolagus
32	289	10.8	388	PAG_HORSE	Q28389 equus cabal
33	288.5	10.7	390	CATD_BOVIN	P80209 bos taurus

34	288	10.7	387	1	PEP1_RABIT	P28712 oryctolagus
35	288	10.7	388	1	PEP1_MACFU	P03954 macaca fusc
36	287	10.7	367	1	PEPA_CHICK	P00793 gallus gall
37	287	10.7	391	1	CATE_CAVPO	P25796 cavia porce
38	287	10.7	396	1	CATE_HUMAN	P14091 homo sapien
39	286	10.6	388	1	PEPA_MACMU	P11489 macaca mula
40	285.5	10.6	387	1	PEPA_CALJA	Q9n2d4 callithrix
41	285	10.6	396	1	CARP_NEUCR	Q01294 neurospora
42	284.5	10.6	386	1	PEPA_PIG	P00791 sus scrofa
43	283	10.5	388	1	PEPF_RABIT	P27823 oryctolagus
44	282.5	10.5	381	1	CHYM_SHEEP	P18276 ovis aries
45	282	10.5	398	1	ASP3_CAEEL	P55956 caenorhabdi

ALIGNMENTS

RESULT 1
BAE2_HUMAN STANDARD; PRT; 518 AA.
ID BAE2_HUMAN
AC Q9Y5Z0; Q9UT6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta secretase 2 precursor (EC 3.4.23.-) (Beta-site APP-cleaving
enzyme 2) (Aspartyl protease 1) (Asp 1) (ASP1) (Membrane-associated
aspartic protease 1) (Memapsin-1).
DE ASPARTIC PROTEASE 1 (Memapsin-1).
GN BACE2 OR ASP21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
beta-secretase activity.";
RL Nature 402:533-537(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Xin H., Stephens J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,
RA Giese K.;
RT "Identification of a novel aspartic-like protease differentially
expressed in human breast cancer cell lines.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;
RT "Cloning of a gene from chromosome 21 Down region encoding a potential
transmembrane aspartyl protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Solans A., Estivill X., de la Luna S.;
RT "Cloning of a novel mammalian aspartyl protease.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20120043; PubMed=10656250;
RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
RT "Identification of a novel aspartic proteinase (Asp 2) as
beta-secretase.";
RL Mol. Cell. Neurosci. 14:419-427(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=20144060; PubMed=10677483;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;

RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
RT beta-amyloid precursor protein."
RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schilhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; AF200342; AAF17078.1; -
DR EMBL; AF117892; AAD45240.1; -
DR EMBL; AF050171; AAD45963.1; -
DR EMBL; AF178532; AAF29494.1; -
DR EMBL; AF204944; AAF26368.1; -
DR EMBL; AF200192; AAF13714.1; -
DR EMBL; AF200192; AAF13714.1; -
DR EMBL; AL163284; CAB90458.1; -
DR EMBL; AL163284; CAB90554.1; -
DR EMBL; BC014453; AAH14453.1; -
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -
DR Genew; HGNC:934; BACE2.
DR MIM; 605668; -
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 ? POTENTIAL.
FT CHAIN ? 518 BETA SECRETASE 2.
FT DOMAIN 21 473 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 474 494 POTENTIAL.
FT DOMAIN 495 518 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 110 110 BY SIMILARITY.
FT ACT_SITE 303 303 BY SIMILARITY.
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 36 A -> T (IN REF. 6).
SQ SEQUENCE 518 AA; 56180 MW; 2E903150823760D3 CRC64;

Query Match 100.0%; Score 2687; DB 1; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.9e-187;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAAPELAPAPFTLPLRVAAATNRVVAFTPGPGTPAERHADGL 60
Db 1 MGALARALLPLLAQWLRAAPELAPAPFTLPLRVAAATNRVVAFTPGPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPQKLQILVDTGSSNPAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPPQKLQILVDTGSSNPAVAG 120
QY 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTGSGWTFVGEDLVTPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTGSGWTFVGEDLVTPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDSLVTOANI PNVFSMOMGAGLPVA 240
Db 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFFDSLVTOANI PNVFSMOMGAGLPVA 240
QY 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIETIKLEIGQSLNLDCREYNADKA 300
Db 241 GSGTNGSLVLGGIEPSLYKGDWYTPIKEWYQIETIKLEIGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDVAVAVARASLIPEFSDGFMTGSOLACWTNSETPWSYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDVAVAVARASLIPEFSDGFMTGSOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIFD 420
Db 361 YLRDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFAASPCAEIAAGAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFAASPCAEIAAGAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG 480
QY 481 ALLVLIVLLLPFRCCRRPRDPEVNDSSLVRHRMK 518
Db 481 ALLVLIVLLLPFRCCRRPRDPEVNDSSLVRHRMK 518

RESULT 2
BACE_RAT STANDARD; PRT; 501 AA.
AC P56819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (BC 3.4.23.-) (Beta-site APP cleaving enzyme)
DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
DE protease 2) (Asp 2) (Asp2) (Membrane-associated aspartic protease 2)
DE (Memapsin-2).
GN BACE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
CC -!- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

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CC -----
DR EMBL; AF190727; AAF04144.1; -.
DR HSSP; P32329; 1YPS.
DR MEROPS; A01.004; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45 POTENTIAL.
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420 BY SIMILARITY.
FT DISULFID 278 443 BY SIMILARITY.
FT DISULFID 330 380 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 501 AA; 55806 MW; 24B445BC8BE87DE3 CRC64;

Query Match 44.2%; Score 1187; DB 1; Length 501;
Best Local Similarity 46.4%; Pred. No. 1.3e-78;
Matches 240; Conservative 82; Mismatches 165; Indels 30; Gaps 9;

QY 9 LLEPLLAQMLLRAPAEIAPAPFT-----LPLRVAATNRVAPTPGP--GTPAERHADGLA 61
Db 1 MAPALRWLLLVGSGMLPAQGTILGIRLPLRSGLA-----GPPLGLRLPRETDE-- 49
QY 62 LALEPALASPAGANFLAMVDNIQDSSGRGYLEMLIGTPPOKQILVDTGSSNFAVAGT 121
Db 50 ---EP--EEPRGRGSFVEMVDNLKSGQGYVEMTVGSPQTLNILLVDTGSSNFAVGAA 104
QY 122 PHSYIDTYFDTERSSYRSKGFVTVKYTGSGWTFVGEDLVTIPIKGFNTSFLVNIATIF 181
Db 105 PHPELHRYRQQLSSTYRDLRKSVYVPYTGKGWELGTDLVSIPIHGPNTVRANIAIT 164
QY 182 ESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMOMCGAGLPV-- 239
Db 165 ESDKFFINGSNWEGILGLAYAEIARPDSDLPEFDSLVKQTHIPNIFSLQCGAGFPLNQ 224
QY 240 -AGSGTNGSLVLGIEPSLYKGIWYTPIKEWYQIEILKEIGQSINLDCREYNAD 298
Db 225 TEALASVGSMTIGGIDHSLYTGSLWYTPIRREWYEVIIIVREYINGQDLKMDCKEYNYD 284
QY 299 KAIYDSGTLLRLPQKVFDAVAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYFPKI 358
Db 285 KSIYDSGTTLRLPKVFEEAAVXSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVI 344
QY 359 SIYLRDENSRSRFRITILPOLYIDPMWAGLNY-ECYRFGISPTNALVIGATVMEGFYV 417
Db 345 SLVLMGEVTNQSFRTITLPQOYLRYVEDVATSQDDCYKFAVGSOSTGTVMGAVIMEGFYV 404
QY 418 IFDRAQKRVGFAASPCAEIAGAIVSEISGPSTEDVASNCVPAOSLSEPIIMVSYALMS 477
Db 405 VFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPTDESTLMTIAYVMAA 464
QY 478 VCGAILLVLLVLLLPFRQR--RPRDPEVNVDESSL 512

Db 465 IC-ALFMLPLCLMVCQWRCLRCLRHQHDDFADDISLL 500
RESULT 3
BACE_MOUSE
ID_BACE_MOUSE STANDARD; PRT; 501 AA.
AC P56818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
DE protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
DE (Memapsin-2).
OS BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
RN [2]
RP REVISIONS TO 6 AND 81-87.
RA Bennett B.D., Vassar R., Citron M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Braashier J.R., Stratan N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomaseilli A.G., Parodi L.A., Heintzson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).
CC -!- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
CC FRAGMENT WHICH IS LATER RELEASE BY GAMMA-SECRETASE (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
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CC -----
DR EMBL; AF190726; AAF04143.2; -.
DR EMBL; AF200346; AAF17082.1; -.
DR HSSP; P56272; 1AMS.
DR MEROPS; A01.004; -.
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 1.

KW	Hydrolase; Aspartyl	protease; Glycoprotein; Zymogen; Transmembrane;
KW	Signal.	
FT	SIGNAL	1 21 POTENTIAL.
FT	PROPEP	22 45 POTENTIAL.
FT	CHAIN	46 501 BETA-SECRETASE.
FT	DOMAIN	22 457 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	458 478 POTENTIAL.
FT	DOMAIN	479 501 CYTOPLASMIC (POTENTIAL).
FT	ACT_SITE	93 93 BY SIMILARITY.
FT	ACT_SITE	289 289 BY SIMILARITY.
FT	DISULFID	216 420 BY SIMILARITY.
FT	DISULFID	278 443 BY SIMILARITY.
FT	DISULFID	330 380 BY SIMILARITY.
FT	CARBOHYD	153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	501 AA; 55747 MW; C085A013145E474E CRC64;

Query Match	44.1%;	Score 1185;	DB 1;	Length 501;
Best Local Similarity	46.0%;	Pred. No. 1.8e-78;		
Matches 237;	Conservative 83;	Mismatches 169;	Indels 26;	Gaps 7;

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QY 9 LILPILAQWLLRAAPELAPAFPT-----LPLRVAATNRVVAPTPGPGTPAERHADGLALA 63
Db 1 MAPALHWWLLLVWGSGMLPAQGTHTLGIIRLPURSGLA-----GPPLGLRLPRETDEES---- 51
QY 64 LEPALASPAGAAFLAMVDNLQDSCGRGYLEMLIGTPPOKQILVDTGSSNFAVAGTPH 123
Db 52 -----EHPGRGGSFVEMVDNLRKSGGQGYVEMTVGSPQTLNITLVDTGSSNFAVGAAPH 106
QY 124 SYIDTYFDTERSSSTYRSKGFVDYTKYIQGSGWTGFVGEDLVTI PKGFNTSFLVNATIFES 183
Db 107 PELHRYYQROLSTSTYRDLRKGVVYPTQGMKEGELGTDLVSI PHGPNVTVRANIAAITES 166
QY 184 ENFFLPGIKWNIGILGLAYATLAKPSSSLETFFDSLVTOANI PNVFSMQMCGAGLPV--A 240
Db 167 DKFFINGSNWEGILGLAYAEIARPDDSLPEFPFDSLVKQTHI PNIFSLQLCGAGFPLNQTE 226
QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWTPPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
Db 227 ALASVGGSMIIGGIDHSLYTGSLWYTPPIREWYEVLIIVREINGQDLKMDCKEYNYDKS 286
QY 301 IVDSGTTLRLRPQKVFDAVVEAVARASLIPEFSDGFWTGSQOLACWNTSETPWSYEPKISI 360
Db 287 IVDSGTTLRLRPKVVEFAAVKSIIKAASITEKFPDGFWLGEQLVCWQA GTTPWNIIFPVISL 346
QY 361 YLRDENSSRSFRITILPOLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATWEGFYVIF 419
Db 347 YLMGEVNTQSFRTITILPQOYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVINEGEFYVVF 406
QY 420 DRAQKRVGFAASPCAETIAGAAVSEISGFSTEDVASNCVPAQSLSEPILTWISYALMSVC 479
Db 407 DRARKRIGFAVSACHVHDEFRTAAVEGPFYIADMEDCGYNI PQTDESTLMTIAYVMAAIC 466
QY 480 GAILLVILVLLLPRFCQR--RPRDPEVVNDESSL 512
Db 467 -ALEMPLCLIMVCQWRCLRCLRHQHDFAADISLL 500

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RESULT 4
BACE_HUMAN
ID _BACE_HUMAN          STANDARD;          PRT;          501 AA.
AC P56817; Q9UJT5; Q9BYC1; Q9BYC0; Q9BYB9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
DE (protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
DE (Memapsin-2) .
DE BACE OR BACE1 .
GN Homo sapiens (Human) .
OS

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A) .
RC TISSUE=Brain;
RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RA "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999) .
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A) , SEQUENCE OF 46-68, AND
RP CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20057171; PubMed=10591214;
RA Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
RA Tatsuno G., Tung J., Schenk D., Seubert P., Suomensaari S.M., Wang S.,
RA Walker D., Zhao J., McConlogue L., Varghese J.;
RA "Purification and cloning of amyloid precursor protein beta-secretase
RT from human brain.";
RL Nature 402:537-540(1999) .
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A) .
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Torry M.C., Pauley A.M.,
RA Braehler J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;
RA "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
RT secretase activity.";
RL Nature 402:533-537(1999) .
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A) .
RX MEDLINE=20120043; PubMed=10656250;
RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
RL secretase.";
RL Mol. Cell. Neurosci. 14:419-427(1999) .
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM B) .
RC TISSUE=Brain, and Pancreas;
RA Michel B., De Pietri Tonelli D., Zacchetti D., Keller P.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
RT human brain and pancreas.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM C) .
RC TISSUE=Pancreas;
RA Zacchetti D., De Pietri Tonelli D., Schnurbus R.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
RT human pancreas.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D) .
RC TISSUE=Brain;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site
RT amyloid precursor protein cleaving enzyme (BACE) and their effect on
RL Neurosci. Lett. 307:9-12(2001) .
RN [8]
RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A) , AND CHARACTERIZATION.
RX MEDLINE=20144060; PubMed=10677483;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;

```

RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
RT beta-amyloid precursor protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=21950860; PubMed=11953458;
RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
RT "The disulphide bonds in the catalytic domain of BACE are critical but
RT not essential for amyloid precursor protein processing activity.";
RL J. Neurochem. 80:1079-1088(2002).
CC -I- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 4 isoforms; A/BACE-1A/BAC-501 (shown here),
CC B/BACE-1B/BACE-1-476; C/BACE-1C/BACE-1-457 and D/BACE-1D/BACE-1-
CC 432; are produced by alternative splicing.
CC -I- TISSUE SPECIFICITY: BRAIN.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF190725; AAF04142.1; -
DR EMBL; AF201468; AAF18982.1; -
DR EMBL; AF200343; AAF17079.1; -
DR EMBL; AF204943; AAF26367.1; -
DR EMBL; AF338816; AAK38374.1; -
DR EMBL; AF338817; AAK38375.1; -
DR EMBL; AB050436; BAB40931.1; -
DR EMBL; AB050437; BAB40932.1; -
DR EMBL; AB050438; BAB40933.1; -
DR EMBL; AF200193; AAF13715.1; -
DR HSSP; P32329; 1YPS.
DR MEROPS; A01.004; -.
DR Genew; HGNC:933; BACE.
DR MIM; 604252; -.
DR InterPro; IPR001461; Aspproteaseal.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420
FT DISULFID 278 443
FT DISULFID 330 380
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 146 189 MISSING (IN ISOFORM C AND ISOFORM D).
FT VARSPLIC 190 214 MISSING (IN ISOFORM B AND ISOFORM D).
SQ SEQUENCE 501 AA; 55763 MW; 377CE4C824ACEF05 CRC64;

Query Match 43.9%; Score 1178.5; DB 1; Length 501;
Best Local Similarity 46.2%; Pred. No. 5.2e-78;

Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;
QY 7 ALLPLLAQLLRAAPELAPAFPT-----LPLRVAATNRVVAPTPGPTPAERHADGLA 61
Db 2 AQLPFWLLMM---GAGVLPAGHTQHGRILPLRSLG-----GAPL-----GLR 42
QY 62 LALE--PALASPAGAAFLAMVDNLQDSGRGYYLEMLICTPPQKLQILVDTGSSNPAA 119
Db 43 LPRETDEEPPEPGRGGSFVENVNLRGKSGGGYVENVTGSPQTLNLTVDTGSSNPAAVG 102
QY 120 GTPHSYIDTYFDTERSSTYRSKGFDTVKYTOGSWTGVGEDLVTPKGFNTSFLVNIAT 179
Db 103 AAPHPFLHRYQROLSTYRDLRKGVVVPYTOGKWEGLGTDLVSIPIHPNVTVRANIYA 162
QY 180 IPESNEFPLPGIKMNGILGLAYATLAKPSSSLFTFPDSLVTOANIPNVFSMOMGAGLPV 239
Db 163 ITESDKFFINGSNWEGILGLAYAEIARPDDSLFPFDSLVKQTHVPLNLSLQCGAGFPL 222
QY 240 AGS---GTNGSLVLGGIEPSLVKGDWYTPRIKEENYQIHLKLEIGQSINLDCREYN 296
Db 223 NQSEVLASVGGSMITIGIDHSLYTGSLWYTPIRRENYEVIIIVREINGQDLKMDCKEYN 282
QY 297 ADKAIVDSGTTLLRLPQKVDVAVEAVARASLIPESDGFWTGSOLACWTNSETPWSYFP 356
Db 283 YDKSIVDSGTTNLRLPKQVFEAAVKSIIKAASSTKPEPDGFWLGEQLVCWQAGTTPNWIFP 342
QY 357 KISIVLRDENSSRSFRITLIPQLYIQPMGAGLNY-ECYRFGISPSTNALVIGATYMEGF 415
Db 343 VISLYLMGEVTNQSFRTITLPQYLRPVEDVATSDQCYKFAISQSSGTGMGAVIMEGF 402
QY 416 YVIFDRAQKRVGFAPSPCAETIAGAAVSEISGPFSTEDVASNCPAQSLSEPILMIVSYAL 475
Db 403 YVVFDRARKRIGFAVSACHVDEFRTAAVEGPFVTLMEDCGYNIPTDESTLMTIAYVM 462
QY 476 MSVCGAILLVLLVLLLPFRQR--RPRDPEVNDDESSL 512
Db 463 AATC-ALFMLPLCLMVCQWRCLRCLRQHQHDDFADDISLL 500
RESULT 5
PEPC_MACFU STANDARD; PRT; 377 AA.
ID PEPC_MACFU
AC P03955;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gastricisin precursor (EC 3.4.23.3) (Pepsinogen C) (Fragment).
GN PG.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gastric mucosa;
RX MEDLINE=92037645; PubMed=1935977;
RA Kageyama T., Tanabe K., Koiwai O.,
RT "Development-dependent expression of isozymogens of monkey
RT pepsinogens and structural differences between them.";
RL Eur. J. Biochem. 202:205-215(1991).
RN [2]
RP SEQUENCE OF 6-377.
RX MEDLINE=86168133; PubMed=3514597;
RA Kageyama T., Takahashi K.;
RT "The complete amino acid sequence of monkey progastricsin.";
RL J. Biol. Chem. 261:4406-4419(1986).
RN [3]
RP SEQUENCE OF 6-65.
RX MEDLINE=85289106; PubMed=3928607;
RA Kageyama T., Takahashi K.;
RT "Monkey pepsinogens and pepsins. VII. Analysis of the activation
RT process and determination of the NH2-terminal 60-residue sequence of

```

RT Japanese monkey progastricsin, and molecular evolution of
RT pepsinogens.";
RL J. Biochem. 97:1235-1246(1985).
CC -I- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC shows preferential cleavage at Tyr-Xaa bonds; high activity
CC towards hemoglobin as substrate.
CC -I- PTM: EACH PEPSINOGEN IS CONVERTED TO CORRESPONDING PEPsin AT PH
CC 2.0 IN PART AS A RESULT OF THE RELEASE OF A 47 AA ACTIVATION
CC SEGMENT AND IN PART AS A RESULT OF STEPWISE PROTEOLYTIC CLEAVAGE
CC VIA AN INTERMEDIATE FORM(S).
CC CC MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES IS REGULATED BY
CC HORMONES AND RELATED SUBSTANCES.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; X59754; CAA42426.1; -.
DR PIR; A00986; PEMQCU.
DR PIR; A22402; A22402.
DR PIR; S19683; S19683.
DR PIR; S16066; S16066.
DR HSSP; P20142; LAVF.
DR MEROPS; A01.003; -.
DR InterPro; IPR001461; Aspproteaseal.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal.
FT SIGNAL 1 1
FT PROPEP 6 31 ACTIVATION PEPTIDE.
FT PROPEP 32 48 ACTIVATION PEPTIDE.
FT CHAIN 49 377 GASTRICSIN.
FT DISULFID 93 98
FT DISULFID 256 260
FT DISULFID 299 332
FT ACT_SITE 80 80
FT ACT_SITE 265 265
FT CONFLICT 331 331 L -> V (IN REF. 2).
FT CONFLICT 349 349 L -> LVY (IN REF. 2).
SQ SEQUENCE 377 AA; 41148 MW; 2CFB8FBF26D77CE CRC64;

Query Match 13.5%; Score 363.5; DB 1; Length 377;
Best Local Similarity 28.9%; Pred. No. 3.9e-19;
Matches 118; Conservative 65; Mismatches 118; Indels 107; Gaps 19;

OY 56 HADGIALALPALASPAGANFLAMVNLQGDSGRGYLLEMIGTPPOKLIIVDTGSSN 115
|:::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 44 HFGLSVSYEP-----MAYMD-----AAYFEISIGTPPNQLVLFDTGSSN 85

OY 116 FAV-----AGTPHSYIDTYFDTERSTRSKGFVDTVKYTOGSWTGVGEDLVTI PK 167
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 86 LWPSVYCQSQACTSHS---RFNPSESISTYSTNGQTFSLOYGSGSLTFEGYDTLTV-- 139

OY 168 GFNTSFLVNIAATIFESENFFLPG----IKWNGILGLAYATLAKPSSSLETFFDSLVTQA 222
140 ---QSIOVPNQEFLSEN--EPGTNFVYAQFDGIMGLAYPTLSVDGAT--TAMQGMVQEG 192

OY 223 NIPN-VFSMQMGAGLPLVAGSGTNGSLVLGIEPSLYKGDIWYTPIKEEWYYQIEIKL 281
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 193 ALTSPIFSVYLSDQ-----QGSSSGAVVFEGVDSLSLTGTQIYWAPVTOELYWQIGIEEF 246

OY 282 EIGGGSLLNDCREYNADKAIVDSGTTLLRLPKQVFDVAVEAVARASLIFEFGDFWTGSQ 341
|||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 247 LIIGGASGW-CSE--GCQAIVDITGTLTLTYPOQYMALIQA-----TGAQ 288

342 LACWTNETSPWSYF-----PKSIYLDENSSRSFRITILLPOLYIQPMGACLNY 391

```

[illegible]

RP X-RAY CRYSTALLOGRAPHY (2.36 ANGSTROMS).
RX MEDLINE=98069649; PubMed=9406551;
RA Khan A.R., Cherney M.M., Tarasova N.I., James M.N.:
RT "Structural characterization of activation 'intermediate 2' on the
RT pathway to human gastricsin.";
RL Nat. Struct. Biol. 4:1010-1015(1997).
CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC shows preferential cleavage at Tyr-Xaa bonds; high activity
CC towards hemoglobin as substrate.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; M18667; AAA60062.1; ALT INIT.
DR EMBL; M18659; AAA60062.1; JOINED.
DR EMBL; M18660; AAA60062.1; JOINED.
DR EMBL; M18661; AAA60062.1; JOINED.
DR EMBL; M18662; AAA60062.1; JOINED.
DR EMBL; M18663; AAA60062.1; JOINED.
DR EMBL; M18664; AAA60062.1; JOINED.
DR EMBL; M18665; AAA60062.1; JOINED.
DR EMBL; M18666; AAA60062.1; JOINED.
DR EMBL; M23077; AAA60063.1; -.
DR EMBL; M23069; AAA60063.1; JOINED.
DR EMBL; M23070; AAA60063.1; JOINED.
DR EMBL; M23071; AAA60063.1; JOINED.
DR EMBL; M23072; AAA60063.1; JOINED.
DR EMBL; M23073; AAA60063.1; JOINED.
DR EMBL; M23074; AAA60063.1; JOINED.
DR EMBL; M23075; AAA60063.1; JOINED.
DR EMBL; J04443; AAA60074.1; -.
DR EMBL; U75272; AAB18273.1; -.
DR PIR; A23458; A23458.
DR PIR; A29937; A29937.
DR PIR; A31811; A31811.
DR PIR; PX0028; PX0028.
DR PDB; 1HTR; 26-JAN-98.
DR PDB; 1AVF; 25-FEB-98.
DR MEROPS; A01.003; -.
DR Genew; HGNC:8890; PGC.
DR MIM; 169740; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal;
KW 3D-structure.
FT SIGNAL 1 16
FT PROPEP 17 59 ACTIVATION PEPTIDE.
FT CHAIN 60 388 GASTRICIN.
FT ACT_SITE 91 91
FT ACT_SITE 276 276
FT DISULFID 104 109
FT DISULFID 267 271
FT DISULFID 310 343
FT CONFLICT 40 41 GE -> ED (IN REF. 6).
FT CONFLICT 52 52 W -> S (IN REF. 6).
SQ SEQUENCE 388 AA; 42426 MW; F862DFDC1438BB92 CRC64;

Query Match 13.1%; Score 353; DB 1; Length 388;
Best Local Similarity 29.1%; Pred. No. 2.3e-18;
Matches 120; Conservative 65; Mismatches 120; Indels 108; Gaps 21;

QY 52 PAERHADG-LALALEPALASPAGAAFLAMVDNLQDGSRGYVLEMLIGTPPKQLQILVD 110
Db 50 PAWKYRFGLDLSVTEP-----MAYMD-----AAVFGELISIGTPPNFLVLF 91

QY 111 TGSNFAV-----AGTPHSYIDTYFEDTERSSTYRSKGFVDVTWKYTGSGWTFVGEDL 162
Db 92 TGSSNLWVPVSVYCSQACTSHS---RFPNSESSTYSTNGQTFSLQYSGSLTGFPGYDT 147
QY 163 VTIPKGFNTSFLVNIATIFESBNFLLPG-----IKWNGILGLAYATLAKPSSSLETFPDS 217
Db 148 LTV-----QSIQVPNQEFGLSEN--ERGTNFVYAQFDGIMGLAYPALSVDEAT--TAMQG 198
QY 218 LVTQANIPN-VFSMOMCAGALPVAGSGTNGSLVLGGIEPSLYKGDIMWTPIKEEMYYQI 276
Db 199 MVQEGALTSVPFVSVYLSNQ-----QGSSGAVVFGVDSSLYTGQIYMAPVTQELYWQI 252
QY 277 ELKLEIGGQSLNLDCREYNADKAIVDSGTTLRLPQKVFDAVAVARASLIPEFSDGF 336
Db 253 GIEEFLIGQASGW-CSE--GCQAIVDGTSLTLVPQQYMSALLQA----- 295
QY 337 WTGSQIACWTNSETPWSYF-----PKISYLRDENSSRSFRITILPOLYIQPMNG 386
Db 296 -TGAQ-----EDEYGFVNCNSIQNLPSLTFTI-----NGVEFPLPSSSYI----- 336
QY 387 AGLNEYCY-RFGISP---STNA---LVIGATWMEGFYIFDRAQKRVGFAAS 431
Db 337 -LSNNGYCTVGVEPTYLSQNGQPLMILGDVFLRSYSVYDLGNRRVGFATA 387

RESULT 7
PEPC_CALJA STANDARD; PRT; 388 AA.
ID PEPC CALJA
AC Q9N2D3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
GN GGC.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 17-26, FUNCTION, AND ENZYME
RP REGULATION.
RC TISSUE=Gastric mucosa;
RX MEDLINE=20250834; PubMed=10788784;
RA Kageyama T.;
RT "New World monkey pepsinogens A and C, and prochymosins. Purification,
RT characterization of enzymatic properties, cDNA cloning, and molecular
RT evolution.";
RL J. Biochem. 127:761-770(2000).
CC -!- FUNCTION: Hydrolyses a variety of proteins.
CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC shows preferential cleavage at Tyr-Xaa bonds; high activity
CC towards hemoglobin as substrate.
CC -!- ENZYME REGULATION: Inhibited by pepstatin.
CC -!- MISCELLANEOUS: The optimal pH is around 2.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; AB038385; BAA90872.1; -.
DR HSSP; P20142; 1AVF.
DR MEROPS; A01.003; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.

RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=84182525; PubMed=6370686;
RA Holm I., Oilo R., Panthier J.-J., Rougeon F.;
RT "Evolution of aspartyl proteases by gene duplication: the mouse renin
RT gene is organized in two homologous clusters of four exons.";
RL EMO J. 3:557-562(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RX MEDLINE=90067953; PubMed=2685761;
RA Kim W.S., Murakami K., Nakayama K.;
RT "Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.";
RL Nucleic Acids Res. 17:9480-9480(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2, and C57BL/10;
RX MEDLINE=90108722; PubMed=2691339;
RA Burt D.W., Mullins L.J., George H., Smith G., Brooks J., Pioli D.,
RA Brannan W.J.;
RT "The nucleotide sequence of a mouse renin-encoding gene, Ren-1d, and
RT its upstream region.";
RL Gene 84:91-104(1989).
RN [4]
RP SEQUENCE OF 1-30 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=84298161; PubMed=6089205;
RA Panthier J.-J., Dreyfus M., Roux D.T.L., Rougeon F.;
RT "Mouse kidney and submaxillary gland renin genes differ in their 5'
RT putative regulatory sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5489-5493(1984).
RN [5]
RP SEQUENCE OF 1-31 FROM N.A.
RX MEDLINE=85085936; PubMed=6392850;
RA Field L.J., Philbrick W.M., Howles P.N., Dickinson D.P.,
RA McGowan R.A., Gross K.W.;
RT "Expression of tissue-specific Ren-1 and Ren-2 genes of mice:
RT comparative analysis of 5'-proximal flanking regions.";
RL Mol. Cell. Biol. 4:2321-2331(1984).
RN [6]
RP SEQUENCE OF 22-37 AND 72-80.
RC STRAIN=C57BL/10ROS X C3H/HEROS; TISSUE=Kidney;
RX MEDLINE=97182599; PubMed=9030738;
RA Jones C.A., Petrovic N., Novak E.K., Swank R.T., Sigmund C.D.,
RA Gross K.W.;
RT "Biosynthesis of renin in mouse kidney tumor As4.1 cells.";
RL Eur. J. Biochem. 243:181-190(1997).
CC -1- FUNCTION: Renin is a highly specific endopeptidase, whose only
CC known function is to generate angiotensin I from angiotensinogen
CC in the plasma, initiating a cascade of reactions that produce an
CC elevation of blood pressure and increased sodium retention by the
CC kidney.
CC -1- CATALYTIC ACTIVITY: Cleaves Leu-|- bond in angiotensinogen to
CC generate angiotensin I.
CC -1- TISSUE SPECIFICITY: KIDNEY.
CC -1- INDUCTION: RENAL RENIN IS SYNTHESIZED BY THE JUXTAGLOMERULAR CELLS
CC OF THE KIDNEY IN RESPONSE TO DECREASED BLOOD PRESSURE AND SODIUM
CC CONCENTRATION.
CC -1- POLYMORPHISM: In inbred mouse strains, there are at least two
CC alleles which can occur at the Ren1 locus: Ren-1d and REN-1C.
CC The sequence shown is that of REN-1C.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; X00810; CAA25391.1; -.
DR EMBL; X00811; CAA25391.1; JOINED.

DR EMBL; X00812; CAA25391.1; JOINED.
DR EMBL; X00813; CAA25391.1; JOINED.
DR EMBL; X00814; CAA25391.1; JOINED.
DR EMBL; X00815; CAA25391.1; JOINED.
DR EMBL; X00816; CAA25391.1; JOINED.
DR EMBL; X00850; CAA25391.1; JOINED.
DR EMBL; X00851; CAA25391.1; JOINED.
DR EMBL; X16642; CAA34636.1; -.
DR EMBL; K02596; AAA40045.1; -.
DR EMBL; M32352; AAA40043.1; -.
DR EMBL; K02800; AAA40044.1; -.
DR EMBL; M34190; AAA40042.1; -.
DR PIR; A00989; REMSK.
DR PIR; S07636; S07636.
DR PIR; A22058; A22058.
DR HSSP; P00796; ISMR.
DR MEROPS; A01.007; -.
DR MGD; MGI:97898; Ren1.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
DR Hydroxylase; Aspartyl protease; Plasma; Glycoprotein; Zymogen;
KW Signal.
FT SIGNAL 1 21
FT PROPEP 22 71 ACTIVATION PEPTIDE.
FT CHAIN 72 402 RENIN.
FT ACT_SITE 102 102 BY SIMILARITY.
FT ACT_SITE 287 287 BY SIMILARITY.
FT DISULFID 115 122 BY SIMILARITY.
FT DISULFID 278 282 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 58 58 W -> R (IN REN-1D).
FT VARIANT 68 68 T -> I (IN REN-1D).
FT VARIANT 160 160 S -> V (IN REN-1D).
FT VARIANT 315 315 E -> D (IN REN-1D).
FT VARIANT 352 352 N -> Y (IN REN-1D).
FT CONFLICT 6 23 MISSING (IN REF. 1).
FT CONFLICT 24 24 T -> I (IN REF. 1).
FT CONFLICT 163 163 V -> VSRV (IN REF. 1).
SQ SEQUENCE 402 AA; 44342 MW; D42920B55E97A38 CRC64;

Query Match 11.9%; Score 320; DB 1; Length 402;
Best Local Similarity 28.6%; Pred. No. 6,1e-16;
Matches 126; Conservative 66; Mismatches 181; Indels 68; Gaps 21;

QY 10 LPLLAQWLRAPELAPFTLPLRVAATNRVAPTPG-PGTPAERHADGIALALE--- 65
DB 6 MPLWALLLL-----WSBCTPSLPTRTATFERIPKKMPSVREILAEKGVDMTRLAEWGV 60
QY 66 ----PA---LASPAGANFLAMVDNLQDGRGYLEMLIGTPPKLQILVDTGSSNFAV 118
DB 61 FTKRPSLTNLTSPVVLNVL---NTQ-----YYGEIGIGTPPQTFKVIPTGSANLWV 110
QY 119 ACTPHSY-----IDTYFDTERSTYRSKGFVTVKYTGQSWTGFGVEDLVTPKGFNTS 172
DB 111 PSTKCSRLYLACGIHSLYESSDSSSYMENGSDFTHYSGRVKGFSLQSDSVTV-GGITVT 169
QY 173 FLVNIATIFESENFPLPGIKMNGILGLAYATLAKPSSSLETFFPSDLVTQANI-PNVFSMQ 231
DB 170 QTFFEVTEPLPIPFML--AKFDGLGMGFP--AQAVGVTPVFDHILSQGLAKEEVSFVY 225
QY 232 MCGAGLPVAGSGTNGSLVLGIEPSLYKGDWYTPIKEEWWYQIEILKLEIGOSLND 291
DB 226 Y-----NRGSHLLGGEVVLGSDPQHYQGNFHVVISIKTDSWQITMKGVSVG--SSTLL 277
QY 292 GREYNADKAIVDSGTTLLRLPQKVFDAVVEAV-ARASLIPEFSDGFWTGSQLAQWNTSET 350
DB 278 CEEGCA--VVVDTGSSSFISAPTSSKLIMQALGAKEKRIEY-----VANC---SQV 324

QY 351 PWSYFPKISITYLRDENSRSFRITILPOLYIQPMGAGL-NYECYRFGISPSTNAL-VIG 408
Db 325 P--TLDPISFDL---GGRAYTSSIDYVLOYPNRDKLCTALHAMDIPPTGPVWVLG 378
QY 409 ATVMEGFYVIFDRAQKRVGFA 429
Db 379 ATFIRKRYTEFDRHNRIGFA 399

RESULT 10
APR1 ORYSA STANDARD; PRT; 509 AA.

ID APR1 ORYSA STANDARD; PRT; 509 AA.
AC Q42456;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aspartic proteinase oryzasin 1 precursor (EC 3.4.23.-).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare / Japonica; TISSUE=Seed;
RX MEDLINE=96048031; PubMed=7556174;
RA Asakura T., Watanabe H., Abe K., Arai S.;
RT "Rice aspartic proteinase, oryzasin, expressed during seed ripening
and germination, has a gene organization distinct from those of
animal and microbial aspartic proteinases.";
RL Eur. J. Biochem. 232:77-83 (1995).
CC -!- DEVELOPMENTAL STAGE: SEED RIPENING AND GERMINATION.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

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CC -----

DR EMBL; D32165; BAA06876.1; -.
DR EMBL; D32144; BAA06875.1; -.
DR HSSP; P42210; IQDM.
DR MEROPS; A01.020; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR InterPro; IPR000004; SapB.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR ProDom; PD001732; SapB; 1.
DR SMART; SM00118; SAPB; 2.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolyase; Aspartyl protease; Zymogen; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 67 POTENTIAL.
FT CHAIN 68 509 ASPARTIC PROTEINASE ORYZASIN 1.
FT DOMAIN 318 416 SPECIFIC TO PLANT ASPARTIC PROTEINASES
FT (BY SIMILARITY).
FT ACT_SITE 103 103 BY SIMILARITY.
FT ACT_SITE 290 290 BY SIMILARITY.
FT DISULFID 116 122 BY SIMILARITY.
FT DISULFID 281 285 BY SIMILARITY.
FT DISULFID 428 465 BY SIMILARITY.
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 509 AA; 54145 MW; 182F5DADA4CB358 CRC64;

Query Match 11.7%; Score 313.5; DB 1; Length 509;
Best Local Similarity 23.0%; Pred. No. 2.5e-15;
Matches 127; Conservative 75; Mismatches 179; Indels 171; Gaps 19;

QY 3 ALARALLPLLAQWILRAAPELAPAPFTLPIRVAATNRVVAPTPGPTPAERHADGLAL 62
Db 5 SVALVLLAAVLLQALLPASAEGLVRIALKKRPIDENSRVAARLSG-----EGARRLGL 59
QY 63 ALBPALASPAGANFLAVNDLQGDSDGRGYILEMLIGTPQKLQILVDTGSSN----- 115
Db 60 RGANSLGGGGEGEDIVALKNYMNAQ----YFGEIGVTPPQKFTVIFDTGSSNLWVPSAK 115
QY 116 --FAVAGTPHSYIDTYFDTERSSSTRSKGFDVYKTTQGSWTFVGEDLVITPKGFNTSF 173
Db 116 CYFSIACFFHS---RYKSGQSTYQKNKPAIQTGTSGIAGFSEDSVTYGD-----V 165
QY 174 LVNIATIFESENF---LPGI-----KNGILGLAYATLAKPSSSLETFPDSLVTQANI 224
Db 166 ----LVVKDQEFIEATKEPGLTFMVAKFDGLIGFOEISVGA-----V 206
QY 225 PNVSQMCG-AGLPVAGSGTN-----GSLVLCGIEPSLYKGDIMWYTPPIKEWYYQI 276
Db 207 PVMYKMWVEQGLVSEPVFSFWFNHSDGEGEIVFGMDPSHYKGNHTYVPVSGKYWQF 266
QY 277 EILKLEIGGQSLNDCREYNADKAIVDSGTTLLRLPQKVDAVEAVARASLIPE----- 331
Db 267 EMGDVLIGKKTGF-CA--SGCSAIDSGTSLAGPTAIIITEINEKIGATGVVSGECKTV 323
QY 332 -----FSDGF----- 336
Db 324 VSQYGOQILDLILAETQPSKICSQVGLCTFDGKHGVSAGIKSVVDEAGESSNLQSGPMC 383
QY 337 -----WTGSLACWNTSETPWSY-----FPKISITYLD 364
Db 384 NACEMAVWMQNLQAKTQDILLINYNQLCDKLPSMGESSVDCGLASMPISFTIGA 443
QY 365 ENSRSFRITILPOLYIQPMGAGLNEYCY---RFGISPSTNAL-VIGATVMEGFYVIF 419
Db 444 K-----KFALKPEEYIL-KVGEGAQAQCSGFTAMDIPPRGPLMILGDVFMGAYHTVF 496
QY 420 DRAQKRVGFAAS 431
Db 497 DYGMKRVGFAXS 508

RESULT 11

PEPC_RAT STANDARD; PRT; 392 AA.

ID PEPC_RAT STANDARD; PRT; 392 AA.
AC P04073;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gastricisin precursor (EC 3.4.23.3) (Pepsinogen C).
GN PGC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=89255508; PubMed=2722863;
RA Ishihara T., Ichihara Y., Hayano T., Katsura I., Sogawa K.,
RA Fujii-Kuriyama Y., Takahashi K.;
RT "Primary structure and transcriptional regulation of rat pepsinogen C
gene.";
RL J. Biol. Chem. 264:10193-10199 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=87054020; PubMed=3780741;
RA Ichihara Y., Sogawa K., Morohashi K., Fujii-Kuriyama Y., Takahashi K.;
RT "Nucleotide sequence of a nearly full-length cDNA coding for
pepsinogen of rat gastric mucosa.";
RL Eur. J. Biochem. 161:7-12 (1986).
RN [3]
RP SEQUENCE OF 16-112.

```

RC STRAIN=Wistar;
RX MEDLINE=84257697; PubMed=6743670;
RA Arai K.M., Muto N., Tani S., Akahane K.;
RT "The N-terminal sequence of rat pepsinogen.";
RL Biochim. Biophys. Acta 788:256-261(1984).
CC -I- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC shows preferential cleavage at Tyr-Xaa bonds; high activity
CC towards hemoglobin as substrate.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; M25993; AAAA41827.1; -.
DR EMBL; M25985; AAAA41827.1; JOINED.
DR EMBL; M25986; AAAA41827.1; JOINED.
DR EMBL; M25987; AAAA41827.1; JOINED.
DR EMBL; M25988; AAAA41827.1; JOINED.
DR EMBL; M25989; AAAA41827.1; JOINED.
DR EMBL; M25990; AAAA41827.1; JOINED.
DR EMBL; M25991; AAAA41827.1; JOINED.
DR EMBL; M25992; AAAA41827.1; JOINED.
DR EMBL; X04644; CAA28305.1; -.
DR PIR; A24608; A24608.
DR PIR; A05145; A05145.
DR PIR; A33510; A33510.
DR HSSP; P20142; IAVF.
DR MEROPS; A01.003; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolyase; Aspartyl protease; Zymogen; Digestion; Signal.
FT SIGNAL 1 16
FT PROPEP 17 62 ACTIVATION PEPTIDE.
FT CHAIN 63 392 GASTRICIN.
FT ACT_SITE 94 94
FT ACT_SITE 280 280
FT DISULFID 107 112 BY SIMILARITY.
FT DISULFID 270 275 BY SIMILARITY.
FT DISULFID 314 347 BY SIMILARITY.
FT CONFLICT 31 31 E -> Q (IN REF. 3).
FT CONFLICT 103 103 S -> A (IN REF. 3).
FT CONFLICT 109 109 S -> L (IN REF. 3).
SQ SEQUENCE 392 AA; 42833 MW; 092A5EAF2783EDD1 CRC64;

Query Match 11.6%; Score 313; DB 1; Length 392;
Best Local Similarity 29.5%; Pred. No. 1.9e-15;
Matches 105; Conservative 56; Mismatches 139; Indels 56; Gaps 16;

QY 92 YYLEMLIGTPPOKLIQIVDTGSSNFAV-----AGTPHSYIDTYFDTERSSYRSKGF 143
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 76 YFGEISIGTPPONFLVLFDTGSSNLWSSVYCQSEACTTHA----RFPNPKSSTYYTEGQ 131

QY 144 DVTVKYTGGSWTGFVGEDLVTIPIKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG 198
   :::|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 132 TFSLQYGTGSLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG 184

QY 199 IAYATLAKPSSSLETFFDSLVTQANIPNVFSQMCGAGLPVAGS--GTNGSLVLGIEP 256
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 185 IAYPGLS--SGATTALQGMIGE-----GALSQPLFGVYL---GSQGSNGGQIVFGVDK 235

QY 257 SLYKGDIMWTPIKEEWYQIETLKLIEIGQSINLDCREYNADKAIVDSGTTLRLPQKVF 316
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 236 NLYTGEITWVPVTOELYWQITIDDFLIGDQASGW-CSSQGC-QGIVDTGTSLVMPAQYL 293

QY 317 DAVEAVARASLIPEFSDEFTGSQLACWTNSETPWSYFPKISIVLRDENSRSFRITLL 376

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Db      294 SELLQTIGAOE--GEYGEYF-----VSCDSVSS-----LPTLSFVL-----NGVQFPPLS 335
Oy      377 POLY-IQPMGAGLNVECFRGISPSSTNALVIGATMEGFVIIPDRAQKRVFAAS 431
Db      336 PSSYIIQEDNFCMWGLSESISTSESGQPLWILGDVFLLRSYAIFDMGNKKVGLATS 391

RESULT 12
PEPE_CHICK
ID PEPE_CHICK STANDARD; PRT; 383 AA.
AC P16476;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Embryonic pepsinogen precursor (EC 3.4.23.-).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227903; PubMed=3131317;
RA Hayashi K., Agata K., Mochii M., Yasugi S., Eguchi G., Mizuno T.;
RT "Molecular cloning and the nucleotide sequence of cDNA for embryonic
RT chicken pepsinogen: phylogenetic relationship with prochymosin.";
RL J. Biochem. 103:290-296(1988).
CC -!- DEVELOPMENTAL STAGE: SPECIFICALLY SECRETED DURING THE EMBRYONIC
CC PERIOD IN THE CHICKEN PROVENTRICULUS (GANADULAR STOMACH).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; D00215; BAA00153.1; -.
DR PIR; A41443; A41443.
DR HSSP; P00794; 4CMS.
DR MEROPS; A01.028; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Digestion; Signal; Glycoprotein.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 383 EMBRYONIC PEPSINOGEN.
FT ACT_SITE 94 94 BY SIMILARITY.
FT ACT_SITE 276 276 BY SIMILARITY.
FT DISULFID 107 112 BY SIMILARITY.
FT DISULFID 267 271 BY SIMILARITY.
FT DISULFID 310 344 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 51 51 T -> S.
SQ SEQUENCE 383 AA; 41719 MW; 1642796871611F54 CRC64;

Query Match 11.5%; Score 310; DB 1; length 383;
Best local Similarity 26.8%; Pred. No. 3e-15;
Matches 106; Conservative 63; Mismatches 136; Indels 90; Gaps 15;

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Db 98 SNLWVSVSCTSPACQSHQMFNPSSQSTYKSTGQNLSTHYGTGDMGTGCDTVAASLM 157
QY 170 NTSFLVNIATIFESSENFLLPGIKMNGIIGLAYATLAKPSSSLETFEDSLVTQANI-PNVF 228
Db 158 DTNQLFGLST-SEPGQFV-YVKFDGILGLGPSLA--ADGITPVFDNMVNESLLEQNLF 213
QY 229 SMQMGAGLPVAGSGTNGSLVLGGIEPSLYKGDWYTPIKEEMYYQIEILKLEIGGQSL 288
Db 214 SVYLSRPEM-----GSMVVEGGIDESYFTGSINWIPVSYQGYWQISMSDIIVNKQEI 265
QY 289 NLDCREYNADKAIVDSGTTLLRLPKYVDVAVEAVARASLIPEFSGFWTGSQACWTNS 348
Db 266 ACS---SGQALIDTGTSLVAGPASPINDIQSAVG-----ANQ 300
QY 349 ETPWSYFPKISIVLRDENSSRSFRITLPOLYIQPMGAGLNY-----ECY 394
Db 301 NTYGEY-----SVNCSHILAMPDVVF--VIG-GIQYPPVALAYTEQNGQGTGM 345
QY 395 RFGISPSTNALVIGATVMEGFYVIFDRAOKRVGFA 429
Db 346 SSFQNSSADLWILGDVFIIRVYYSIFDRANNRVGLA 380
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RESULT 13
CATD_HUMAN
ID CATD_HUMAN STANDARD; PRT; 412 AA.
AC P07339;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN CTSD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=85270436; PubMed=3927292;
RX Faust P.L., Kornfeld S., Chirgwin J.M.;
RT "Cloning and sequence analysis of cDNA for human cathepsin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4910-4914(1985).
RN [2]
RP MEDLINE=87231068; PubMed=3588310;
RX Westley B.R., May F.E.B.;
RT "Oestrogen regulates cathepsin D mRNA levels in oestrogen responsive
RL human breast cancer cells.";
RL Nucleic Acids Res. 15:3773-3786(1987).
RN [3]
RP MEDLINE=91299158; PubMed=2069717;
RX Redecker B., Heckendorf B., Grosch H.W., Mersmann G., Hasilik A.;
RT "Molecular organization of the human cathepsin D gene.";
RL DNA Cell Biol. 10:423-431(1991).
RN [4]
RP MEDLINE=91299158; PubMed=2069717;
RX Redecker B., Heckendorf B., Grosch H.W., Mersmann G., Hasilik A.;
RT "Molecular organization of the human cathepsin D gene.";
RL DNA Cell Biol. 10:423-431(1991).
RN [5]
RP MEDLINE=94085791; PubMed=8262386;
RX May F.E., Smith D.J., Westley B.R.;
RT "The human cathepsin D-encoding gene is transcribed from an estrogen-
RL regulated and a constitutive start point.";
RL Gene 134:277-282(1993).
RN [6]
RP MEDLINE=95021301; PubMed=7935485;
RX Augereau P., Miralles F., Cavailles V., Gaudelot C., Parker M.,
RA Rochefort H.;
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RT "Characterization of the proximal estrogen-responsive element of
RT human cathepsin D gene.";
RL Mol. Endocrinol. 8:693-703(1994).
RN [7]
RP MEDLINE=93342076; PubMed=8393577;
RX TISSUE=Liver;
RC TISSUE=Liver;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RL Submitted (JUN-1992) to the SWISS-PROT data bank.
RN [8]
RP VARIANT VAL-58.
RX MEDLINE=20179010; PubMed=10716266;
RA Papassotiropoulos A., Bagli M., Kurz A., Kornhuber J., Forstl H.,
RA Maier W., Pauls J., Lautenschlager N., Heun R.;
RT "A genetic variation of cathepsin D is a major risk factor for
RT Alzheimer's disease.";
RL Ann. Neurol. 47:399-403(2000).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RC TISSUE=Spleen;
RX MEDLINE=93223670; PubMed=8467789;
RA Metcalf P., Fusek M.;
RT "Two crystal structures for cathepsin D: the lysosomal targeting
RT signal and active site.";
RL EMBO J. 12:1293-1302(1993).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC TISSUE=Liver;
RX MEDLINE=93342076; PubMed=8393577;
RA Baldwin E.T., Bhat T.N., Gulnik S., Hosur M.V., Sowder R.C. II,
RA Cachau R.E., Collins J., Silva A.M., Erickson J.W.;
RT "Crystal structures of native and inhibited forms of human cathepsin
RT D: implications for lysosomal targeting and drug design.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6796-6800(1993).
CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
CC Involved in the pathogenesis of several diseases such as breast
CC cancer and possibly Alzheimer's disease.
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-His5 bond in B
CC chain of insulin.
CC -!- SUBUNIT: CONSISTS OF A LIGHT CHAIN AND A HEAVY CHAIN.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- POLYMORPHISM: The Val-58 allele is significantly overrepresented
CC in demented patients (11.8%) compared with nondemented controls
CC (4.9%). Carriers of the Val-58 allele have a 3.1-fold increased
CC risk for developing AD than noncarriers.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M11233; AAB59529.1; -
DR EMBL; X05344; CAA28955.1; -
DR EMBL; M63138; AAA51922.1; -
DR EMBL; M63134; AAA51922.1; JOINED.
DR EMBL; M63135; AAA51922.1; JOINED.
DR EMBL; M63136; AAA51922.1; JOINED.
DR EMBL; M63137; AAA51922.1; JOINED.
DR EMBL; BC016320; AAH16320.1; -
DR EMBL; L12980; AAA16314.1; -
DR EMBL; S74689; AAD14156.1; -
DR EMBL; S52557; AAD13868.1; -
DR PIR; A25771; KKHUO.
DR PDB; 1LYA; 3I-JAN-94.
DR PDB; 1LYB; 3I-JAN-94.
DR MEROPS; A01.009; -
DR SWISS-2DPAGE; P07339; HUMAN.
```

DR Siena-2DPAGE; P07339; -.
DR Genew; HGNC:2529; CTSD.
DR MIM; 116840; -.
DR InterPro; IPR001461; Aspproteaseal.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Lysosome; Signal; Zymogen;
KW Polymorphism; Alzheimer's disease; 3D-structure.
FT SIGNAL 1 18
FT PROPEP 19 64
FT CHAIN 65 412
FT CHAIN 65 161
FT CHAIN 169 412
FT ACT_SITE 97 97
FT ACT_SITE 295 295
FT DISULFID 91 160
FT DISULFID 110 117
FT DISULFID 286 290
FT DISULFID 329 366
FT CARBOHYD 134 134
FT CARBOHYD 263 263
FT VARIANT 58 58
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
A -> V (ASSOCIATED WITH INCREASED RISK IN
AD, POSSIBLY INFLUENCES SECRETION AND
INTRACELLULAR MATURATION; IN
DBSNP:17571).
/FTid=VAR_011621.

FT TURN 343 344
FT STRAND 345 349
FT HELIX 351 354
FT STRAND 355 357
FT TURN 359 362
FT STRAND 365 368
FT STRAND 370 372
Query Match 11.5%; Score 308.5; DB 1; Length 412;
Best Local Similarity 27.1%; Pred. No. 4.3e-15;
Matches 121; Conservative 75; Mismatches 180; Indels 71; Gaps 22;
QY 9 LPLPLAQLRLRAPAPFTPLRLVAAATNRVAPPPG-----PGTPAERHADGLAL 62
Db 6 LPLPLAL--CLLAAP--ASALVRIPLHKFTSIRRTMSEVGSVEDLIAKGPVSKYQAVPA 61
QY 63 ALPEPALSPAGANFLAMVDNLQDSDGRGYLLEMLIGTPQKLIQILVDTGSSNFAVAGTP 122
Db 62 VTGEPF--PEVLKNYM-----DAQYGEIGIGTPQCFTVYFDTGSSNLWVPSIH 109
QY 123 HSYIDT-----YFDTERRSTYRSKGFVDVTVKYTGQSWTGFVEDLVITP--KGFNTSFL 174
Db 110 CKLLDIACWIHHKYNSSDKSSTYVKNGTSPDIHYGSGLSGYLSQDTVSVPCQASASSAL 169
QY 175 --VNIAITFESSENFPLPGI-----KNGILGLAYATLAKPSSSLETFFDSLVTOANI--PN 226
Db 170 GGAVKVERQVFGEATKQPGITFIAKFDGILGMAYPRIS--VNNVLPVFDMLOQLVDQN 227
QY 227 VFSMQMCGAGLPVAGSGTNGSLVLGIEPSLYKGDIMWYTPIKEWYQIEILKLEIGGQ 286
Db 228 IFSFY-----LSRDPDAQPGELMLGTDTSKYKGSLSYLNTVRKAYWQVHLDDQEV--AS 281
QY 287 SLNLDREYNADKAIYDSGTTLLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSQLAQWT 346
Db 282 GLTL-CKE--GCEAIVDTGTSIMWGP---VDEVRELQKAIGAVPLIQGEY----MIPC-- 329
QY 347 NSETPWSYFPKISITYLKDENSRSFRITILPQLYIQPMGAGLNYECYRF--GISPSTN 403
Db 330 ---EKVSTLPAITLKL---GGKGYKLS--PEDYTLKVSQAGKTLCLSGFMGMDIPPSG 380
QY 404 AL-VIGATWMEGFYVIFDRAQKRVGFA 429
Db 381 PLWILGDVFTGRYYTVFDRDNNRVGFA 407
RESULT 14
CATD_MOUSE STANDARD; PRT; 410 AA.
ID CATD_MOUSE
AC P18242;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN CTSD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=91088345; PubMed=2263503;
RA Dietrich J.F., Staskus K.A., Retzel E.F., Haase A.T.;
RT "Nucleotide sequence of a cDNA encoding mouse cathepsin D.";
RL Nucleic Acids Res. 18:7184-7184 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90326544; PubMed=2374732;
RA Grusby M.J., Mitchell S.C., Glimcher L.H.;
RT "Molecular cloning of mouse cathepsin D.";
RL Nucleic Acids Res. 18:4008-4008 (1990).
RN [3]
RP SEQUENCE FROM N.A.

```

RC STRAIN=C57BL/6J;
RX MEDLINE=94280622; PubMed=8011168;
RA Helman M., Perschl A., Saitfi P., von Figura K., Peters C.;
RT "Mouse cathepsin D gene: molecular organization, characterization of
RT the promoter, and chromosomal localization.";
RL DNA Cell Biol. 13:419-427(1994).
CC -1- FUNCTION: Acid protease active in intracellular protein breakdown.
CC -1- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
CC chain of insulin.
CC -1- SUBUNIT: CONSISTS OF A LIGHT CHAIN AND A HEAVY CHAIN.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
-----
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CC
CC EMBL; X53337; CAA37423.1; -
CC DR EMBL; X52886; CAA37067.1; -
CC DR EMBL; X68378; CAA48453.1; -
CC DR EMBL; X68379; CAA48453.1; JOINED.
CC DR EMBL; X68380; CAA48453.1; JOINED.
CC DR EMBL; X68381; CAA48453.1; JOINED.
CC DR EMBL; X68382; CAA48453.1; JOINED.
CC DR EMBL; X68383; CAA48453.1; JOINED.
CC DR PIR; S14704; KHM5D.
CC DR HSSP; P07339; LLYB.
CC DR MEROPS; A01.009; -.
CC DR MGD; MGI:88562; Ctsd.
CC DR InterPro; IPR001461; AspproteaseA1.
CC DR InterPro; IPR001969; Aspprotease_site.
CC DR Pfam; PF00026; asp; 1.
CC DR PRINTS; PR00792; PEPsin.
CC DR PROSITE; PS00141; ASP_PROTEASE; 2.
CC KW Hydroxylase; Aspartyl1 protease; Glycoprotein; Lysosome; Zymogen; Signal.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT PROPEP 21 64 ACTIVATION PEPTIDE (POTENTIAL).
CC FT CHAIN 65 410 CATHEPSIN D.
CC FT ACT_SITE 97 97 BY SIMILARITY.
CC FT DISULFID 293 293 BY SIMILARITY.
CC FT DISULFID 91 160 BY SIMILARITY.
CC FT DISULFID 110 117 BY SIMILARITY.
CC FT DISULFID 284 288 BY SIMILARITY.
CC FT DISULFID 327 364 BY SIMILARITY.
CC FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
CC FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
CC SQ SEQUENCE 410 AA; 44954 MW; DC4928EC46928BF0 CRC64;

Query Match 11.4%; Score 306.5; DB 1; Length 410;
Best Local Similarity 27.5%; Pred. No. 5.9e-15;
Matches 103; Conservative 64; Mismatches 123; Indels 85; Gaps 15;

QY 92 YLLEMLIGTPPOKLQILVDTGSSNFAVAGTPHSYIDT-----YEDTERSTYRSKGFV 145
DB 79 YYGDIGIGTPPOCFTVVFEDTGSNLMWPSIHCKILDIACWVHHKXNSDKSSTVYKNGTSF 138
QY 146 TVKTYQGSWTFVGEDLVITIPKGFNTSFLVNIAT--IFESENFLPGI-----KWNIGIL 197
DB 139 DIHYGSGSLSGYLSQDTVSVPCKSDSGKARGIKVEKQIF-GEATKQGIIVFAAKFDGIL 197
QY 198 GLAVATLAKPSSSLETFDFSLSVTQANI-PNVFSQMCGAGLPVAGSGTNGSGSLVLGIEP 256
DB 198 GMGYPHIS--VNNVLPVFEDNLMQOKLVDKNIFSFY-----LNRDPEGQPGELMLGTD 250
QY 257 SLYGKDIWYTPRIKEWYYQIEILKLEIGGOSLNDCREYNADKALVDSGTTLLRLPQKVF 316
DB 251 KYHGBELSYLVNTRKAYWQVHMQLVEGNE-LTL-CK--GGCEALVDITGTSLLVGPVEEV 306

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QY      317 DAVEAVAPASLIPEFSDGFWTGSQLACWNTSETPWSYFPKRISIVLRDENSRSFRITIL 376
       :|::|||-----:|-----:-----PSTNALVIGATVMEG 414
Db      307 KELOKAIGAVPLI-----:-----QGEMYIPCEKVSSL 333
QY      377 POLYIQPMWGAGLNYEC---YREGIS-----PSTNALVIGATVMEG 414
       |:||:|:|||||-----:|-----:-----PSTNALVIGATVMEG 414
Db      334 PTVYLK--LG-GKNVELHPDKYIIKVSQGGKTICLSGFMGMIDPPPSGPLMILGDVFICS 390
QY      415 FYVIFDRAQKRVGEFA 429
       :|:||| |||||
Db      391 YTVTFDRDNRRVGFEA 405

RESULT 15
RENS_MOUSE STANDARD; PRT; 401 AA.
ID _RENS_MOUSE AC P00756; P97955; Q62155; P70229;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Renin precursor, submandibular gland (EC 3.4.23.15)
DE (Angiotensinogenase).
GN REN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE OF 64-351 AND 354-401.
RX MEDLINE=83014991; PubMed=6812055;
RA Misono K.S., Chang J.-J., Inagami T.;
RT "Amino acid sequence of mouse submaxillary gland renin.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4858-4862(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82220074; PubMed=6283373;
RA Panthier J.-J., Foote S., Chambraud B., Strosberg A.D., Corvol P.,
RA Rougeon F.;
RT "Complete amino acid sequence and maturation of the mouse
RT submaxillary gland renin precursor.";
RL Nature 298:90-92(1982).
RN [3]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=84298161; PubMed=6089205;
RA Panthier J.-J., Dreyfus M., Roux D.T.L., Rougeon F.;
RT "Mouse kidney and submaxillary gland renin genes differ in their 5'
RT putative regulatory sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5489-5493(1984).
RN [4]
RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=90108722; PubMed=2691339;
RA Burt D.W., Mullins L.J., George H., Smith G., Brooks J., Pioli D.,
RA Brammar W.J.;
RT "The nucleotide sequence of a mouse renin-encoding gene, Ren-1d, and
RT its upstream region.";
RL Gene 84:91-104(1989).
RN [5]
RP SEQUENCE OF 1-30 FROM N.A.
RX MEDLINE=85085936; PubMed=6392850;
RA Field L.J., Philbrick W.M., Howles P.N., Dickinson D.P.,
RA McGowan R.A., Gross K.W.;
RT "Expression of tissue-specific Ren-1 and Ren-2 genes of mice:
RT comparative analysis of 5'-proximal flanking regions.";
RL Mol. Cell. Biol. 4:2321-2331(1984).
RN [6]
RP SEQUENCE OF 267-292 FROM N.A.
RX MEDLINE=84057744; PubMed=6357783;
RA Panthier J.-J., Rougeon F.;
RT "Kidney and submaxillary gland renins are encoded by two non-allelic
RL genes in Swiss mice.";
EMBO J. 2:675-678(1983).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

```

RX MEDLINE=92301530; PubMed=1608447;
RA Dhanaraj V., Dealwis C.G., Frazao C., Badasso M., Sibanda B.L.,
RA Tickle I.J., Cooper J.B., Driesen H.P.C., Newman M., Aguilar C.,
RA Wood S.P., Blundell T.L., Hobart P.M., Geoghegan K.F., Ammirati M.J.,
RA Danley D.E., O'Connor B.A., Hoover D.J.;
RT "X-ray analyses of peptide-inhibitor complexes define the structural
basis of specificity for human and mouse renins.";
RL Nature 357:466-472(1992).
CC -!- FUNCTION: RENIN IS A HIGHLY SPECIFIC ENDOPEPTIDASE, RELATED TO
CC PEPsin, WHOSE ONLY KNOWN FUNCTION IS TO GENERATE ANGIOTENSIN I
CC FROM ANGIOTENSINOGEN IN THE PLASMA, INITIATING A CASCADE OF
CC REACTIONS THAT PRODUCE AN ELEVATION OF BLOOD PRESSURE & INCREASED
CC SODIUM RETENTION BY THE KIDNEY. ITS FUNCTION IN THE SALIVARY GLAND
CC IS NOT UNDERSTOOD.
CC -!- CATALYTIC ACTIVITY: Cleaves Leu-|- bond in angiotensinogen to
CC generate angiotensin I.
CC -!- SUBUNIT: DIMER OF A HEAVY CHAIN AND A LIGHT CHAIN JOINED BY A
CC DISULFIDE BOND.
CC -!- TISSUE SPECIFICITY: SUBMANDIBULAR GLAND.
CC -!- MISCELLANEOUS: THE ACTIVE ENZYME ISOLATED FROM THE SUBMANDIBULAR
CC GLAND HAS CATALYTIC AND ANTIGENIC ACTIVITIES SIMILAR TO RENAL
CC RENIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN HAVING 195-198
CC LEU-SER-ARG-SER, WHICH IS DUE TO A SHIFT IN THE TRANSLATION
CC READING FRAME, AND 395-VAL. THE AUTHORS' TRANSLATION FOR 99 AGREES
CC WITH THAT SHOWN BUT DOES NOT AGREE WITH THE NUCLEIC ACID SEQUENCE.
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DR EMBL; J00621; AAA40050.1; ALT_FRAME.
DR EMBL; K02597; AAA40048.1; -.
DR EMBL; M34191; AAA40046.1; -.
DR EMBL; AF237860; AAA40047.1; -.
DR PIR; A00988; REMS.
DR PIR; B22058; B22058.
DR PDB; 1SMR; 31-JAN-94.
DR MEROPS; A01.008; -.
DR MGD; MGI:97899; Ren2.
DR InterPro; IPR001461; Aspproteasea1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Plasma; Signal; Zymogen;
KW Submandibular gland; 3D-structure.
FT SIGNAL 1 25 PROBABLE.
FT PROPEP 26 63 ACTIVATION PEPTIDE.
FT CHAIN 64 351 HEAVY CHAIN.
FT CHAIN 354 401 LIGHT CHAIN.
FT ACT_SITE 101 101
FT ACT_SITE 286 286
FT DISULFID 114 121
FT DISULFID 277 281
FT DISULFID 320 357
FT CONFLICT 13 13
FT STRAND 69 69 L -> W (IN REF. 4).
FT STRAND 71 78
FT TURN 79 81
FT STRAND 82 89
FT TURN 90 93
FT STRAND 94 101
FT TURN 102 103
FT STRAND 107 101
FT TURN 112 111
FT TURN 116 113
FT TURN 117 117
FT HELIX 119 123

FT	STRAND	127	127
FT	HELIX	129	131
FT	TURN	133	134
FT	STRAND	136	146
FT	TURN	147	148
FT	STRAND	149	162
FT	TURN	163	164
FT	STRAND	165	176
FT	HELIX	179	182
FT	TURN	183	184
FT	STRAND	189	192
FT	HELIX	196	198
FT	HELIX	200	202
FT	HELIX	206	212
FT	TURN	213	214
FT	STRAND	216	216
FT	STRAND	220	225
FT	STRAND	234	238
FT	HELIX	243	245
FT	STRAND	246	254
FT	STRAND	257	257
FT	TURN	258	261
FT	STRAND	262	270
FT	TURN	271	272
FT	STRAND	276	276
FT	TURN	278	279
FT	STRAND	281	285
FT	TURN	287	288
FT	STRAND	289	289
FT	STRAND	292	294
FT	HELIX	296	306
FT	TURN	307	307
FT	STRAND	309	312
FT	TURN	313	314
FT	STRAND	315	319
FT	HELIX	320	325
FT	STRAND	329	333
FT	TURN	334	335
FT	STRAND	336	340
FT	HELIX	342	345
FT	STRAND	346	346
FT	TURN	347	348
FT	STRAND	356	359
FT	STRAND	361	363
FT	TURN	368	370
FT	STRAND	374	376
FT	HELIX	378	381
FT	TURN	382	383
FT	STRAND	384	389
FT	TURN	390	393
FT	STRAND	394	400
SO	SEQUENCE	401 AA; 44282 MW; D938931F91F82980 CRC64;	
Query Match 11.4%; Score 305.5; DB 1; Length 401;			
Best Local Similarity 27.1%; Pred. No. 6.8e-15;			
Matches 121; Conservative 69; Mismatches 177; Indels 79; Gaps 21;			
QY	10 LPLLAQWLRAPELAPFTLPKRVAAATNRVVAPTPGPTPA-----ERHADGLALA 63		
Db	6 MFLWALLLL-----WSPCTFSLP-----TGTFPERIPLKMPSVREILERGVDMTRL 54		
QY	64 LE-----PALASPAGANFLAMVDNLQDSDGRGYLLEMLIGTPPOKQIIVDTGS 113		
Db	55 AEWDVFTKRSSLTDLISPVVLTNYL-----NSQ-----YYGEIGIGTPPQTFKVIPTDGS 104		
QY	114 SNEAVAGTPHSY-----IDTYFDTERRSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTI 167		
Db	105 ANLWVPSTKCSRLYLACGIHSLYESSDSSSVENGDDEFTIHYGSGRVKGFUSQDSVT 163		
QY	168 GFNTSFLVNIATIFESSENFLLPGIKWNGILGLAYATLAKPSSSLETFPSGLVTOANI 226		
Db	164 GITVTQTGFGEVTELPILIPFML--AQFDGVLGNGFP--AQAVGVTPTVFPHILSOGVL 219		

QY 227 VFSMQMCGAGLPVAGSGTNGSLVLGIEPSLYKGDIWYTPIKEWYQIEILKLEIGQ 286
Db 220 VFSVYY-----NRGPHLLGGEVVLGSGSDPEHYQDFHYSLSKTDSWQITMKGVSVG-- 271
QY 287 SLNLDCREYNADKAIYVDSGTTLLRLPQKVFDAVEAV-ARASLIPEFSDGFWTGSQIACW 345
Db 272 SSTLLCEE--GCEVVVDTGSSSFISAPTSCLKLIMQALGAKERKLEHY-----VWSC- 320
QY 346 TNSETPWSYFEPKISIVLRDENSRSFRITILPOLYIQPMGAGL-NYECYRFGISPSTNA 404
Db 321 --SQVP--TLPDISFNL----GGRAYTLUSDYVLQYPNRRDKLCTVALHAMDIPPTGP 372
QY 405 L-VIGATVMEGFYVIFDRAQKRVGFA 429
Db 373 VVVLGATPIRKFYTEFDRHNNRIGFA 398

Search completed: April 1, 2003, 11:32:44
Job time : 17 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:29:48 ; Search time 92 Seconds
(without alignments)
1160.135 Million cell updates/sec

Title: US-09-668-314C-2

Perfect score: 2687

Sequence: 1 MGALARALLPLLAQWLRA.....RPRDEVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: SPTREMBL_21:*
 - 2: sp_archaea:*
 - 3: sp_bacteria:*
 - 4: sp_fungi:*
 - 5: sp_human:*
 - 6: sp_invertebrate:*
 - 7: sp_mammal:*
 - 8: sp_mhc:*
 - 9: sp_organelle:*
 - 10: sp_phage:*
 - 11: sp_plant:*
 - 12: sp_rodent:*
 - 13: sp_virus:*
 - 14: sp_vertebrate:*
 - 15: sp_unclassified:*
 - 16: sp_rvirus:*
 - 17: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2395	89.1	514	11 Q9JL18	Q9JL18 mus musculu
2	2375	88.4	468	4 Q9NZL2	Q9NZL2 homo sapien
3	2293	85.3	439	4 Q9H2V8	Q9H2V8 homo sapien
4	1966	73.2	396	4 Q9NZL1	Q9NZL1 homo sapien
5	1246	46.4	255	11 Q9R1P7	Q9R1P7 mus musculu
6	1183.5	44.0	532	4 Q9ULS1	Q9ULS1 homo sapien
7	1068	39.7	476	4 Q9BYC1	Q9BYC1 homo sapien
8	1025.5	38.2	457	4 Q9BYC0	Q9BYC0 homo sapien
9	925	34.4	432	4 Q9BYB9	Q9BYB9 homo sapien
10	651	24.2	266	11 Q9CUT5	Q9CUT5 mus musculu
11	461	17.2	213	4 Q9P0D2	Q9P0D2 homo sapien
12	386	14.4	244	5 Q8WQY9	Q8WQY9 aphrocallis
13	367.5	13.7	383	13 Q9DEC3	Q9DEC3 xenopus lae
14	361.5	13.5	389	6 Q9GMY4	Q9GMY4 sorex ungui
15	355.5	13.2	384	13 Q91322	Q91322 rana catesb
16	355	13.2	389	13 Q9PWK1	Q9PWK1 gallus gall

17	355	13.2	389	13 Q9W643	Q9W643 gallus gall
18	351.5	13.1	389	6 Q9GMY5	Q9GMY5 suncus muri
19	351.5	13.1	389	6 Q9GMY3	Q9GMY3 rhinolophus
20	335.5	12.5	388	6 Q9GMY2	Q9GMY2 oryctolagus
21	334.5	12.4	391	5 Q9VKP6	Q9VKP6 drosophila
22	326	12.1	399	13 Q93458	Q93458 podarcis si
23	324.5	12.1	372	5 Q9VLK3	Q9VLK3 drosophila
24	324.5	12.1	383	13 Q9DEL4	Q9DEL4 salvelinus
25	322.5	12.0	390	6 Q8SQ41	Q8SQ41 canis fami
26	322.5	12.0	397	13 Q9W6D4	Q9W6D4 hynobius le
27	320	11.9	387	13 Q9DEC4	Q9DEC4 rana catesb
28	319.5	11.9	387	13 Q9DDV5	Q9DDV5 salvelinus
29	319	11.9	419	5 Q95VA2	Q95VA2 cionorchis
30	318.5	11.9	396	13 Q93428	Q93428 chionodraco
31	316	11.8	378	13 Q9PUR9	Q9PUR9 pseudopleur
32	316	11.8	392	11 Q9D7R7	Q9D7R7 mus musculu
33	315.5	11.7	396	13 Q9DEX3	Q9DEX3 clupea hare
34	313	11.6	383	5 Q76856	Q76856 dictyosteli
35	312.5	11.6	354	5 Q9GXX7	Q9GXX7 boophilus m
36	305	11.4	384	13 Q9DEC2	Q9DEC2 xenopus lae
37	302	11.2	398	13 P87370	P87370 oncorhynch
38	301.5	11.2	401	11 Q91X66	Q91X66 mus musculu
39	300.5	11.2	386	6 Q9BGU5	Q9BGU5 bos taurus
40	295.5	11.0	390	6 Q9GK10	Q9GK10 camelus dro
41	295	11.0	376	13 Q9PUR8	Q9PUR8 pseudopleur
42	295	11.0	387	6 Q9GMY8	Q9GMY8 sorex ungui
43	294	10.9	413	3 Q14413	Q14413 pichia angu
44	293.5	10.9	386	6 Q9GMY7	Q9GMY7 rhinolophus
45	292	10.9	386	6 Q9GMY6	Q9GMY6 canis fami

ALIGNMENTS

RESULT 1

ID	Q9JL18	PRELIMINARY;	PRT;	514 AA.
AC	Q9JL18;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Aspartyl protease 1.			
GN	BACE2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Choi D.K., Sugano S., Sakaki Y.;			
RT	"Molecular characterization of the mouse Aspl gene, a homolog of the			
RL	human Aspl (Down Syndrome Region aspartyl protease).";			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF216310; AAF36599.1; -.			
DR	HSSP; P32329; 1YPS.			
DR	MEROPS; A01.041; -.			
DR	MGD; MGI:1860440; Bace2.			
DR	InterPro; IPR001461; AspproteaseA1.			
DR	InterPro; IPR001969; Aspprotease_site.			
DR	Pfam; PF00026; asp; 1.			
DR	PRINTS; PR00792; PEPsin.			
DR	PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.			
KW	Protease.			
SQ	SEQUENCE 514 AA; 55799 MW; A70725F2CIDF5B47 CRC64;			

Query Match 89.1%; Score 2395; DB 11; Length 514;
Best Local Similarity 88.6%; Pred. No. 1.4e-173;
Matches 459; Conservative 20; Mismatches 35; Indels 4; Gaps 1;

QY	1 MGALARALLPLLAQWLRAAPAPFTLPLRYAAATNRVVAAPTGGTPAERRADGL 60
DB	1 MGALLRALLLLVLAQWLASVAPALAPAPFTLPLQVAGATNHRASAVPGLGTPELRADGL 60

QY	61	ALLALEPALASPAGAA	NFLAMVDNL	OGDSGRGYL	EMLIGTP	POKLQIL	VDTCSSN	FAVAG	120		
Db	61	ALLALEPVRAT---	ANFLAMVDNL	OGDSGRGYL	EMLIGTP	POKQOIL	VDTCSSN	FAVAG	116		
QY	121	TPHSYIDTYFDTER	SSTYRSKGF	VDVYKYTQ	GSWTFV	GEDLVTI	PKGFNTS	FLVNIATI	180		
Db	117	APHSYIDTYFDSE	SSSTYHSKGF	VDVYKYTQ	GSWTFV	GEDLVTI	PKGFNTS	FLVNIATI	176		
QY	181	FESENFLLPGIK	MNGILGLAY	ATLAKPSS	LETFD	SLVTOANI	PNVFS	MOGAGLPVA	240		
Db	177	FESENFLLPGIK	MNGILGLAY	ATLAKPSS	LETFD	SLVAQAKI	PDIFSMQ	GAGLPVA	236		
QY	241	GSCTNGGSLVL	GIEPSLYK	GDIMWTP	PIKEWYQ	IEILKLEI	GGOSL	NLDCREYNADKA	300		
Db	237	GSCTNGGSLVL	GIEPSLYK	GDIMWTP	PIKEWYQ	IEILKLEI	GGONL	NLDCREYNADKA	296		
QY	301	IVDSGTLLRL	POKVFDA	VVEAVARAS	LIPESD	GFWTG	SOLAC	WTNSETPM	SYEPKISI	360	
Db	297	IVDSGTLLRL	POKVFDA	VVEAVART	SLIPESD	GFWTG	AQOLAC	WTNSETPM	SYAEPKISI	356	
QY	361	YLRDENSSRS	FRITIL	POLYIQ	PMGAGL	NYECYR	FGIS	PSTNAL	VIGATVMEGEFYI	420	
Db	357	YLRDENASRS	FRITIL	POLYIQ	PMGAGF	NYECYR	FGISS	STNAL	VIGATVMEGEFYV	416	
QY	421	RAQKRVGF	FAASPCAEI	AGA	AVSEIS	GFSTED	VASNC	VPAQSL	SEPI	WIVSYALMSVCG	480
Db	417	RAQKRVGF	FAVSPCAE	IEG	TTVSEI	SGFSTED	IASNC	VPAQAL	NEPIL	WIVSYALMSVCG	476
QY	481	ALLVLIVL	LLLPFR	CQRR	PRD	PEV	VNDESS	LVHRWK	518		
Db	477	ALLVLIVL	LLLP	LHCR	HAPR	D	PEV	VNDESS	LVHRWK	514	

RESULT 2

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ID Q9NZL2 PRELIMINARY; PRT; 468 AA.
AC Q9NZL2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de La Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL CytoGenet. Cell Genet. 89:177-184(2000).
DR EMBL; AF188276; AAF35835.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; Aspproteaseal.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp. 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

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Query Match	88.4%;	Score 2375;	DB 4;	Length 468;
Best Local Similarity	90.3%;	Pred. No. 4e-172;		
Matches 468; Conservative	0;	Mismatches	0;	Indels 50; Gaps 1;

QY	1	MGALARALLLP	LIAQWLLRAAP	ELAPAPFTL	PLRVAATNR	VVAPT	PGPGT	PAERHADGL	60
Db	1	MGALARALLLP	LIAQWLLRAAP	ELAPAPFTL	PLRVAATNR	VVAPT	PGPGT	PAERHADGL	60
QY	61	ALALEPALLAS	PAGAANFLAM	VNDLQGD	SGRGYYLEML	ICTP	POKLQIL	VDVTGSSN	FAVG 120

Db	61	ALALEPALASPAGAAFLAMVDNLQDSDGRGYLLEMLIGTPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTFEDTERSSSTYRSKGFVDTVKYYTQGSWTFVGEDLVITPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTFEDTERSSSTYRSKGFVDTVKYYTQGSWTFVGEDLVITPKGFNTSFLVNIATI	180
Qy	181	FESENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCAGLPVA	240
Db	181	FESENFPLPGIKMNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMCAGLPVA	240
Qy	241	GSGTNGGSLVLGGIEPSSLYKGDWYTPRIKEWYQIETLKLIEIGQSLNLDCREYNADKA	300
Db	241	GSGTNGGSLVLGGIEPSSLYKGDWYTPRIKEWYQIETLKLIEIGQSLNLDCREYNADKA	300
Qy	301	IYDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQLAOWTNSPTMWSYFPKISI	360
Db	301	IYDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFMTGSQLAOWTNSPTMWSYFPKISI	360
Qy	361	YLRDENSRSRFRITILPOLYIDPMMGAGLNYECYRFGTISPSTNALVIGATVMGEFYIFD	420
Db	329	-----LYIQPMMGAGLNYECYRFGTISPSTNALVIGATVMGEFYIFD	370
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG	480
Db	371	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCG	430
Qy	481	AILLVLLVLLLLPFCQRRPRDPEVYNDESSLVRHRWK	518
Db	431	AILLVLLVLLLLPFCQRRPRDPEVYNDESSLVRHRWK	468

RESULT 3

ID	Q9H2V8	PRELIMINARY;	PRT;	439 AA.
AC	Q9H2V8;			
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)		
DE	CDAL3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PHEOCHROMOCYTOMA;			
RA	Li Y., Huang Q., Peng, Y, Song H., Yu Y., Xu S., Ren S., Chen Z.,			
RA	Han Z.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF212252; AAG41783.1; -.			
DR	HSSP; P00797; 2REN.			
DR	InterPro; IPR001461; AspproteaseA1.			
DR	InterPro; IPR001969; Aspprotease_site.			
DR	Pfam; PF00026; asp; 1.			
DR	PRINTS; PR00792; PEPsin.			
DR	PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.			
SO	SEQUENCE 439 AA; 48275 MW; 02EC0E0E50F11602 CRC64;			

Query Match	85.3%;	Score 2293;	DB 4;	Length 439;
Best Local Similarity	100.0%;	Pred. NO. 6.1e-166;		
Matches 439;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Db 121 AYATLAKPSSSLETFEFDLSLVTOANIPNVFSMOMCGAGLPVAGSGTNGSLVLGGIEPSLY 180
QY 260 KGDIMWTPRIKEEMWYQIEILKLEIGGOSLNLDCREYNADKAIVDSGTTLLRLPQKVFDAV 319
Db 181 KGDIMWTPRIKEEMWYQIEILKLEIGGOSLNLDCREYNADKAIVDSGTTLLRLPQKVFDAV 240
QY 320 VEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISITYLRDENSSRSFRITILPOL 379
Db 241 VEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISITYLRDENSSRSFRITILPOL 300
QY 380 YIQPMMGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFDRAQKRVGFAASPCAETIAGA 439
Db 301 YIQPMMGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFDRAQKRVGFAASPCAETIAGA 360
QY 440 AVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCGAILLVLLVLLLPFCQRR 499
Db 361 AVSEISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCGAILLVLLVLLLPFCQRR 420
QY 500 PRDPEVYNDESSLVRHRWK 518
Db 421 PRDPEVYNDESSLVRHRWK 439

RESULT 4

Q9NZL1 ID Q9NZL1 PRELIMINARY; PRT; 396 AA.
AC Q9NZL1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de la Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RL Alzheimer's amyloid precursor protein beta-secretase.";
RL Cytogenet. Cell Genet. 89:177-184(2000).
DR EMBL; AF188277; AAF35836.1; -.
DR HSSP; P00797; ZREN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match 73.2%; Score 1966; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.7e-141;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWMLRAAPELAPAPFTLPLRVAATNRVVAFTPGGTPAERHADGL 60
Db 1 MGALARALLPLLAQWMLRAAPELAPAPFTLPLRVAATNRVVAFTPGGTPAERHADGL 60
QY 61 ALALBPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPQKLIQILVDTGSSNFAVAG 120
Db 61 ALALBPALASPAGANFLAMVDNLQDSGRGYLLEMLIGTPQKLIQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTVFDTERSSSTYRSKGFVTVKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTVFDTERSSSTYRSKGFVTVKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFFLPGIKMGNGILGLAVATLAKPSSSLETFEFDLSLVTOANIPNVFSMOMCGAGLPVA 240
Db 181 FESENFFLPGIKMGNGILGLAVATLAKPSSSLETFEFDLSLVTOANIPNVFSMOMCGAGLPVA 240

QY 241 GSGTNGGSLVLGGIEPSLYKGDIMWTPRIKEEMWYQIEILKLEIGGOSLNLDCREYNADKA 300
Db 241 GSGTNGGSLVLGGIEPSLYKGDIMWTPRIKEEMWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISI 360
QY 361 YLRDENSSRSFRITILPOL 378
Db 361 YLRDENSSRSFRITILPOL 378

RESULT 5

Q9R1P7 ID Q9R1P7 PRELIMINARY; PRT; 255 AA.
AC Q9R1P7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Aspartyl protease (Fragment).
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Acciarino M., Fumagalli P., Taramelli R., Ottolenghi S.;
RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
RT transmembrane protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051150; AAD45964.1; -.
DR MEROPS; A01.041; -.
DR MGD; MGI:1860440; Bace2.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
KW Protease.
FT NON TER 1 1
SQ SEQUENCE 255 AA; 28685 MW; 53DE317815996D63 CRC64;

Query Match 46.4%; Score 1246; DB 11; Length 255;
Best Local Similarity 91.0%; Pred. No. 9.5e-87;
Matches 232; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 264 WYTPRIKEEMWYQIEILKLEIGGOSLNLDCREYNADKAIVDSGTTLLRLPQKVFDAVEAV 323
Db 1 WYTPRIKEEMWYQIEILKLEIGGOSLNLDCREYNADKAIVDSGTTLLRLPQKVFDAVEAV 60
QY 324 ABASLIPEFSDGFWTGSQIACWTNSETPWSYFPKISITYLRDENSSRSFRITILPOLYIQP 383
Db 61 ARTSLIPEFSDGFWTGSQIACWTNSETPWAYFPKISITYLRDENASRSFRITILPOLYIQP 120
QY 384 MNGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFDRAQKRVGFAASPCAETIAGA VSE 443
Db 121 MNGAGLNYECYRFGISPSSTNALVIGATWMEGFYVIFDRAQKRVGFAASPCAETIAGT VSE 180
QY 444 ISGPFSTEDVASNCVPAQSLSEPILMIVSYALMSVCGAILLVLLVLLLPFCQRRPRDP 503
Db 181 ISGPFSTEDIASNCVPAQALNEPILMIVSYALMSVCGAILLVLLVLLLPFCRHAPRDP 240
QY 504 EVYNDESSLVRHRWK 518
Db 241 EVYNDESSLVRHRWK 255

RESULT 6

Q9ULS1 ID Q9ULS1 PRELIMINARY; PRT; 532 AA.
AC Q9ULS1;

DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE KIAA1149 protein (Fragment).
GN KIAA1149.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirose M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
DR EMBL; AB032975; BAA86463.2; -.
DR HSSP; P56272; 1AM5.
DR MEROPS; A01.004; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;

Query Match 44.0%; Score 1183.5; DB 4; Length 532;
Best Local Similarity 47.8%; Pred. No. 1.6e-81;
Matches 231; Conservative 81; Mismatches 154; Indels 17; Gaps 6;

QY 44 APTPGGTPAERHADGLAL-----EPALASPAGANFLAVNDLQDSGRGYLYE 95
DB 52 APSTASGCPCAAAMGAPLGLRLPRETDEEP--EPPGRGSEVENVNLRGKSGQGYVE 109
QY 96 MLIGTPPOKQILVDTGSSNFPAVAGTPHSDYIDYFDTERSSYRSKGFDTVKYQGSWT 155
DB 110 MTWVGSPQNTNITVDTGSSNFPAVGAHPHRLHRYQRLSSTYRDLRKGVVPTQKWE 169
QY 156 GFVGEDLVTPKGFNTSFLVNATIFESSENFPLPGIKWNGILGLAVATLAKPSSSLETFE 215
DB 170 GELGTDLVSPHGPNTVRANIAAITESDKRFINGSNWEGILGLAVAEIARPDLSLPFF 229
QY 216 DSLVTQANIPNVFSMOMGAGLPVAGS---GTNGSLVLGIEPSLYKGDIMYTPIKEEW 272
DB 230 DSLVKQTHVPLFSLQLCGAGPLNQSEVLASVSGSMIIGIDHSLYTGSLWYTPIRREW 289
QY 273 YYQIEILKLEIGQSLNLDREYNADKAIYDSGTTLLRLPKQVFDVAVEAVARASLIPEF 332
DB 290 YVEVITVRVEINGQDLKMDCKEYNYDKSIYDSGTTNLRPLPKVFEAAVKSIIKAASSTEF 349
QY 333 SDGFWTGSLACWTNSETPWSYFPKISILYRDENSSRSFRITILPOLYIQPMGAGLNY- 391
DB 350 PDGFWLGEQLVCWQAGTTPWNIFFVISLYLMEGVNQSFRITILPOQYLRPVEDVATSD 409
QY 392 ECFRFGISPSTNALVIGATWMEGFYVIFDRAQKRVGFAASPCAETAGAAVSEISGFSTE 451
DB 410 DCYKFAISQSGTVMGAVIMEGFYVFDRAKRIQFAVSACHVHDEFRTAAVEGPFVTL 469
QY 452 DVASNCVPAQSLSEPIILWISYALMSVCGAILLVLLVLLPFCQR--RPRDPEVND 509
DB 470 DMEDCGYNIPQIDESTLMTIAYMAAIC-ALEFMLPLCLMVCQWRCRLRQOHDDFADDI 528
QY 510 SSL 512
DB 529 SLL 531

RESULT 7
ID Q9BYC1 PRELIMINARY; PRT; 476 AA.
AC Q9BYC1;

DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-476.
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tananashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
RT production.";
RL Neurosci. Lett. 307:9-12(2001).
DR EMBL; AB050436; BAB40931.1; -.
DR HSSP; P32329; 1YPS.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 476 AA; 52907 MW; 6C8C87F8A953AF66 CRC64;

Query Match 39.7%; Score 1068; DB 4; Length 476;
Best Local Similarity 43.2%; Pred. No. 8.2e-73;
Matches 224; Conservative 78; Mismatches 159; Indels 58; Gaps 10;

QY 7 ALLPPLAQWLLRAPELAPAPT-----LPLRVAAATNRVVAPTPGTPAERHADGLA 61
DB 2 AQALFWLLWM--GAGVLAHGTQHGIRLPLRSLG-----GAPL-----GLR 42
QY 62 LALE--PALASPAGANFLAVNDLQDSGRGYLYEMLIGTPPOKQILVDTGSSNFAVA 119
DB 43 LPRETDEEPEPGRGSEFENVNLRGKSGQGYVEMTVGSPQNTNITVDTGSSNFAVG 102
QY 120 GTPHSDYIDYFDTERSSYRSKGFDTVKYQGSWTGSEVGEDLVTPKGFNTSFLVNAT 179
DB 103 AAPHFLHRYQRLSSTYRDLRKGVVPTQKMEGELGTDLVSPHGPNTVRANIAA 162
QY 180 IFESSENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMOMGAGLPV 239
DB 163 ITESDKRFINGSNWEGILGLAVAEIAR-----LCGAGFPL 197
QY 240 AGS---GTNGSLVLGIEPSLYKGDIMYTPIKEEWYQIEILKLEIGQSLNLDREYN 296
DB 198 NQSEVLASVSGSMIIGIDHSLYTGSLWYTPIRREWYEVITVRVEINGQDLKMDCKEYN 257
QY 297 ADKAIYDSGTTLLRLPKQVFDVAVEAVARASLIPEFSDGFWTGSLACWTNSETPWSYFP 356
DB 258 YDKSIYDSGTTNLRPLPKVFEAAVKSIIKAASSTEFPDGFWLGEQLVCWQAGTTPWNIFF 317
QY 357 KISILYRDENSSRSFRITILPOLYIQPMGAGLNY-ECYRFGISPSTNALVIGATWMEGF 415
DB 318 VISLYLMEGVNQSFRITILPOQYLRPVEDVATSDCYKFAISQSGTVMGAVIMEGF 377
QY 416 YVIFDRAQKRVGFAASPCAETAGAAVSEISGFSTEDVASNVCVPAQSLSEPIILWISYAL 475
DB 378 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQIDESTLMTIAYMA 437
QY 476 MSVCGAILLVLLVLLPFCQR--RPRDPEVND 512
DB 438 AAIC-ALEFMLPLCLMVCQWRCRLRQOHDDFADDISLL 475

RESULT 8
ID Q9BYC0 PRELIMINARY; PRT; 457 AA.
AC Q9BYC0;
DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Beta-site APP cleaving enzyme I-457 (Beta-site APP cleaving enzyme
DE type C).
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=21408467; Pubmed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
RT production";
RL Neurosci. Lett. 307:9-12(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=EXOCRINE PANCREAS;
RA Zaccetci D., De Pietri Tonelli D., Schnurbus R.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
RT human pancreas";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050437; BAB40932.1; -.
DR EMBL; AF338817; AAK38375.1; -.
DR HSSP; P32329; 1YPS.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 457 AA; 51068 MW; C794C9A9E85FE7A2 CRC64;

Query Match 38.2%; Score 1025.5; DB 4; Length 457;
Best Local Similarity 42.1%; Pred. No. 1.3e-69;
Matches 206; Conservative 75; Mismatches 139; Indels 69; Gaps 7;

QY 48 GPQT-PAERHADGLALALPALA-----SPAGANFLAMVDNLQDGS 89
Db 13 GAGVLPAGHTQHGI RLPLRSLGLGAPLGLRLPRETDEEPEEPGRGSGFVEMVDNLRGKSG 72
QY 90 RGYLEMLIGTPQKQLIVDTGSSNFAVAGTPHSYIDTYFDTERSSYRSKGFDTVKY 149
Db 73 QGYVEMTVGSPQTLNITLVDTGSSNFAVGAAPFLHRYQRQLSSTYRDLRKGVVVPY 132
QY 150 TGGSWTGFVGEDLVTPKGFNTSFLVNIAITFESENFFLPGIKNGILGLAYATLAKPSS 209
Db 133 TQKMEGELGTDL-----PDD 148
QY 210 SLETFPDSLVTQANIPNVFSMOMGAGLPVAGS---GTNGSLVGGIEPSLYKGDWYT 266
Db 149 SLEPFDSLVKQTHVFNLFSLQCGAGFP LNQSEVLASVGSMTIGIDHSLYTGSLWYT 208
QY 267 PIKEWYQIEILKLEIGGOSLNDCREYNADKAIYDSGTTLLRLPQKVEDAVEAVARA 326
Db 209 PIRREWYEVIIIVREINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIIKA 268
QY 327 SLIPFSDGFWTGSQSLACWTNSETPWSYFPKISITLRDENSRSFRITILPQLYIQPMG 386
Db 269 SSTEKFPDGFMLGEOQLVCWQAGTTPWNIFFVISLYLMEVTVNOSFRITILPQQLRPVED 328
QY 387 AGLNLY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAETAGAAVSEIS 445
Db 329 VATSQDDCYKFAISQSSTGTVMGAVIMEGFYVIFDRARKRIGFAVSACHVHDEFRTAAVE 388
QY 446 GPSTEDVASNVCVPAQSLSEPIIIVSYALMSVCGAILLVLLLPFRQOR--RPRDP 503
Db 389 GPFVTLDMEDCGYNIPTDESTLMTIAYVMAAIC-ALFMLPLCLMVCQWRCLRCLRQOH 447
QY 504 EVVNDSSL 512
: : | | |

Db 448 DFADDISLL 456

RESULT 9
Q9BYB9 PRELIMINARY; PRT; 432 AA.
AC Q9BYB9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Beta-site APP cleaving enzyme I-432.
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=21408467; Pubmed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
RT production";
RL Neurosci. Lett. 307:9-12(2001).
DR EMBL; AB050438; BAB40933.1; -.
DR HSSP; P32329; 1YPS.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 432 AA; 48212 MW; 96FC81E6F0EED01B CRC64;

Query Match 34.4%; Score 925; DB 4; Length 432;
Best Local Similarity 38.5%; Pred. No. 5.2e-62;
Matches 200; Conservative 72; Mismatches 145; Indels 102; Gaps 10;

QY 7 ALLPLLAQWLLRAPELAPFT-----LPLRVAAATNRVVAPTPGTTPAERHADGLA 61
Db 2 AQALFWLLWM---GAGVLPAGHTQHGI RLPLRSLGLG-----GAPL-----GLR 42
QY 62 LALE--PALAPAGANFLAMVDNLQDSGRGYYLEMLIGTPQKQLIVDTGSSNFAVA 119
Db 43 LPRETDEEPEEPGRGSGFVEMVDNLRGKSGQGYVEMTVGSPQTLNITLVDTGSSNFAVG 102
QY 120 GTPHSYIDTYFDTERSSYRSKGFDTVKYTGSGWTFVGEDLVTPKGFNTSFLVNIAIT 179
Db 103 AAPHPFLHRYQRQLSSTRDLRKGVVVPYTGKMEGELGTDL----- 145
QY 180 IFESENFFLPGIKNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMOMGAGLPV 239
Db 146 -----LCGAGFPL 153
QY 240 AGS---GTNGSLVGGIEPSLYKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYN 296
Db 154 NQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREWYEVIIIVREINGQDLKMDCKEYN 213
QY 297 ADKAIYDSGTTLLRLPQKVEDAVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFP 356
Db 214 YDKSIYDSGTTNLRPLPKVFEAAVKSIIKAASSTEFDPGFWLGEQLVCWQAGTTPWNIFFP 273
QY 357 KISITLRDENSRSFRITILPQLYIQPMGAGLNLY-ECYRFGISPSTNALVIGATVMEGF 415
Db 274 VISLYLMEVTVNOSFRITILPQQLRPVEDVATSGDDCYKFAISQSSTGTVMGAVIMEGF 333
QY 416 YVIFDRAQKRVGFAASPCAETAGAAVSEISGPFSTEDVASNVCVPAQSLSEPIIIVSYAL 475
Db 334 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPTDESTLMTIAYVM 393
QY 476 MSVCGAILLVLLLPFRQOR--RPRDEVVNDSSL 512
Db 394 AAIC-ALFMLPLCLMVCQWRCLRCLRQOHDFADDISLL 431

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RESULT 10
O9CUTS
ID Q9CUT5 PRELIMINARY; PRT; 266 AA.
AC Q9CUT5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Beta-site App cleaving enzyme (Fragment).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyoko-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014390; BAB29317.1; -.
DR MEROPS; A01.004; -.
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; AspproteaseA1.
DR Pfam; PF00026; asp; 1.
FT NON_TER 1
SQ SEQUENCE 266 AA; 30201 MW; B9113FDA8ADAB4238 CRC64;

Query Match 24.2%; Score 651; DB 11; Length 266;
Best Local Similarity 45.5%; Pred. No. 1.6e-41;
Matches 121; Conservative 55; Mismatches 86; Indels 4; Gaps 3;

QY 250 VLGIEPSLYKGDIMWYPIKEEYQIILKLEIGGQSLNLDREYNADKAIVDSGTTLL 309
DB 1 IIGGIDHSLYTGLWYTPIRREWEYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 60

QY 310 RLPQKVFDAVEAVARASLIPEFSDGFMTGSQACWTNSETPWSYFPKISYLRDENSRR 369
DB 61 RLPKVFDAVAVKSIKAASSTKFPDGFMLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQ 120

QY 370 SFRITLIPOLYIQPMGAGLNY-ECYRFGISPTNALVIGATVMEGFYIFDRAQKRVGF 428
DB 121 SFRITLPQYLRPEVDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVFDRAKRIGF 180

QY 429 AASPCAELAGAAVSEISGFSTEDVASNCVPAQSLSEPILVISYALMSVCGAILLVLI 488
DB 181 AVSACHVHDERRTAAVEGPFVTADMEDCGNIPQTDSTLMTIAYVMAIC-ALFMLPLC 239

QY 489 LLLLPFRQR--RPRDPEVNDSSSL 512
DB 240 LNVQWQRLRCLRHQHDDFADDISLL 265

RESULT 11
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Q9P0D2
ID Q9P0D2 PRELIMINARY; PRT; 213 AA.
AC Q9P0D2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE HSPC104 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORD BLOOD;
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161367; AAF28927.1; -.
DR InterPro; IPR001461; AspproteaseA1.
DR Pfam; PF00026; asp; 1.
FT NON_TER 1
SQ SEQUENCE 213 AA; 24338 MW; EC9D3FA31CFA835C CRC64;

Query Match 17.2%; Score 461; DB 4; Length 213;
Best Local Similarity 51.5%; Pred. No. 3.2e-27;
Matches 84; Conservative 27; Mismatches 42; Indels 10; Gaps 1;

QY 252 GGIEPSLYKGDIMWYPIKEEYQIILKLEIGGQSLNLDREYNADKAIVDSGTTLLRL 311
DB 1 GGIDHSLYTGLWYTPIRREWEYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNRL 60

QY 312 POKYVDAVEAVARASLIPEFSDGFMTGSQACWTNSETPWSYFPKISYLRDENSRRSF 371
DB 61 PKKYVEAAVKSIIKAASSTKFPDGFMLGEQLVCWQAGTTPWNIFPVISLYLMGEVTQSF 120

QY 372 RITLIPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMEG 414
DB 121 RITLIPQYLRP-----WKWMPRPKTTVTVCCLTVIHG 153

RESULT 12
Q8WQY9
ID Q8WQY9 PRELIMINARY; PRT; 244 AA.
AC Q8WQY9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Aspartate protease (Fragment).
GN APP.
OS Aphrocallistes vastus.
OC Eukaryota; Metazoa; Porifera; Hexactinellida; Hexasterophora;
OC Lysacinosida; Rossellidae; Aphrocallistes.
OX NCBI_TaxID=83887;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller W.E.G., Mueller I.M., Grebenjuk V.A.;
RT "Urmatazoa: Origin and evolution of the common ancestor of Metazoa.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ304863; CAC83293.1; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00026; asp; 1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN 1.
KW Protease.
FT NON_TER 244
SQ SEQUENCE 244 AA; 26366 MW; 6536902661E0E4C7 CRC64;

Query Match 14.4%; Score 386; DB 5; Length 244;
Best Local Similarity 39.3%; Pred. No. 2e-21;
Matches 97; Conservative 33; Mismatches 95; Indels 22; Gaps 8;
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